



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 98953

TO: Phillip Gambel
Location: 8b03 / 9e12
Monday, July 21, 2003
Art Unit: 1644
Phone: 308-3997
Serial Number: 09 / 751797

From: Jan Delaval
Location: Biotech-Chem Library
CM1-1E07
Phone: 308-4498

jan.delaval@uspto.gov

Search Notes

09/751797

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
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jan.delaval@uspto.gov

48953

Delaval, Jan

From: Gambel, Phillip
Sent: Wednesday, July 16, 2003 10:25 AM
To: Delaval, Jan
Subject: 09 / 751,797 decloux brief

jan

please perform a sequence and a sequence interference search for

09 / 751,797 dumotier brief

note that two of the squences are genomic sequences

thanx

phillip gambel
art unit 1644
308-3997

1644 maiblox 9e12

- 1) SEQ ID NO: 7
- 2) SEQ ID NO: 8
- 3) SEQ ID NO: 24
- 4) SEQ ID NO: 25

Jan Delaval
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Biotechnology & Chemical Library
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Access DB# 98953

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ Examiner # _____ Date: _____
An Unit _____ Phone Number 30 _____ Serial Number _____
Mail Box and Bldg. Room Location _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

ADDITIONAL INFORMATION
800-000-0000 - 2000 FAX
AMERICAN CHEMICAL SOCIETY
LIBRARY INFORMATION
SERIALS SECTION

STAFF USE ONLY

Searcher Jan
Searcher Phone # 4496
Searcher Location _____
Date Searcher Requested 7/16/03
Date Completed 7/21/03
Searcher Prep & Review Time _____
Client Prep Time 20
Billing Time 15

Type of Search

NA Sequence (#) ✓
AA Sequence (#) _____
Structure (#) _____
Bibliographic _____
Litigation _____
Full-text _____
Patent Family _____
Other _____

Vendors and cost where applicable

STN _____
Dialog _____
Questel Orbit _____
Index _____
Webis Nexis _____
Sequence Systems ✓
WWW Internet _____
Other vendors _____

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:06:30 ; Search time 979.633 Seconds
(without alignments)
18499.535 Million cell updates/sec

Title: us-09-751-797-7

Perfect score: 1119
Sequence: 1 taacagcagctccctccac.....tgcatacataaaaaaaaa 1119

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_procl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	618	55.2	700	11	AK005228 Mus muscu
2	173	15.5	256	9	AV030414 AV030414
3	76.8	6.9	562	17	AZ449260 AZ449260
4	76	6.8	1101	17	CNS0056VL CNS0056VL
5	73.8	6.6	637	17	AL069706 Drosophi
6	71.2	6.4	1092	17	CNS036CC CNS036CC

Result No.	Score	Query Match	Length	ID	Description
7	71.2	6.4	1101	17	CNS0039G CNS0039G
8	71	6.3	1092	17	CNS020K7 CNS020K7
9	70.8	6.3	1043	17	CNS0145P CNS0145P
10	70.8	6.3	1101	17	CNS016L1 CNS016L1
11	70.2	6.3	1201	17	CNS016E1 CNS016E1
12	70	6.3	1101	17	CNS00E07 CNS00E07
13	69.4	6.2	1101	17	CNS00E0L CNS00E0L
14	69.2	6.2	1101	17	CNS00WYL CNS00WYL
15	69.2	6.2	1101	17	CNS017ZQ CNS017ZQ
16	68.8	6.1	987	17	CNS014PQ CNS014PQ
17	68.8	6.1	1101	17	CNS00EVL CNS00EVL
18	67.8	6.1	928	17	CNS00DKY CNS00DKY
19	67.8	6.1	1083	12	BF271806 BF271806
20	67.8	6.1	1225	17	CNS0161D CNS0161D
21	67.6	6.0	340	9	AL513755 AL513755
22	67.6	6.0	1203	17	CNS015WU CNS015WU
23	67.4	6.0	843	17	CNS00CS1 CNS00CS1
24	67	6.0	1101	17	CNS00FMC CNS00FMC
25	66.6	6.0	1101	17	CNS00BO1 CNS00BO1
26	66.2	5.9	945	17	CNS04DOK CNS04DOK
27	65.8	5.9	713	17	CNS06C1J CNS06C1J
28	65.6	5.9	1101	17	CNS001F8 CNS001F8
29	65.6	5.9	1190	17	CNS02ON7 CNS02ON7
30	65.6	5.9	1190	17	CNS02ON7 CNS02ON7
31	65.4	5.8	1101	17	CNS016L1 CNS016L1
32	64.4	5.8	836	17	CNS02WQ2 CNS02WQ2
33	64	5.7	1101	17	CNS00EOL CNS00EOL
34	63.8	5.7	1029	17	CNS01ZGM CNS01ZGM
35	63.8	5.7	1225	17	CNS0161D CNS0161D
36	63.6	5.7	958	17	CNS0074D CNS0074D
37	63.2	5.6	1101	17	CNS0039G CNS0039G
38	63.2	5.6	1101	17	CNS003BD CNS003BD
39	62.8	5.6	895	17	CNS06FSV CNS06FSV
40	62.8	5.6	1043	17	CNS0145P CNS0145P
41	62.6	5.6	804	17	A0895941 A0895941
42	62.6	5.6	1029	17	CNS01ZGM CNS01ZGM
43	62.2	5.6	732	17	A0325717 A0325717
44	62.2	5.6	981	17	CNS02BD8 CNS02BD8
45	62.2	5.6	1101	17	CNS00E07 CNS00E07

ALIGNMENTS

RESULT 1
LOCUS AK005228 700 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500012D04:interleukin 10-related T cell-derived inducible factor, full insert sequence.
ACCESSION AK005228
VERSION AK005228.1 GI:12837639
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:G57BL/6J) adult male cerebellum cDNA to mRNA, clone:1500012D04.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL MEDLINE
PUBMED

REFERENCE	TITLE	JOURNAL	PUBLISHED	AUTHORS
3	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Katsunari, T., Teshiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, K., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwaigi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsutani, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	RIKEN Integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)	20030913	
REFERENCE	TITLE	JOURNAL	PUBLISHED	AUTHORS
4	Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Komno, H., Adachi, U., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Komodo, S., Yamana, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Sato, R., Kadota, K., Maruyama, H., Aeburner, M., Batelov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuhen, P., Lewis, S., Matsuo, Y., Mikaloid, I., Pesole, G., Quackenbush, J., Schiraldi, L.M., Staudt, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsch, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bull, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, D., Hune, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, F., Mombeaerts, P., Nordone, P., Ring, B., Ritzwald, M., Rodriguez, I., Sakamoto, N., Sasai, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Konttsuki, S. and Hayashizaki, Y.	Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)	21085660	
REFERENCE	TITLE	JOURNAL	PUBLISHED	AUTHORS
5	(bases 1 to 700) Adachi, U., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bull, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hirooka, T., Horii, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kaida, S., Kato, H., Kawai, J., Kojima, Y., Komno, H., Kouda, M., Koysa, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schiraldi, L., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Teijima, Y., Toya, T., Yamamura, T., Yamana, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.	Direct Submission Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Riken Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopaedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAAGGAAGATCCAGAGCTTTTCTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequences' 5'-GGAGGAGAGGGCGCAGTAATTTCGACTTAATTAATTAATCCCCCCC 3'. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3'			

Db		697 CA 698	
RESULT 2			
LOCUS AV030414		256 bp mRNA linear EST 31-AUG-1999	
DEFINITION AV030414 Mus musculus adult C57BL/6J cerebellum Mus musculus cDNA clone 1500012D04, mRNA sequence.			
ACCESSION AV030414			
VERSION AV030414.1		GI:4823962	
KEYWORDS EST.			
SOURCE house mouse.			
ORGANISM Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
REFERENCE 1 (bases 1 to 256)			
AUTHORS Carninci,F., Shibata,K., Ozawa,Y., Kono,H., Itoh,M., Aizawa,K., Akhira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Horii,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,U., Kluchl,N., Kojima,Y., Matsuyama,T., Nitsuma,H., Oda,H., Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tomioka,N., Muramatsu,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.			
TITLE RIKEN Mouse ESTs			
JOURNAL Unpublished (1999)			
COMMENT Contact: Chile Owa			
Genome Science Laboratory			
RIKEN 3-1-1 Koyada, Tsukuba, Ibaraki 305-0074, Japan			
Tel: 81-298-36-9145			
Fax: 81-298-36-9098			
Email: genome-res@rc.riken.go.jp			
The most stableization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))			
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))			
Please visit our web site (http://genome.rtc.riken.go.jp/) for further details.			
FEATURES			
Source			
Location/Qualifiers			
1..256			
/organism="Mus musculus"			
/strain="C57BL/6J"			
/db_xref="taxon:10090"			
/clone_1id="1500012D04"			
/clone_1lb="Mus musculus adult C57BL/6J cerebellum"			
/sex="male"			
/tissue_type="cerebellum"			
/dev_stage="adult"			
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (ctr) primer 15'			
TGTTACCAATCTGAAGTCGGAGCGCCGGAATGTTTTTTTTTTTTTTTTTTTTTTT			
T 3 J ; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. library constructed and normalized by Bento Soares and M.Felina Bonaldi."			
Bonaldi."			
BASE COUNT 88 a 29 c 41 g 98 t			
ORIGIN			
Query Match 15.5%; Score 173; DB 9; Length 256;			
Best Local Similarity 90.3%; Pzed. No. 5.7e-25;			
Matches 196; Conservative 0; Mismatches 20; Indels 1; Gaps 1;			
992 TAGAAAAAAGCTTGTAATTCTTCATATCATCAATATTTATATGTAAAGTTAT 951			
40 TGGAGAGATAGCTATGCTATCTCTTCCTTCACATACGCATCTTTATATATGAGATTAT 99			

QY	952	TTATTTAAAGTAAACATTTTATTTATGTCAGTTATTTATTAATGAGTTATTTATTAAGAAAC	1011
Db	100	TTATTTAAAGTAAACATTTTATTTATGTCAGTTATTTATTAATGAGTTATTTATTAAGAAAC	159
QY	1012	ATTATCTGCATATGATATTT-AGTATTAAGGCAATAATATTTATGACAAATACTATGAA	1070
Db	160	ATTATCTGCATATGATATTTAGTATTAAGGCAATAATATTTATGATTAATACTATGAA	219
QY	1071	ACAAGATATCTTAGGCTTTATTAATTAACATGATATC	1107
Db	220	ACAAGATATCTTAGGCTTTATTAATTAACATGATATC	256
RESULT 3			
LOCUS	AZ449260	562 bp DNA linear	GSS 04-OCT-2000
DEFINITION	1M0247J21F Mouse 10kb plasmid UGCGIM library	musculus genomic	
ACCESSION	AZ449260		
VERSION	AZ449260.1	GI:10602872	
KEYWORDS	GSS.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 562) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weis University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0247 row: 5 column: 21 Seq primer: CGTGTAAACGACGCGCACT Class: plasmid ends High quality sequence stop: 562. Location/Qualifiers 1. 562 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UGCGIM0247J21" /clone_1kb="Mouse 10kb plasmid UGCGIM library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI1473114[gb AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells		

BASE COUNT 119 a 155 c 116 g 172 t
ORIGIN

Query Match 6.8%; Score 76.8; DB 17; Length 562;
Best Local Similarity 96.7%; Pred. No. 1.4e-05;
Matches 89; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 304 GCTAAAGATGCTGCTGCTGATGAGAGAGTGTCTCACTGACCTGGAGAGCGTTCTG 363
DB 472 GTTAGAGATGCTGCTGCTGATGAGAGAGTGTCTCACTGACCTGGAGAGCGTTCTG 530
QY 364 CTCCCGCAGTCAGACAGTTCAGCCCTACAT 395
DB 531 CTCCCGCAGTCAGACAGTTCAGCCCTACAT 562

RESULT 4
CNS006VL 1101 bp DNA linear GSS 04-JUN-1999
LOCUS
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL069706.1 GI:4949849
VERSION
KEYWORDS
SOURCE
ORGANISM Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuo Osoegawa and
Aaron Mamonos in Peter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCT-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source

1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR29B23"
/clone_id="RPCT-98"
/note="end : T7"

BASE COUNT 419 a 91 c 60 g 299 t 232 others
ORIGIN

Query Match 6.8%; Score 76; DB 17; Length 1101;
Best Local Similarity 36.0%; Pred. No. 1.8e-05;
Matches 180; Conservative 93; Mismatches 220; Indels 7; Gaps 2;

QY 620 GCTCTTCTGCTCTTAAAGAAACAATAGATCCCTGATGAGCTTTTACTAAAG 679
DB 472 GCTCTTCTGCTCTTAAAGAAACAATAGATCCCTGATGAGCTTTTACTAAAG 679
QY 660 AAGAGAGAGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 739
DB 500 AAGAGAGAGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 559

QY 740 AAAAAAGAAATAGTGTCAAGTGTGCTGAGACCGAGGATGATGATTAACCAAGA 799
DB 560 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 617
QY 800 TTCAATGACATATTTATTTATGTCACGTATGATGATGATGATGATGATGATGAT 859
DB 618 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 677
QY 860 ATTGTTGAAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 919
DB 678 TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 737
QY 920 CCAATGCTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 979
DB 738 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 792
QY 980 CAGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1039
DB 793 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 852
QY 1040 GCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1099
DB 853 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 912
QY 1100 TGATATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1119
DB 913 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 932

RESULT 5
CNS036CC/ 637 bp DNA linear GSS 15-MAY-2000
LOCUS
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Orl end of clone
215L21 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL229845.1 GI:7888840
VERSION
KEYWORDS
SOURCE
ORGANISM Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/tetraodon>.

FEATURES
source
1..637
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="215L21"
/clone_id="G"

/nc="Genoscope sequence ID : COAG215CF131SP1-end :
PUC-ori"
BASE COUNT 180 a 95 c 80 g 224 t 58 others
Query Match 5.6%; Score 73.8; DB 17; Length 637;
Best Local Similarity 43.2%; Pred. No. 5.6e-05;
Matches 144; Conservative 36; Mismatches 153; Indels 0; Gaps 0;
QY 787 ATAAACCAAGATTCATTGCAATATTTTATGTGCACTGATGATACAGCAAGAAATAA 846
Db 629 AAAAAAAAAAAAAAAAAAAAAAAAAATTTTTTTTTTTTTTAAAAAATAAAAAAWAW 570
QY 847 TGTACTTAAAAAATGTTGAAAGGAGGTACTCTCATTCCTTTGAAAAAAGCTTA 906
Db 569 WAAAAAAAAAAAAAAAAATTTTWWAAAAAAATTTATATTTTTTTTTWWAAAAAAA 510
QY 907 TGTACTTCATTTCCATATCCAAATATTTTATATGTAAGTTTATATTATTAAGTATAC 966
Db 509 WTTTTTTTTTAAAAAAAAAAAAATTTTTTWWAAWTTTTTTTWWTTTTTTTTTTTWWAA 450
QY 967 ATTTATTTATGTGCACTTATTTAATATGATTTATTTATAGAAAATATATCTGCTATTGA 1026
Db 449 AAATTTTTTTTTTTTTTTTTTATWWAAAAAAATWGGGGAATTTTTTTTTTTTTTTTT 390
QY 1027 TATTAGTATPAGCAATAATATTATTGACAAATPACTATGGAACAATATTTTGGC 1086
Db 389 TTTTWWAAAAAAATWWAAAAAAATTTTTTTVAAAAAATTTTWWGWWTTWT 330
QY 1087 TTTAATTAACATGATATCATATAAAAAAAA 1119
Db 329 TTWAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 297
RESULT 6
CNS020K/c
LOCUS
DEFINITION
Tetradon nigroviridis genome survey sequence T7 end of clone
22L11 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION
AL175696
VERSION
AL175696.1
KEYWORDS
GSS, genome survey, sequence.
SOURCE
Tetradon nigroviridis.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE
1 (bases 1 to 1092)
Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence
Unpublished
2 (bases 1 to 1092)
Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
Unpublished
3 (bases 1 to 1092)
Genoscope.
Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large
scale clone and sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.
FEATURES
location/Qualifiers
1..1092

/organism="Heterodon nigriviridis"
 /db_xref="taxon:99883"
 /clone="222L11"
 /clone_id="G"
 /note="Genoscope sequence ID : COAG222CF061P1-end : 17"
 BASE COUNT 383 a 169 c 165 g 262 t 113 others
 ORIGIN
 Query Match 6.4%; Score 71.2; DB 17; Length 1092;
 Best Local Similarity 37.7%; Pred. No. 0.00017;
 Matches 121; Conservative 58; Mismatches 142; Indels 0; Gaps 0;
 QY 799 ATTCATGACAAATTTTATTTGTCACGATGATCAACAGAAAATAATGACTTTAAA 858
 Db 967 WTTTATATTTTTTTTTTTTTTTTWTAAAAAAAAMAAAAAAMTTTAAAMWTAA 908
 QY 859 AATGTTGAAGAGGTTACCTCTCATCTCTTAGAAAAAAGCTATGTACTTCAT 918
 Db 907 AAAAAAAMWTMTTTTTTTTAAATTTTTTTTTTTTAAATTTAAATTTTAA 848
 QY 919 TCATATCCAAATTTTATATATGTAAGTTATTTATTAAGTATCAATTTATG 978
 Db 847 MAATATTTTWTMTTTTTTAAATAAATMTTTTTTTTAAATTAATAAAMWTATWTAA 788
 QY 979 TCAGTTATTAATATGATTTATTTATAGAAACATATTCGCTATGATATTGATAA 1033
 Db 787 AATTAAMAMWTMTTTTTTTTAAAAAAAAMAAATMTTWTMTTTTTTTTAA 728
 QY 1039 GGCAAAATTAATTTATGACATATACTATGAAACAATATCTAGGCTTAATAACAC 1098
 Db 727 TTAATTTTTTTTTTTTTTTTTTAAAAAAMAAAAAAMTTTTTTTAAAMWTAA 668
 QY 1099 ATGATATCATAAAAAAA 1119
 Db 667 WMTTWTTTTTTTTAAAAAAA 647
 RESULT 7
 CNS0039G/c
 LOCUS
 DEFINITION
 Drosophila melanogaster genome survey sequence Tenz end of BAC # 939
 BACR08K10 of RPc1-98 library from Drosophila melanogaster (fruit
 fly); genomic survey sequence.
 AL063921
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Drosophila melanogaster.
 Drosophila melanogaster.
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mosmoser in Pictet de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPc1-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 Escherichia coli strain Y2, cn bw sp, the same strain used for the BDGP's
 P1 and BGT libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 Location/Qualifiers

project grant. The DNA was prepared from embryos by Alain Bucheton

and Genevieve Payan. It has been constructed in the vector pBelBAC11.

FEATURES
source

1. 1201
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN15C13"
/clone_id="DrosBAC"
/plasmid="pBelBAC11"
/note="end : SP6"

BASE COUNT 448 a 136 c 161 g 336 t 120 others
ORIGIN

Query Match 6.3%; Score 70.2; DB 17; Length 1201;
Best Local Similarity 40.0%; Pred. No. 0.00027;
Matches 152; Conservative 53; Mismatches 174; Indels 1; Gaps 1;

QY 740 AAAAGAGAAATGTCAGTTCATGACGACGAGGTAAGTATACCAAGAGA 799
DB 708 ATNAAAGAAATATGTGTWYTHYBYYYRRGRRRAAAARARAAAGRW 767
QY 800 TTCAATGCAATATTTATGCTGCTGATGACACAGAAATTAATGCTTAAAAA 859
DB 768 KTGSTTAATATCTTAAAMAAATATTTTATTTAAATTTTGGGAT 827
QY 860 ATTGTTGAAAGAGGTACCTCATCTCTTAAAGAAAGCTTAATGTAATTT 919
DB 828 AAAAATWMAAAAGGA-AMATTTTWTWMAAAATTAATTTT 886
QY 920 CCAATCCATATTTTATATGTAAGTTTATTTATTAAGTATACATTTATTT 979
DB 887 ANAAAAATWMAATATTTTAAANAAATGKTWMAAAAMWTTTATTTT 946
QY 980 CAGTTTATATGATTTTATGTAAGAAACATTTCTGCTGATTTAGTATTAAG 1039
DB 947 WMAAAATTTTATTTATTTATGTAAGAAATTTTATTAATTTTAAATTA 1006
QY 1040 GCAATATATTTATGCAATATGTAAGAAAGATATCTTAAATTAAGACA 1099
DB 1007 AAAAAAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 1066
QY 1100 TGGATATCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1119
DB 1067 AATTTWAKTAAAAA 1086

RESULT 12

CNS00E07/c

LOCUS 1101 bp DNA linear GSS 04-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR29P01 of RPEC-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION AL069440
VERSION AL069440.1 GI:4949583

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

COMMENT

Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Oseegawa and
Aaron Mammoxer in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPEC-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source

1. 1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR29P01"
/clone_id="RPEC-98"
/note="end : TET3"

BASE COUNT 366 a 66 c 104 g 351 t 214 others
ORIGIN

Query Match 6.3%; Score 70; DB 17; Length 1101;
Best Local Similarity 38.3%; Pred. No. 0.0003;
Matches 173; Conservative 68; Mismatches 200; Indels 4; Gaps 2;

QY 648 TAAGATCCGATGAGCTTTTCTAAGAGAAAGTGAAGTACGTCATCATCAT 707
DB 964 TMTATATCATTAATTTTATATGCAATTTAAATTAATTAATTAATTA 905
QY 708 TAGAAGATTCACATGAACTGCTGCTGAGAAAGAAATAGTCAAGTTCAT 767
DB 904 WCATTTTATTAATTAATTTTATTAATTAATTAATTAATTAATTAATTA 845
QY 768 GAGACGAGAGTGAAGTGAATTAACCAAGATTCATGCAATTTTATGCTG 827
DB 844 AATWATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 785
QY 828 TGAATACAGCAAAATTAATGCTTAAATTAATTTGTAAGAGGATTCAT 887
DB 784 TTTTAAATTAATTAATTAATTAATTTTAAATTAATTAATTAATTTAT 725
QY 888 CTTTAAAGAAAGGCTTATGATCAATTTCCATATCCATATTTATATATG 947
DB 724 T-WTATTAATTAATTTTATTAATTTTAAATTTTAAATTAATTAATTA 666
QY 948 TTAATTAATTAATTAATTAATTTATGATGATTTATTAATTAATTA 1007
DB 665 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTTC 609
QY 1008 AATCATTAATGCTATGATTTATTAATTAATTAATTAATTAATTAAT 1067
DB 608 WTTAAATTAATTAATTAATTAATTAATTTTATTAATTAATTAATTA 549
QY 1068 GAAACAGATATCTTAGGCTTAAT 1092
DB 548 TATTAATTAATTTATTAATTTGAT 524

RESULT 13

CNS00E0L

LOCUS 1101 bp DNA linear GSS 04-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29M12 of RPEC-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION AL069526
VERSION AL069526.1 GI:4949669

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

COMMENT

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammeter in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers

1..1101

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="BACR29M12"

/clone_1ib="RPCI-98"

/note="Tend : T7"

BASE COUNT 249 a 72 c 234 g 360 t 186 others

ORIGIN

Query Match 6.2%; Score 69.4; DB 17; Length 1101;
Best Local Similarity 41.1%; Pred. No. 0.00039;
Matches 127; Conservative 42; Mismatches 140; Indels 0; Gaps 0;

811 TATTTATGTCTGATGATACACAGAAAAATATGACTTTAAAAATGTTGAA 870

734 TTTTATTTTAAWAAAAATTTAAAAAAATTTTAAWAAWAAWAAWAAWAAWAA 793

871 GGAGTACCTCTATCTCTTAAAGAAAAAGCTTATGTAATCTTCAATTCAT 930

794 TAAATTTAAATTTTAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAA 853

931 ATTATATATATGTAAGTTATTTATTAAGTATATATTTATTTATTTATTTAT 990

854 AAATTTTATATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 913

991 TATGATTTATTTATAGAAACATATCTGCTATTGATATTTAGTAAGGCAAT 1050

914 WTAATATATTTTAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 973

1051 TTATGACATATACATGAAACAGATATCTTAGGCTTTATTAACATGATATCT 1110

974 ATTATATATATTTTAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAA 1033

1111 AAAAAAAA 1119

1034 AATWTAAMW 1042

RESULT 14

CNS00YWL 1101 bp DNA linear GSS 26-JUL-1999

LOCUS Drosophila melanogaster genome survey sequence Sp6 end of BAC

DEFINITION BACN01G13 of DrosBAC library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

ACCESSION AL096927.1 GI:5608538

VERSION AL096927.1 GI:5608538

KEYWORDS GSS.

SOURCE Drosophila melanogaster.

ORGANISM Drosophila melanogaster.

REFERENCE Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,

Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,

Ephydroidea, Drosophilidae, Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.

FEATURES

Location/Qualifiers

1..1101

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="BACN01G13"

/clone_1ib="DrosBAC"

/plasmid="pBelOBAC11"

/note="end : Sp6"

BASE COUNT 424 a 119 c 129 g 248 t 181 others

ORIGIN

Query Match 6.2%; Score 69.2; DB 17; Length 1101;
Best Local Similarity 36.5%; Pred. No. 0.00043;
Matches 119; Conservative 69; Mismatches 137; Indels 1; Gaps 1;

795 AAGATTCATTCGACATATTTTATGTCTGATGATACACAGAAAAATATGACTTT 854

1101 AAATATATATATATATATATTTTAAWAAWAAWAAWAAWAAWAAWAAWAAW 1042

855 AAAAAATTTGTAAGAGAGCTTACCTCTATTCCTTTAGAAAAAGCTTATGTA 914

1041 TATTAATATATATTTTAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 982

915 CATTCGATTCGACATATTTTATATATGTAAGTTATTTATTAAGTATATTTAT 974

981 TATATATATATATATATTTTAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 922

975 TATGATTTATTTATAGAAACATATCTGCTATTGATATTTAGTAAGGCAAT 1033

921 WTTAATATTTTAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 862

1034 TATAGCAAAATATATTTATGACATATCTTAGGCTTTATTAACATGATATCT 1093

861 TTWTTTATATATATTTTAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 802

1094 AACCATGATATCTATTAACAAAAA 1119

801 AAACAAATCABATWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 776

RESULT 15

CNS017ZQ 1101 bp DNA linear GSS 26-JUL-1999

LOCUS Drosophila melanogaster genome survey sequence Sp6 end of BAC

DEFINITION BACN37P08 of DrosBAC library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

ACCESSION AL108704 GI:562808

VERSION AL108704 GI:562808

KEYWORDS GSS.

SOURCE Drosophila melanogaster.

ORGANISM Drosophila melanogaster.

REFERENCE Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,

Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,

Ephydroidea, Drosophilidae, Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -

<http://www.edgp.ebi.ac.uk> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

FEATURES
Location/Qualifiers

source 1..1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN37P08"
/clone_11b="DrosBAC"
/plasmid="pBelobAC11"
/note="end : SP6"

BASE COUNT 291 a 108 c 105 g 365 t 232 others

ORIGIN

Query Match 6.2%; Score 69.2; DB 17; Length 1101;
Best Local Similarity 32.4%; Pred. No. 0.0043;
Matches 106; Conservative 82; Mismatches 139; Indels 0; Gaps 0;

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OY 792 CACAAAGATTCATGACATATTTATGTGACCTGATGATGACAGAAAAATATGTAC 851
Db 720 CATMAHKYNNKKGITGTHGKGWGYGGKTHHBSGKGGTAAGKAMGTCGDARWCCG 779
OY 852 TTAAAAAATTGTTGAAGAGGTTACCTCATTCCTTAGAAAAAGCTTATGTAA 911
Db 780 KTCMASWAMCAVCKRBAABAAAMAMWMTKHYCTTTMATYVMTGRTMAAPAA 839
OY 912 CTTCAATTCATCCAAATATTTATATATGTAAGTTATTTATATAGTATACATTT 971
Db 840 MKRMDNKKAKATVATAMWAMATATTTATAMWATWATWMTKYTYTTBTATW 899
OY 972 ATTTATGTCAGTTATTAATATGATTTATTTATAGAAACATATCTGCTATGATTT 1031
Db 900 WTAATATATTAATATATATATATATATATATATATATATATATATATATAT 959
OY 1032 AGTATTAAGCAAAATATATTTATGACATTAAGTAAACAGATATCTTAGCTTAA 1091
Db 960 ATAMATATYMTAAAMATATATATATATATATATATATATATATATATATAT 1019
OY 1092 TAAACACATGATATCAAAAAAAA 1118
Db 1020 WTATWATATWTTATATATATATATATA 1046
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Search completed: July 19, 2003, 19:39:03
Job time : 982.883 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: July 19, 2003, 09:02:25 ; Search time 153.463 Seconds
(without alignments)
16420.772 Million cell updates/sec

Title: US-09-751-797-7

Perfect score: 1119

Sequence: 1 taacacagctctctctcacc.....tggatcatcctcaaaaaaaaa 1119

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

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4: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

7: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*

8: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*

9: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

10: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

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12: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*

13: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

14: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

15: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*

16: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*

17: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*

18: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*

19: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*

20: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

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22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

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24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1119	100.0	1119	21	Mouse T cell indu
2	1119	100.0	1119	22	Mouse CDNA encodin
3	1119	100.0	1119	24	Mouse TIF alpha CD
4	1119	100.0	1119	24	Mouse T cell deriv
5	1107.8	99.0	1166	21	Mouse GIL-19 prot
6	1047.8	93.6	1111	21	Mouse T cell indu
7	1047.8	93.6	1111	22	Mouse CDNA for T c
8	1047.8	93.6	1111	24	Mouse TIF beta CDN
9	1047.8	93.6	1111	24	Mouse T cell deriv

10	768.4	68.7	778	22	AAD09746	Mouse ZCYTO18 CDNA
11	601.4	53.7	7444	21	AAA28815	Murine T cell indu
12	601.4	53.7	7445	22	AA514859	Mouse partial geno
13	601.4	53.7	7445	24	AAD30628	Mouse TIF alpha ge
14	601.4	53.7	7445	24	AAD27134	Mouse T cell deriv
15	555.2	49.6	5935	21	AAA28818	Murine T cell indu
16	555.2	49.6	5935	22	AA514878	Mouse partial geno
17	555.2	49.6	5935	24	AAD30660	Mouse TIF beta gen
18	555.2	49.6	5935	24	AAD27153	Mouse T cell deriv
19	535.2	47.8	1177	21	AA081773	Human PRO10096 CDN
20	524.8	46.9	1152	22	AA092134	Nucleotide sequenc
21	524.8	46.9	1152	22	AA087053	Human angiogenesis
22	524.8	46.9	1152	24	AB195737	CDNA encoding huma
23	524.8	46.9	1152	24	AB11847	Human PRO10096 CDN
24	524.8	46.9	1152	24	AB188248	CDNA encoding huma
25	524.8	46.9	1152	24	ABX3657	Human cytokine, ZC
26	524.4	46.9	1116	22	AAD09719	Human IL-TIF polyp
27	524.4	46.9	1116	22	AA083741	Human CDNA encodin
28	524.4	46.9	1116	24	ABX10503	Human EXCS encodin
29	521.8	46.6	1132	22	AA084310	Human interleukin-
30	520	46.5	1139	22	AA028841	Mouse secreted exp
31	448.2	40.1	504	21	AAA43454	Human T cell indu
32	409.2	36.6	690	21	AAA28839	Human TIF DNA frag
33	409.2	36.6	690	22	AA514875	Human CDNA encodin
34	409.2	36.6	690	24	AAD30645	Human TIF CDNA
35	409.2	36.6	690	24	AAD27150	Human T cell deriv
36	306	27.3	537	22	AA028842	Human interleukin-
37	288.4	25.8	501	22	AAD09720	Degenerate sequenc
38	223.6	20.0	418	24	AAD30638	Human T cell indu
39	126	11.3	4796	21	AAA28840	Human T cell indu
40	126	11.3	4797	22	AA514876	Human partial geno
41	126	11.3	4797	24	AAD30646	Human TIF genomic
42	126	11.3	4797	24	AAD27151	Human T cell deriv
43	63	5.6	65	24	ABN54694	Mouse spliced tran
44	60.8	5.4	7047	24	ABX28386	DNA transcription
45	60.6	5.4	12025	24	ABX3298	Human immune syste

ALIGNMENTS

RESULT 1	AAA28815	standard; CDNA; 1119 BP.
ID	AAA28815	
AC	AAA28815;	
XX		
DT	04-SEP-2000	(first entry)
XX		
DE	Murine T cell inducible factor alpha CDNA.	
XX		
KW	TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;	
XX	Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist; ss.	
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	52..591
FT		/*tag= a
XX		
XX	WO200024758-A1.	
XX		
PD	04-MAY-2000.	
XX		
PF	18-OCT-1999;	99WO-US24424.
XX		
XX	26-OCT-1998;	98US-0178973.
PR	16-JUL-1999;	99US-0354243.
XX		
PA	(LUDWIG-) LUDWIG INST CANCER RES.	
XX		
XX	Dumontier L, Louhed J, Renaud J,	
XX		

PS Example 6; Page 49; 64pp; English.

CC The invention relates to nucleic acid molecules encoding T cell
CC derived inducible factors (TIFs) also known as interleukin-21 (IL-21)
CC TIF polynucleotides are upregulated by the cytokine, IL-9, IL-TIF or
CC IL-21 molecules are implicated in activation of STAT transcription
CC factors, acute phase proteins and inflammation. The present sequence
CC is mouse TIF alpha cDNA.

50 Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;

Query Match	100.0%	Score 1119; DB 24;	Length 1119;
Best Local Similarity	100.0%	Pred. No. 2, 1e-230;	
Matches 1119; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0

OY	1	TTAAACAGGCTCCCTCTCACTTATCAACGTGTGACACTGTGTCATCTGTATGCTGTGC	60
Db	1	TAAACAGGCTCCTCTCACTTATCAACGTGTGACACTGTGTCATCTGTATGCTGTGC	60
OY	61	CTGCAGAAATCTATGAGTTTTCCCTTATGGGGACTTGGCCGACGCTGCTCTTC	120
Db	61	CTGCAGAAATCTATGAGTTTTCCCTTATGGGGACTTGGCCGACGCTGCTCTTC	120
OY	121	ATTGCGCTGTGGGCCAGAGGCAATGGCTGCCCCCTCAACACCCGGTGCAGCTTGAG	180
Db	121	ATTGCGCTGTGGGCCAGAGGCAATGGCTGCCCCCTCAACACCCGGTGCAGCTTGAG	180
OY	181	GTGTCCAACTTCAGAGCCGTACATCGTCAACCGACCTTATGCTGGCCAAAGAGGCC	240
Db	181	GTGTCCAACTTCAGAGCCGTACATCGTCAACCGACCTTATGCTGGCCAAAGAGGCC	240
OY	241	AGCCTTGAGATPACACACAGACGTCGGGCTCATTCGGGGAGAACTGTTCCGAGAGTC	300
Db	241	AGCCTTGAGATPACACACAGACGTCGGGCTCATTCGGGGAGAACTGTTCCGAGAGTC	300
OY	301	AGTGTAAAGATCAGTGTCTACTGTATGAAGCAGGTGCTCACTTCACTTGGAAACGTT	360
Db	301	AGTGTAAAGATCAGTGTCTACTGTATGAAGCAGGTGCTCACTTCACTTGGAAACGTT	360
OY	361	CTGCTCCCCAGTCAGACAGGTGTCACGCCCTTACATGACAGAGAGTGTACTTCTGCACC	420
Db	361	CTGCTCCCCAGTCAGACAGGTGTCACGCCCTTACATGACAGAGAGTGTACTTCTGCACC	420
OY	421	AAACTCAGCAATCAGTCACTCTGTCACATCAGCGGTGACGACCCAGAACATCCAGAA	480
Db	421	AAACTCAGCAATCAGTCACTCTGTCACATCAGCGGTGACGACCCAGAACATCCAGAA	480
OY	481	AATGTCAGAAAGCTGAAGGAGACAGTGAATAAGCTTGGAGAGATGAGAGATCAAGGCG	540
Db	481	AATGTCAGAAAGCTGAAGGAGACAGTGAATAAGCTTGGAGAGATGAGAGATCAAGGCG	540
OY	541	ATTGGGGAACTGGACCTGCTGTTTATGTCCTGAGAAATGCTTGGGCTGACGAGAAAG	600
Db	541	ATTGGGGAACTGGACCTGCTGTTTATGTCCTGAGAAATGCTTGGGCTGACGAGAAAG	600
OY	601	AGCTAGAAAACGAGAACTGCTCTTCTCTGCTTCTTAAAGAACATTAAGATCCCTGAA	660
Db	601	AGCTAGAAAACGAGAACTGCTCTTCTCTGCTTCTTAAAGAACATTAAGATCCCTGAA	660
OY	661	TGGACTTTTTTACTTAAAGGAAAGTGAGAGCTTACATCATCTTGAAGATTTCAC	720
Db	661	TGGACTTTTTTACTTAAAGGAAAGTGAGAGCTTACATCATCTTGAAGATTTCAC	720
OY	721	ATGAAAACCTGGCTCAGTTGAAAAGAAAATAGTGTCAAGTTGTCATGAGACCAAGGTA	780
Db	721	ATGAAAACCTGGCTCAGTTGAAAAGAAAATAGTGTCAAGTTGTCATGAGACCAAGGTA	780
OY	781	GACTTGATACCAAGAAATTCATTCACAATATTTATGTCACTGATGATCAACAGAA	840
Db	781	GACTTGATACCAAGAAATTCATTCACAATATTTATGTCACTGATGATCAACAGAA	840
OY	841	AAATATGATCTTAAAAAATTTGTTGAAAGAGGTACTCTCATTTCTTTTGAATAAA	900
Db	841	AAATATGATCTTAAAAAATTTGTTGAAAGAGGTACTCTCATTTCTTTTGAATAAA	900

Db	841	AAATAATGACTTTAAAAAAATGTTGTAAGAGGTTACCTCCTCATTCCTTTAGAAAAA	900
Qy	901	AGCTTATGMACTTCATTTCCCAATCCAAATTTTATATATGTAAGTTTATTTATATA	960
Db	901	AGCTTATGTAACCTTCATTCCTATCCCAATTTTATATATGTAAGTTTATTTATATA	960
Qy	961	GTATACATTTATTTATGTCAAGTTTATTAATATGATTTTATTTAGAAACATTATCGC	1020
Db	961	GTATACATTTTATTTATGTCAAGTTTATTTAATATGATTTTATTTAGAAACATTATCGC	1020
Qy	1021	TATTGATATTTAGTATAAGGCAAAATAATTTTATGACACATACATGGAACAAGATATC	1080
Db	1021	TATTGATATTTAGTATAAGGCAAAATAATTTTATGACACATACATGGAACAAGATATC	1080
Qy	1081	TTAGGCTTAAATAAACCATGATATCATTAATAAAAAA	1119
Db	1081	TTAGGCTTAAATAAACCATGATATCATTAATAAAAAA	1119

ID	AA027133	standard; DNA; 1119 BP.
XX	AA027133;	
AC	09-APR-2002	(first entry)
DT	Mouse T cell derived inducible factor (TIF) alpha cDNA.	
XX	T cell derived inducible factor; TIF, cytokine; interleukin-9; IL-9;	
KM	protein therapy; STAT activation; differentiation; mouse; ss.	
XX	Mus musculus.	
OS		
XX		
FH	Key	Location/Qualifiers
FT	CDS	52..591
FT		/*tag= a
FT		/product= "Mouse TIF alpha"
XX		
PM	US6331613-B1.	
PD	18-DEC-2001.	
XX		
PF	18-OCT-1999;	99US-0419568.
XX		
PR	26-OCT-1998;	98US-0178973.
PR	16-JUL-1999;	99US-0354243.
XX		
PA	(LUDM-) LUDWIG INST CANCER RES.	
PI	Dumoutier L, Louhed J, Renaud J;	
XX		
DR	WPI; 2002-105277/14.	
DR	P-PSDB; AAE16553.	
XX		
PT	Nucleic acids encoding T cell derived inducible factors useful for	
XX	inducing STAT activation in cells -	
PS	Claim 1; Column 17-20; 24pp; English.	
XX		
CC	The present invention relates to an isolated nucleic acid molecule, which	
CC	encodes a T cell derived inducible factor comprising an amino acid	
CC	sequence encoded by 6 defined nucleotide sequences. The nucleic acid	
CC	molecules are shown to be up regulated by the cytokine interleukin-9	
CC	(IL-9) and are described as T Cell Derived Inducible Factors (TIFs). The	
CC	invention is used in protein therapy. The nucleic acid molecules encode	
CC	proteins which induce STAT activation in cells. They can be used, for	
CC	example, in the stimulation of regeneration of targeted tissues.	
CC	Further, their inhibitors or antagonists can be used to retard, prevent	
CC	or inhibit differentiation of other tissues. The present sequence is	
XX	mouse TIF alpha cDNA.	
XX		
SQ	Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;	

Query Match 100.0%; Score 1119; DB 24; Length 1119;
 Best Local Similarity 100.0%; Pred. No. 2.1e-230;
 Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 TAAACAGGCTCTCTCTCACTTATCAAGCTTGTGACACTTGTGCGATCTGTAGAGGCTGTC 60
DB 1 TAAACAGGCTCTCTCTCTCACTTATCAAGCTTGTGACACTTGTGCGATCTGTAGAGGCTGTC 60
QY 61 CTGACAGAAATCTATGAGTTTTCCTTATGAGGACTTTGGCCGCCAGCTGCTGCTTC 120
DB 61 CTGACAGAAATCTATGAGTTTTCCTTATGAGGACTTTGGCCGCCAGCTGCTGCTTC 120
QY 121 ATTGCTCTGTGGGCCCAAGAGGCAAAATGGCTGCTCCGTCACACCCGGTGCAGCTTGAG 180
DB 121 ATTGCTCTGTGGGCCCAAGAGGCAAAATGGCTGCTCCGTCACACCCGGTGCAGCTTGAG 180
QY 181 GTGTCCAACTTCCAGAGCCGTATCATCGTCAACCGGACCTTTATGTGGCCCAAGAGGCC 240
DB 181 GTGTCCAACTTCCAGAGCCGTATCATCGTCAACCGGACCTTTATGTGGCCCAAGAGGCC 240
QY 241 AGCCTTGCAGATTAACAACAAGAGCTCCGGCTCATCGGAGAGAACTGTTCCGAGAGTGC 300
DB 241 AGCCTTGCAGATTAACAACAAGAGCTCCGGCTCATCGGAGAGAACTGTTCCGAGAGTGC 300
QY 301 AGTGTAAAGATCAGTGTCTACCTGATGAGCAGGTGCTCACTTCACTTCCGAAAGCTT 360
DB 301 AGTGTAAAGATCAGTGTCTACCTGATGAGCAGGTGCTCACTTCACTTCCGAAAGCTT 360
QY 361 CTGCTCCCGCAGCAGACAGGTTCCAGCCCTATCATGAGAGGTTGATCCTTCCGAGC 420
DB 361 CTGCTCCCGCAGCAGACAGGTTCCAGCCCTATCATGAGAGGTTGATCCTTCCGAGC 420
QY 421 AAACCTCAGCAATCAGCTCAGCTCTGTCAATCAGCGGTGACACAGCAATCCAGAG 480
DB 421 AAACCTCAGCAATCAGCTCAGCTCTGTCAATCAGCGGTGACACAGCAATCCAGAG 480
QY 481 AATGTGAGAGGCTGAGAGAGAGAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGCGC 540
DB 481 AATGTGAGAGGCTGAGAGAGAGAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGCGC 540
QY 541 ATTGGGGAAGTGAAGCTGCTGTTATGTCTGAGAAATGCTTGGCTGAGGAGAGAG 600
DB 541 ATTGGGGAAGTGAAGCTGCTGTTATGTCTGAGAAATGCTTGGCTGAGGAGAGAG 600
QY 601 AGCTAGAAAACGAAGAACTGCTCTCTCTCTCTTCTTAAAGAAACAAATAGATCCCTGAA 660
DB 601 AGCTAGAAAACGAAGAACTGCTCTCTCTCTCTTCTTAAAGAAACAAATAGATCCCTGAA 660
QY 661 TGGACTTTTCTTAAAGAAAGTGAAGAGCTTACGTCATCATCTTAAAGATTTTCAAC 720
DB 661 TGGACTTTTCTTAAAGAAAGTGAAGAGCTTACGTCATCATCTTAAAGATTTTCAAC 720
QY 721 ATGAAACCTGGCTCAGTTGAAAAAGAAATAGTGTCAAGTTGTCATGAGACCAAGAGTA 780
DB 721 ATGAAACCTGGCTCAGTTGAAAAAGAAATAGTGTCAAGTTGTCATGAGACCAAGAGTA 780
QY 781 GACTGATTAACCAAGAAAGTTCATGCAATATTTTATGTCTGATGATGATGATGATGATG 840
DB 781 GACTGATTAACCAAGAAAGTTCATGCAATATTTTATGTCTGATGATGATGATGATGATG 840
QY 841 AATAAATGTAATTAATAAATGTTGAAAGAGAGTTCATCTTCTTGAAGAAAA 900
DB 841 AATAAATGTAATTAATAAATGTTGAAAGAGAGTTCATCTTCTTGAAGAAAA 900
QY 901 AGCTTATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 960
DB 901 AGCTTATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 960
QY 961 GTATACATTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
DB 961 GTATACATTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020

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QY 1021 TATGATATTTAGTATTAAGGCAATATATTTATGACATATATGAAACAGATATTC 1080
 DB 1021 TATGATATTTAGTATTAAGGCAATATATTTATGACATATATGAAACAGATATTC 1080
 QY 1081 TTAGCTTTAATTAACACATGATATCAATTAATAAAAAA 1119
 DB 1081 TTAGCTTTAATTAACACATGATATCAATTAATAAAAAA 1119

RESULT 5
 AAC81774
 ID AAC81774 standard; cDNA; 1166 BP.
 XX
 AC AAC81774;
 XX
 DT 23-FEB-2001 (first entry)
 XX
 DE Murine GIL-19 protein coding sequence.
 XX
 KW Mouse; GIL-19/AE289; IL-10; interleukin-10; nutrition;
 KW cell proliferation; immune stimulation; immune suppression;
 KW haematopoiesis regulation; tissue growth; inflammation; cancer; ss.
 OS Mus sp.
 XX
 PN WO200065027-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 28-APR-2000; 2000MO-US11479.
 XX
 PR 28-APR-1999; 99US-0131473.
 XX
 PA (GENY) GENETICS INST INC.
 XX
 PI Jacobs K, Fouser L, Spaulding V, Xuan D;
 XX
 DR WPI; 2000-687325/67.
 XX
 PT Human GIL-19 protein that shows a high degree of homology to IL
 PT (interleukin)-10, useful in upregulation of humoral immune responses,
 PT as an antiinflammatory agent and as a modulator of immune responses
 PT associated with injury -
 XX
 PS Disclosure; Fig 1; 60bp; English.
 XX
 CC The present invention provides the protein and coding sequences for the
 CC novel human GIL-19/AE289 protein. The protein shows homology to
 CC interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used
 CC in the regulation of cell proliferation and differentiation,
 CC haematopoiesis, immune stimulation or suppression, tissue growth and
 CC tumour inhibition. In addition, it also has uses in the treatment of
 CC inflammation and in nutrition.
 XX
 SQ Sequence 1166 BP; 375 A; 241 C; 244 G; 306 T; 0 other;

Query Match 99.0%; Score 1107.8; DB 21; Length 1166;
 Best Local Similarity 99.4%; Pred. No. 5.3e-228;
 Matches 1112; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

QY 1 TAAACAGGCTCTCTCTCACTTATCAAGCTTGTGACACTTGTGCGATCTGTAGAGGCTGTC 60
DB 24 TAAACAGGCTCTCTCTCTCACTTATCAAGCTTGTGACACTTGTGCGATCTGTAGAGGCTGTC 83
QY 61 CTGACAGAAATCTATGAGTTTTCCTTATGAGGACTTTGGCCGCCAGCTGCTGCTTC 120
DB 84 CTGACAGAAATCTATGAGTTTTCCTTATGAGGACTTTGGCCGCCAGCTGCTGCTTC 143
QY 121 ATTGCTCTGTGGGCCCAAGAGGCAAAATGGCTGCTCCGTCACACCCGGTGCAGCTTGAG 180
DB 144 ATTGCTCTGTGGGCCCAAGAGGCAAAATGGCTGCTCCGTCACACCCGGTGCAGCTTGAG 203
QY 181 GTGTCCAACTTCCAGAGCCGTATCATCGTCAACCGGACCTTTATGTGGCCCAAGAGGCC 240

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OY 303 TGCTAAAGATCAGTGTCTACGTATGAAGAGGTCCTCACTTCAACCTGGAGAGAGCTTCT 362
DB 301 TGTCTAAGATCAGTGTCTACGTATGAAGAGGTCCTCACTTCAACCTGGAGAGAGCTTCT 360
OY 363 GCTCCCCCAGTGAAGAGGTCCTGCTTCAATGACAGAGGTCCTTCTCTGACCAA 422
DB 361 GCTCCCCCAGTGAAGAGGTCCTGCTTCAATGACAGAGGTCCTTCTCTGACCAA 420
OY 423 ACTCAGCAATCAGCTCAGTCTCTGCTCAATCAGCGGTGACGACGAGAACATCCAGAA 482
DB 421 ACTCAGCAATCAGCTCAGTCTCTGCTCAATCAGCGGTGACGACGAGAACATCCAGAA 480
OY 483 TGTCAAGAGGTCGAGAGGAGACAGTGAAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTC 542
DB 481 TGTCAAGAGGTCGAGAGGAGACAGTGAAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTC 540
OY 543 TGGGGAAGTGAAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTC 602
DB 541 CGGGGAAGTGAAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTC 600
OY 603 CTAGAAAAAGAGAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 662
DB 601 CTAGAAAAAGAGAGGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
OY 663 GACTTTTCTTAAAGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAG 722
DB 661 GACTTTTCTTAAAGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAG 720
OY 723 GAAACCTGGCTCAGTGAAGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTC 782
DB 721 GAAACCTGGCTCAGTGAAGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTC 780
OY 783 CTGTAATACCAAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTC 842
DB 781 CTGTAATACCAAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTC 840
OY 843 ATAAATGATCTTAAAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAG 902
DB 841 ATAAATGATCTTAAAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAGGTCGAGAG 900
OY 903 CTATGATACCTCATTGATCAATCAATATTTTATATATATATATATATATATATATAT 962
DB 901 CTATGATACCTCATTGATCAATCAATATTTTATATATATATATATATATATATATAT 960
OY 963 ATACATTTTATATATATATATATATATATATATATATATATATATATATATATATAT 1022
DB 961 ATACATTTTATATATATATATATATATATATATATATATATATATATATATATATAT 1020
OY 1023 TTGATATTT-AGTATTAAGCAAAATATATATATATATATATATATATATATATAT 1081
DB 1021 TTGATATTTAGATATTAAGCAAAATATATATATATATATATATATATATATATAT 1080
OY 1082 TAGGCTTTAATAACATGATATATATATATATATATATATATATATATATATATAT 1112
DB 1081 TAGGCTTTAATAACATGATATATATATATATATATATATATATATATATATATAT 1111

```

RESULT 7
AAS14860

ID AAS14860 standard; cDNA; 1111 BP.

XX AAS14860;

XX 19-DEC-2001 (first entry)

XX Mouse cDNA for T cell derived inducible factor, TIFbeta.

XX Mouse; T cell derived inducible factor; TIFbeta; ss; anti-IL-9; IL-9; STAT transcription factor;
XX anti-leukemic; cytokine; interleukin-9; IL-9; STAT transcription factor;
XX cancer; lymphoma; immune system disorder; allergy; asthma;
XX acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
XX thyroiditis; melanoma; hepatoma.

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OS Mus musculus.
XX
XX US2001024652-A1.
XX
XX 27-SEP-2001.
XX
XX 29-DEC-2000; 2000US-0751797.
XX
XX 18-OCT-1999; 99US-0419568.
XX 26-OCT-1998; 98US-0178973.
XX 16-JUL-1999; 99US-0354243.
XX
XX (DUMC/) DUMOUTIER L.
XX (LOUH/) LOUHED J.
XX (RENA/) RENAULD J.
XX
XX Dumoutier L, Louhed J, Renauld J;
XX WPI; 2001-638496/73.
XX
XX New isolated nucleic acid molecules encoding T cell inducible factors,
XX useful as markers for expression or effect of interleukin (IL)-9 in a
XX subject and diagnosing susceptibility to asthma or allergy -
XX Claim 1, Page 14; 26pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule, which encodes
XX a T cell derived inducible factor (TIF) which are upregulated by the
XX cytokine interleukin-9 (IL-9) and induce STAT transcription factor
XX activation. The TIF proteins (or their nucleins) may be used to test IL-9
XX and/or agonists for their potency against lymphomas, immune system
XX disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
XX autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
XX or inhibit differentiation of tissue types in which they are active and
XX therefore be used to develop treatments for melanomas and hepatomas.
XX The present sequence is a cDNA for mouse TIFbeta.
XX
XX Sequence 1111 BP; 346 A; 232 C; 236 G; 297 T; 0 other;
XX
XX Query Match 93.6%; Score 1047.8; DB 22; Length 1111;
XX Best Local Similarity 97.0%; Pred. No. 3.8e-215;
XX Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

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Db      421 ACTCAGCAATCAGCTCAGCTCCTGTCACATCAGTGTGACGACCAAGACATCCAGAGAA 480
Oy      483 TGTCAAGAGCTGAAGAGAGACAGTGAAGAAAGCTGGAGAGAGTGAAGATCAAGCCAT 542
Db      481 TGTCAAGAGCTGAAGAGAGACAGTGAAGAAAGCTGGAGAGAGTGAAGATCAAGCCAT 540
Oy      543 TGGGGAAGCTGAGCTGCTGTTATGTCCTGTGAGAAATGCTGCTGAGCGAGAGAAAG 602
Db      541 CGGGGAAGCTGAGCTGCTGTTATGTCCTGTGAGAAATGCTGCTGAGCGAGAGAAAG 600
Oy      603 CTAGAAAGAGAGAACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 662
Db      601 CTAGAAAGAGAGAACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
Oy      663 GACTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 722
Db      661 GACTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Oy      723 GAAACCTGCTCAGTGAAGAAAGAAATAGTGTCAAGTTGCTCCATGAGACCAAGGTAGA 782
Db      721 GAAACCTGCTCAGTGAAGAAAGAAATAGTGTCAAGTTGCTCCATGAGACCAAGGTAGA 780
Oy      783 CTGATTAACCAAGAGATTCATTCATATTTTATGTCATCTGATGATACACAGAAA 842
Db      781 CTGATTAACCAAGAGATTCATTCATATTTTATGTCATCTGATGATACACAGAAA 840
Oy      843 ATATGATCTTTTAAATTTGTTTGAAGAGTTACCTCTCACTTCTCTCTCTCTCTCTCTCT 902
Db      841 ATATGATCTTTTAAATTTGTTTGAAGAGTTACCTCTCACTTCTCTCTCTCTCTCTCTCT 900
Oy      903 CTATATGATCTTTTAAATTTGTTTGAAGAGTTACCTCTCACTTCTCTCTCTCTCTCTCTCT 962
Db      901 CTATATGATCTTTTAAATTTGTTTGAAGAGTTACCTCTCACTTCTCTCTCTCTCTCTCTCT 960
Oy      963 ATATGATCTTTTAAATTTGTTTGAAGAGTTACCTCTCACTTCTCTCTCTCTCTCTCTCT 1022
Db      961 ATATGATCTTTTAAATTTGTTTGAAGAGTTACCTCTCACTTCTCTCTCTCTCTCTCTCT 1020
Oy      1023 TTGATATTTTAAATTTGTTTGAAGAGTTACCTCTCACTTCTCTCTCTCTCTCTCTCT 1081
Db      1021 TTGATATTTTAAATTTGTTTGAAGAGTTACCTCTCACTTCTCTCTCTCTCTCTCTCT 1080
Oy      1082 TAGGCTTTTAAATTTGTTTGAAGAGTTACCTCTCACTTCTCTCTCTCTCTCTCTCT 1112
Db      1081 TAGGCTTTTAAATTTGTTTGAAGAGTTACCTCTCACTTCTCTCTCTCTCTCTCTCT 1111

```

RESULT 8

AA030629 standard; cDNA; 1111 BP.

AA030629;

21-MAY-2002 (first entry)

Mouse TIF beta cDNA.

T cell derived inducible factor; TIF; interleukin-21; IL-21; mouse;

STAT transcription factor; acute phase protein; inflammation; ss.

Mus musculus.

Location/Qualifiers

Key 50.589 /tag= a /product= "Mouse TIF beta protein"

MO000210393-A2.

07-FEB-2002.

27-JUN-2001; 2001MO-US20485.

```

PR      27-JUN-2000; 2000US-0626617.
XX
PA      (LUDW-) LUDWIG INST CANCER RES.
XX
PI      Dumoutier L, Renaud J;
XX
DR      WPI; 2002-195964/25.
XX
P-PSDB; AAE19236.
XX
PS      Stimulating expression of STAT transcription factor and inducing
PT      production of acute phase protein in a cell, involves contacting a cell
PT      capable of expressing STAT with T cell derived inducible factors -
XX
XX      Example 9; Page 53; 64pp; English.
XX
CC      The invention relates to nucleic acid molecules encoding T cell
CC      derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
CC      TIF polynucleotides are upregulated by the cytokine, IL-9, IL-TIF or
CC      IL-21 molecules are implicated in activation of STAT transcription
CC      factors, acute phase proteins and inflammation. The present sequence
CC      is mouse TIF beta cDNA.
XX
SQ      Sequence 1111 BP; 346 A; 232 C; 236 G; 297 T; 0 other;
XX
Query Match          93.6%; Score 1047.8; DB 24; Length 1111;
Best Local Similarity 97.0%; Pred. No. 3.8e-215;
Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

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```

Db      661 GACCTTTTCTAAAGAAAGTGAAGCTTAACGTCACCCATCATTAAGAGTTTCACAT 720
Qy      723 GAAACCTGGCTCACTGTAAGAAAGAAATAGTGTCAAGTGTCCATGAGACGAGGTAGA 782
Db      721 GAAACCTGGCTCACTGTAAGAAAGAAATAGTGTCAAGTGTCCATGAGACGAGGTAGA 780
Qy      783 CTGTATTAACCAAGATTCATTGACATATTTTATTTGTCAGTGTATGATACACAGAAA 842
Db      781 CTGTATTAACCAAGATTCATTGACATATTTTATTTGTCAGTGTATGATACACAGAAA 840
Qy      843 ATAATGACTTTAAATAATGTTTGAAGAGAGTACCTCATTCCTTTAGAAAAAAG 902
Db      841 AGTATGACTTTAAATAATGTTTGAAGAGAGTACCTCATTCCTTTAGAAAAAAG 900
Qy      903 CTATGTACTTCATTTCCATATCCAAATATTTATATATGTAAGTTATTTATTTATTAAGT 962
Db      901 CCTATGTACTTCATTTCCATATCCAAATATTTATATATGTAAGTTATTTATTTATTAAGT 960
Qy      963 ATACATTTTATTTATGTCAGTTTATTAATATGATTTATTTATAGAAAACATTATCTGCTA 1022
Db      961 ATACATTTTATTTATGTCAGTTTATTAATATGATTTATTTATAGAAAACATTATCTGANG 1020
Qy      1023 TTGATATTT-AGTATTAAGCAATATATTTATGACATATCTATGGAAGAGATATCT 1081
Db      1021 TTGATATTTGATTAAGCAATATATTTATGATTAATATCTATGGAAGAGATATCT 1080
Qy      1082 TAGGCTTTAATTAACACATGATATCATTA 1112
Db      1081 TAGGCTTTAATTAACACATGATATCATTA 1111

```

RESULT 9

AAD27135
ID AAD27135 standard; DNA; 1111 BP.

XX AAD27135;

XX 09-APR-2002 (first entry)

XX Mouse T cell derived inducible factor (TIF) beta cDNA.

XX T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;
XX protein therapy; STAT activation; differentiation; mouse; ss.

XX Mus musculus.

XX US6331613-B1.

XX 18-DEC-2001.

XX 18-OCT-1999; 99US-0419568.

XX 26-OCT-1998; 98US-0178973.

XX 18-JUL-1999; 99US-0354243.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Dumoulier L, Louhed J, Renaud J;

XX WPI; 2002-105277/14.

XX Nucleic acids encoding T cell derived inducible factors useful for
XX inducing STAT activation in cells -

XX Claim 1; Column 25-26; 24DP; English.

XX The present invention relates to an isolated nucleic acid molecule, which
XX encodes a T cell derived inducible factor comprising an amino acid
XX sequence encoded by 6 defined nucleotide sequences. The nucleic acid
XX molecules are shown to be up regulated by the cytokine interleukin-9
XX (IL-9) and are described as T cell derived inducible factors (TIFs). The
XX invention is used in protein therapy. The nucleic acid molecules encode

CC proteins which induce STAT activation in cells. They can be used, for
CC example, in the stimulation of regeneration of targeted tissues.
CC Further, their inhibitors or antagonists can be used to retard, prevent
CC or inhibit differentiation of other tissues. The present sequence is
CC mouse TIF beta cDNA.

XX Sequence 1111 BP; 346 A; 232 C; 236 G; 297 T; 0 other;

Query Match 93.6%; Score 1047.8; DB 24; Length 1111;
Best Local Similarity 97.0%; Pred. No. 3.8e-215;
Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

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Qy      3 AACAGGCTCCCTCCTCACTTATCAACCTTTGACACTTGTGAGTCGGGAGGCTGCTCT 62
Db      1 AACAGGCTCCCTCCTCACTTATCAACCTTTGACACTTGTGAGTCGGGAGGCTGCTCT 60
Qy      63 GCAGAAATCTATGAGTTTTCCTTAATGAGGAGCTTTGAGGAGCTGCTGCTTCTCAT 122
Db      61 GCAGAAATCTATGAGTTTTCCTTAATGAGGAGCTTTGAGGAGCTGCTGCTTCTCAT 120
Qy      123 TGCCCTGTGGCCCGAGAGGCAATGCGCTGCCGTCAACACCCGGTGCAGCTTGAAGT 182
Db      121 TGCCCTGTGGCCCGAGAGGCAATGCGCTGCCGTCAACACCCGGTGCAGCTTGAAGT 180
Qy      183 GTCCAACTTCCAGCAGCCGTATCATCTCAACCGCACTTTATGCTGGCCAAAGAGCCAG 242
Db      181 GTCCAACTTCCAGCAGCCGTATCATCTCAACCGCACTTTATGCTGGCCAAAGAGCCAG 240
Qy      243 CCTGCAATATACAAACACAGACGTCGGCTCATGCGGAGAGAACTGTTCCGAGAGTCA 302
Db      241 CCTGCAATATACAAACACAGACGTCGGCTCATGCGGAGAGAACTGTTCCGAGAGTCA 300
Qy      303 TGCTAAAGATCAGTGTCACTGATGAGAGAGTGTCACTTCACTCCGTGAAGAAGCTTCT 362
Db      301 TGCTAAAGATCAGTGTCACTGATGAGAGAGTGTCTCACTTCACTCCGTGAAGAAGCTTCT 360
Qy      363 GCTCCCGCAGTCAAGAGTTCACGCCCTTACATGACAGAGGTGTACTTCTGACCAA 422
Db      361 GCTCCCGCAGTCAAGAGTTCACGCCCTTACATGACAGAGGTGTACTTCTGACCAA 420
Qy      423 ACTGAGAACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
Db      421 ACTGAGAACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy      483 TGTCAAGAGCTGAAGAGACAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGGCGAT 542
Db      481 TGTCAAGAGCTGAAGAGACAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGGCGAT 540
Qy      543 TGGGGAACCTGACCTGCTGTTATGCTCTGAGAAATGCTTGTGCTGAGCGAAGAG 602
Db      541 CGGGGAACCTGACCTGCTGTTATGCTCTGAGAAATGCTTGTGCTGAGCGAAGAG 600
Qy      603 CTGAAGAAAGAGAAACGCTCCCTCCCTCCCTTCTAAGAAAGAAACATTAAGCCCTGATG 662
Db      601 CTGAAGAAAGAGAAACGCTCCCTCCCTTCTAAGAAAGAAACATTAAGCCCTGATG 660
Qy      663 GACTTTTCTTAAGAGAAAGTGAAGAGCTTAACGTCATCATCTTAAGAGATTTCAAT 722
Db      661 GACTTTTCTTAAGAGAAAGTGAAGAGCTTAACGTCATCATCTTAAGAGATTTCAAT 720
Qy      723 GAAACCTGGCTCACTGTAAGAAAGAAATAGTGTCAAGTGTTCATGAGACGAGGTAGA 782
Db      721 GAAACCTGGCTCACTGTAAGAAAGAAATAGTGTCAAGTGTTCATGAGACGAGGTAGA 780
Qy      783 CTGTATTAACCAAGATTCATTGACATATTTTATTTGTCAGTGTATGATACACAGAAA 842
Db      781 CTGTATTAACCAAGATTCATTGACATATTTTATTTGTCAGTGTATGATACACAGAAA 840
Qy      843 ATAATGACTTTAAATAATGTTTGAAGAGAGTTCATTCATCTTTAGAAAAAAG 902
Db      841 AGTATGACTTTAAATAATGTTTGAAGAGAGTTCATTCATCTTTAGAAAAAAG 900
Qy      903 CTATGTACTTCATTTCCATATCCAAATATTTATATATGTAAGTTATTTATTAAGT 962

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Db      |||||
901 CCTATGTAACCTTCCATTCACCAACTTATATATGTAAGTTATTTATATATAGT 960
Qy      963 ATACATTTTATTTATGTCAGTTTATTTATATGATTTTATATAGAAACATTATCTGCTA 1022
Db      961 ATACATTTTATTTATGTCAGTTTATTTATATGATTTTATATAGAAAAATATCTGATG 1020
Qy      1023 TTGATATTT-AGTATAGGCAAAATATTTATATGACATTAATGAAACAGATATCT 1081
Db      1021 TTGATATTTGATATAGCAAAATATTTATATGATTAATTAAGTAAGAAACAGATATCT 1080
Qy      1082 TAGGCTTATATTAACACATGATATATCAATPAA 1112
Db      1081 TAGGCTTATATTAACACATGATATATCAATPAA 1111

RESULT 10
AAD09746
ID      AAD09746 standard; cDNA; 778 BP;
XX
XX      AAD09746;
XX
XX      10-SEP-2001 (first entry)
XX
XX      Mouse ZCYTO18 cDNA.
XX
XX      Mouse; cytoskeletal; cytokine; ZCYTO18 protein; genetic abnormality;
XX      cancer; inflammation; gene therapy; ss.
XX
XX      Mus musculus.
XX
XX      Key      Location/Qualifiers
XX      CDS      47..586
XX              /*tag= a
XX              /Product= "Mouse ZCYTO18 protein"
XX
XX      sig_peptide 47..145
XX              /*tag= b
XX      mat_peptide 146..583
XX              /*tag= c
XX              /Product= "Mouse mature ZCYTO18 protein"
XX
XX      WO200146422-A1.
XX
XX      28-JUN-2001.
XX
XX      PD      22-DEC-2000; 2000WO-US35308.
XX
XX      PF      23-DEC-1999; 99US-0471767.
XX      PR      01-DEC-2000; 2000US-0250841.
XX
XX      PA      (ZYMO) ZYMOGENETICS INC.
XX
XX      PI      Presnell SR, Kindsvogel W;
XX      WI      MPI; 2001-408648/43.
XX      DR      P-PSDB; AAE05052.
XX
XX      Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -
XX
XX      Example 5; Page 160-162; 167pp; English.
XX
XX      The patent discloses novel human cytokine, ZCYTO18 protein and its
XX      corresponding DNA. ZCYTO18 protein induces proliferation of cells
XX      expressing ZCYTO18, a receptor for ZCYTO18 or induces cytotoxicity
XX      in K562 cells. ZCYTO18 DNA is useful for detecting a genetic
XX      abnormality in a patient. ZCYTO18 DNA and its antibodies are useful
XX      for detecting cancer and inflammation. ZCYTO18 protein is useful for
XX      killing cancer cells. It is useful for increasing platelets in a
XX      patient or injured tissue. It is also used in gene therapy.
XX      The present sequence is a cDNA encoding mouse cytokine, ZCYTO18.
XX
XX      Sequence 778 BP; 213 A; 193 C; 197 G; 175 T; 0 other;
XX
XX

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Query Match      68.7%; Score 768.4; DB 22; Length 778;
Best Local Similarity 99.2%; Pred. No. 2.8e-155;
Matches 772; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      6 AGGCTTCCTCTCACTTATATCACTGTGTGGAGTCTGTATGGCTGTCCGCA 65
Db      1 AGGCTTCCTCTCACTTATATCACTGTGTGACCTGTGTGGAGTGTGTGTGTGCA 60
Qy      66 GAATCTATAGTGTTCCTTATGGGACCTTTGGCCGCGAGTGCCTGCTTCATTGC 125
Db      61 GAATCTATAGTGTTCCTTATGGGACCTTTGGCCGCGAGTGCCTGCTTCATTGC 120
Qy      126 CTTGTGGGCCCGAGGAGCAATGGCTGCGCCGTCAACACCCGGTGCAAGCTTGAGGTTC 185
Db      121 CTTGTGGGCCCGAGGAGCAATGGCTGCGCCGTCAACACCCGGTGCAAGCTTGAGGTTC 180
Qy      186 CAATCTCCAGCAGCCGTCATCTGTCACCCGACCTTTATGCTGGCCAAAGGCGCAGCT 245
Db      181 CAATCTCCAGCAGCCGTCATCTGTCACCCGACCTTTATGCTGGCCAAAGGCGCAGCT 240
Qy      246 TGCAGATPACAACACAGACGTCGGGCTCATGCGGGAGAACTGTTCCGAGAGTCAGTGC 305
Db      241 TGCAGATPACAACACAGATGTCGGGCTCATGCGGGAGAACTGTTCCGAGAGTCATGTC 300
Qy      306 TAAAGATCAGTGTCTACCTGATGAAGCAGGTCTCACTTCAACCTGGAAGACGTTCTGCT 365
Db      301 TAAAGATCAGTGTCTACCTGATGAAGCAGGTCTCACTTCAACCTGGAAGACGTTCTGCT 360
Qy      366 CCCCAGTCAGACAGGTTCCAGCCCTTACATGACAGAGGTGTGATCTTTCCTGACCAACT 425
Db      361 CCCCAGTCAGACAGGTTCCAGCCCTTACATGACAGAGGTGTGATCTTTCCTGACCAACT 420
Qy      426 CAGCAATAGCTCAGCTCCTCTCATGAGGGGTGAGAGCAGAAACATCCAGAAATGT 485
Db      421 CAGCAATAGCTCAGCTCCTCTCATGAGGGGTGAGAGCAGAAACATCCAGAAATGT 480
Qy      486 CAGAAAGCTGAAGGAGCAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGCGCATTTGG 545
Db      481 CAGAAAGCTGAAGGAGCAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGCGCATTTGG 540
Qy      546 GGAATGGAAGCTGCTGTTTATGTCTCTAGAAAGTCTTGCGTCTGAGGAGAAAGCTGA 605
Db      541 GGAATGGAAGCTGCTGTTTATGTCTCTAGAAAGTCTTGCGTCTGAGGAGAAAGCTGA 600
Qy      606 GAAACGAAAGAACTGCTCCTTCTTAAAGAAACATATAGATCCCTGAATGAC 665
Db      601 GAAACGAAAGAACTGCTCCTTCTTAAAGAAACATATAGATCCCTGAATGAC 660
Qy      666 TTTTCTTAAAGAAAGTGAAGCTAAGCTCATCATCTTAAAGATTTACATGAA 725
Db      661 TTTTCTTAAAGAAAGTGAAGCTAAGCTCATCATCTTAAAGATTTACATGAA 720
Qy      726 ACTGCTCAGTTGAAAAAAGAAATAGTGTCAAGTTGTCATGAGAACAGAGGTAGAC 783
Db      721 ACTGCTCAGTTGAAAAAAGAAATAGTGTCAAGTTGTCATGAGAACAGAGGTAGAC 778

RESULT 11
AAA28816
ID      AAA28816 standard; DNA; 7444 BP.
XX
XX      AAA28816;
XX
XX      04-SEP-2000 (first entry)
XX
XX      Murine T cell inducible factor alpha genomic DNA.
XX
XX      TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;
XX      Anti-asthmatic; anti-allergic; cytoskeletal; inhibitor; antagonist; ss.
XX
XX      Mus sp.
XX
XX      Key      Location/Qualifiers
XX

```

FT	exon	1908..1932
FT		/*tag= a
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FT	CDS	2080..6615
FT		/*tag= b
FT		/product= TIF-alpha
FT	intron	1933..2032
FT		/*tag= c
FT	exon	2033..2262
FT		/*tag= d
FT		/number= 1b
FT	intron	2263..2654
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FT	exon	2655..2720
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FT		/number= 2
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FT	exon	3931..3996
FT		/*tag= j
FT		/number= 4
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FT		/*tag= k
FT	exon	6539..7137
FT		/*tag= l
FT		/number= 5
XX		
XX		WO200024758-A1.
XX		
XX		04-MAY-2000.
XX		
XX		18-OCT-1999;
XX		99WO-US24424.
XX		
XX		26-OCT-1998;
XX		98US-.0178973.
XX		16-JUL-1999;
XX		99US-0354243.
XX		
XX	PA	(LUDW-) LUDWIG INST CANCER RES.
XX		
XX	PI	Dumoutier L, Louhed J, Renaud J;
XX		
XX	DR	WPI; 2000-422495/36.
XX		
XX	P-PSDB;	AAI92877.
XX		
XX	PT	New nucleic acid molecule encoding a T cell derived inducible factor
XX	PT	for treating asthma, an allergy or lymphoma
XX		
XX		Claim 1; Page 34-37; 46pp; English.
XX		
XX		This DNA encodes T cell derived inducible factor (TIF) alpha identified
XX		by subtraction cloning from a murine lymphoma cell line BW5147 in the
XX		presence or absence of interleukin 9 (IL-9). BW5147, can be grown in
XX		vitro, without the need to add any cytokines to its culture medium. Many
XX		IL-9 activities are mediated by activation of STAT transcription
XX		factors. The novel TIFs were expressed in the presence of IL-9, but not
XX		in its absence. TIFs induce STAT activation in cells. They can be used,
XX		e.g. in the stimulation of regeneration of targeted tissues. Their
XX		inhibitors or antagonists can be used to retard, prevent or inhibit
XX		differentiation of other tissues. The TIFs and their coding sequences are
XX		useful in the treatment of asthma, allergies and lymphoma (claimed). They
XX		are also useful for identifying compounds that inhibit or activate T cell
XX		induced factor activity in a cell (claimed).
XX		
XX		Sequence 7444 BP; 2058 A; 1570 C; 1596 G; 2220 T; 0 other;
XX		
XX		Query Match 53.7%; Score 601.4; DB 21; Length 7444;
XX		Best local similarity 99.8%; Pred. No. 3.7e-119;
XX		Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY	510	AAAGCTTGAGAGAGGTGGAGATCAAGAGCGCAATTGGGGAACTGGACCTGCGTTTAATGTC	565
Db	6534	ATAGCTTGGAAAGAGGTGGAGATCAAGAGCGCAATTGGGGAACTGGACCTGCGTTTAATGTC	6593
QY	570	TCTGGAAGAAATCCTTGGCGCTGAGGAGAGAAAGACTAGAAAAACGAAGAAGTGCCTCTCT	629
Db	6594	TCTGGAAGAAATCCTTGGCGCTGAGGAGAGAAAGACTAGAAAAACGAAGAAGTGCCTCTCTCT	6593
QY	630	GCGTTCTTAAAAAAGAACAAATAAGATCCCTGAATGGACCTTTTTTACTAAAGAAAGTGAGAA	689
Db	6654	GCGTTCTTAAAAAAGAACAAATAAGATCCCTGAATGGACCTTTTTTACTAAAGAAAGTGAGAA	6713
QY	680	GCTAAACCTCCATCATCATTTAGAAATTTTCACATGAACCTGGCTCAGTTGAAAAAGAAA	749
Db	6714	GCTAAACCTCCATCATCATTTAGAAATTTTCACATGAACCTGGCTCAGTTGAAAAAGAAA	6773
QY	750	TAGTGTCAAGTGTGCATGAGACGAGAGGTGAGCTTGATPAAACGACAAAGATTCTTGACA	809
Db	6774	TAGTGTCAAGTGTGCATGAGACGAGAGGTGAGCTTGATPAAACGACAAAGATTCTTGACA	6833
QY	810	ATATTTTATTTGTCACTGATGATACACAGAAAAATTAATGACTTTTAAAAAAATGTTTGA	869
Db	6834	ATATTTTATTTGTCACTGATGATACACAGAAAAATTAATGACTTTTAAAAAAATGTTTGA	6893
QY	870	AGGAGGTTACTCTTCATCTCTTTGAAAAAAAAGCTTAGTATGACTTCAATTCACAA	929
Db	6894	AGGAGGTTACTCTTCATCTCTTTGAAAAAAAAGCTTAGTATGACTTCAATTCACAA	6953
QY	930	TATTTTATATATGTAGTTTATTTATATAGTATATGATTTTATTTATGTCAGTTTATTA	989
Db	6964	TATTTTATATATGTAGTTTATTTATATAGTATATGATTTTATTTATGTCAGTTTATTA	7013
QY	990	ATATGATTTTATTTATAGAAAAACATTATCTGCTATTTGATATTTAGTATPAGCAATATATA	1049
Db	7014	ATATGATTTTATTTATAGAAAAACATTATCTGCTATTTGATATTTAGTATPAGCAATATATA	7073
QY	1050	TTTATGACATATPACTATGAAAAACAGATATCTTGAGCTTTATATPAAACATGATATCAT	1109
Db	7074	TTTATGACATATPACTATGAAAAACAGATATCTTGAGCTTTATATPAAACATGATATCAT	7133
QY	1110	AAA 1112	
Db	7134	AAA 7136	
RESULT 12			
AAS14859			
ID	AAS14859	standard; DNA; 7445 BP.	
XX	AC	AAS14859;	
XX	DT	19-DEC-2001 (first entry)	
XX	DE	Mouse partial genomic DNA for T cell derived inducible factor, TIFalpa.	
XX	XX	Mouse; T cell derived inducible factor; TIFalpa; ds; antiallergic;	
XX	KW	antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;	
XX	KW	cancer; lymphoma; immune system disorder; allergy; asthma;	
XX	KW	acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;	
XX	KW	thyroiditis; melanoma; hepatoma.	
OS	XX	Mus musculus.	
PN	XX	US2001024652-A1.	
XX	XX	27-SEP-2001.	
XX	PD	29-DEC-2000; 2000US-0751797.	
XX	PF	18-OCT-1999; 99US-0419568.	
XX	PR	26-OCT-1998; 98US-0178973.	
XX	PR	16-JUL-1999; 99US-0354243.	
XX	XX		

PA (DUMO/) DUMOUTIER L.
 PA (LOUA/) LOUAHD J.
 PA (RENA/) RENAULD J.
 XX
 PI Dumoutier L, Louahed J, Renauld J;
 XX
 XX WPI; 2001-638496/73.
 DR
 XX
 PT New isolated nucleic acid molecules encoding T cell inducible factors,
 PT useful as markers for expression or effect of interleukin (IL)-9 in a
 PT subject and diagnosing susceptibility to asthma or allergy
 XX
 XX
 XX Claim 1; Page 11-14; 26pp; English.
 CC
 CC The invention relates to an isolated nucleic acid molecule, which encodes
 CC a T cell derived inducible factor (TIF) which are upregulated by the
 CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor
 CC activation. The TIF proteins (or their mutants) may be used to test IL-9
 CC ant/agonists for their potency against lymphomas, immune system
 CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
 CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
 CC or inhibit differentiation of tissue types in which they are active and
 CC therefore be used to develop treatments for melanomas and hepatomas.
 CC The present sequence a partial genomic sequence for mouse TIFalpha.
 CC
 XX
 SQ Sequence 7445 BP; 2058 A; 1570 C; 1597 G; 2220 T; 0 other;

Query Match 53.7%; Score 601.4; DB 22; Length 7445;
 Best Local Similarity 99.8%; Pred. No. 3.7e-119;
 Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 510 AAAGCTTGAGAGAGATGAGATCAAGGCGATTGGGGAAGCTGCTGTTATGTC 569
 DB 6535 ATAGCTTGAGAGAGATGAGATCAAGGCGATTGGGGAAGCTGCTGTTATGTC 6594
 OY 570 TCTGAGAATGCTGCTGCTGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAG 629
 DB 6595 TCTGAGAATGCTGCTGCTGAGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAG 6654
 OY 630 GCGCTTCTAAAAAGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 689
 DB 6655 GCGCTTCTAAAAAGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6714
 OY 690 GCTAACGTCATCATCATTAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 749
 DB 6715 GCTAACGTCATCATCATTAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6774
 OY 750 TAGTGTCAAGTGTGCATGAGACAGAGGTAGACTTGATTAACCAAGAGATTCATGACA 809
 DB 6775 TAGTGTCAAGTGTGCATGAGACAGAGGTAGACTTGATTAACCAAGAGATTCATGACA 6834
 OY 810 ATATTTTATGTCATGATGATACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 869
 DB 6835 ATATTTTATGTCATGATGATACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6894
 OY 870 AGAGAGTAACTCTCATTCCTTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 929
 DB 6895 AGAGAGTAACTCTCATTCCTTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6954
 OY 930 TATTTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 989
 DB 6955 TATTTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7014
 OY 990 ATATGATTTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1049
 DB 7015 ATATGATTTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7074
 OY 1050 TTATGACACATTAAG 1109
 DB 7675 TTATGACACATTAAG 7134
 OY 1110 AAA 1112
 |||

DB 7135 AAA 7137

RESULT 13

AAD30628
 ID AAD30628 standard; DNA; 7445 BP.

AC AAD30628;

DT 21-MAY-2002 (first entry)

DE Mouse TIF alpha genomic DNA

XX T cell derived inducible factor; TIF; interleukin-21; IL-21; mouse;

XX STAT transcription factor; acute phase protein; inflammation; ds.

OS Mus musculus.

PN WO200210393-A2.

PD 07-FEB-2002.

PF 27-JUN-2001; 2001WO-US20485.

PR 27-JUL-2000; 2000US-0626617.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Dumoutier L, Renauld J;

DR WPI; 2002-195964/25.

XX Stimulating expression of STAT transcription factor and inducing

PT production of acute phase protein in a cell, involves contacting a cell

PT capable of expressing STAT with T cell derived inducible factors

PS Example 7; Page 49-53; 64pp; English.

XX The invention relates to nucleic acid molecules encoding T cell

CC derived inducible factors (TIFs) also known as interleukin-21 (IL-21).

CC TIF polynucleotides are upregulated by the cytokine, IL-9. IL-TIF or

CC IL-21 molecules are implicated in activation of STAT transcription

CC factors, acute phase proteins and inflammation. The present sequence

CC is mouse TIF alpha genomic DNA.

CC Sequence 7445 BP; 2059 A; 1568 C; 1597 G; 2221 T; 0 other;

Query Match 53.7%; Score 601.4; DB 24; Length 7445;

Best Local Similarity 99.8%; Pred. No. 3.7e-119;

Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 510 AAAGCTTGAGAGAGATGAGATCAAGGCGATTGGGGAAGCTGCTGTTATGTC 569
 DB 6535 ATAGCTTGAGAGAGATGAGATCAAGGCGATTGGGGAAGCTGCTGTTATGTC 6594
 OY 570 TCTGAGAATGCTGCTGCTGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 629
 DB 6595 TCTGAGAATGCTGCTGCTGAGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6654
 OY 630 GCGCTTCTAAAAAGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 689
 DB 6595 GCGCTTCTAAAAAGAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6714
 OY 690 GCTAACGTCATCATCATTAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 749
 DB 6715 GCTAACGTCATCATCATTAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6774
 OY 750 TAGTGTCAAGTGTGCATGAGACAGAGGTAGACTTGATTAACCAAGAGATTCATGACA 809
 DB 6775 TAGTGTCAAGTGTGCATGAGACAGAGGTAGACTTGATTAACCAAGAGATTCATGACA 6834
 OY 810 ATATTTTATGTCATGATGATACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 869
 |||

	Best Local Similarity	99.8%	Pred. No. 3.7e-119;	Matches 602;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	510	AAAGCTTGGAGAGGTGGAGATCAAGGCGCATTTGGGAACTGGACCTGCTGTTATATGTC	569					
Db	6535	ATAGCTTGAGAGAGTGGAGAGATCAAGGCCATTTGGGAACTGGACCTGCTGTTATATGTC	6594					
QY	570	TCTGGAAGAAATGCTTGCCTGTGAGGAGAGAGAAGCTAGAAAAGAAAGAACTGCTCTTCT	629					
Db	6595	TCTGGAAGAAATGCTTGCCTGTGAGGAGAGAGAAGCTAGAAAAGAAAGAACTGCTCTTCT	6654					
QY	630	GCCTTCTTAAAGAACAACTAAGATCCTGAATGGAATGGAATTTTACTTAAAGGAAGTGAGA	689					
Db	6655	GCCTTCTTAAAGAACAACTAAGATCCTGAATGGAATGGAATTTTACTTAAAGGAAGTGAGA	6714					
QY	690	GCTAACGCGCCATCATTCATTGAGAAATTTCCATGAACCTGGGCTCAGTTGAAAAAGAAA	749					
Db	6715	GCTAACGCGCCATCATTCATTGAGAAATTTCCATGAACCTGGGCTCAGTTGAAAAAGAAA	6774					
QY	750	TAGTGTCAAGTTGTCCATGAGACGAGAGGTAGACTTGATTAACCAAAAGATTCAATTGACA	809					
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AC								
XX								
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XX								
DE	Murine T cell inducible factor beta genomic DNA.							
XX								
KW	TIF-beta; T cell derived inducible factor; interleukin 9; STAT; IL-9;							
KW	Anti-asthmatic; anti-allergic; cyostatic; inhibitor; antagonist; ss.							
XX								
OS	Mus sp.							
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:03:00 ; Search time 1874.61 Seconds

(without alignment)

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Title: US-09-751-797-7

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Perfect score: 1119

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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41: gb_ov.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1119	100.0	1119	6	AR165226 Sequence
2	1119	100.0	1119	6	AR201397 Sequence
3	1119	100.0	1119	6	AX459953 Sequence
4	1119	100.0	1121	10	MMU249491 Sequence
5	1056.4	94.4	1118	10	MMU249492 Sequence
6	1047.8	93.6	1111	6	AR165228 Sequence
7	1047.8	93.6	1111	6	AR201399 Sequence
8	1047.8	93.6	1111	6	AX459955 Sequence
9	768.4	68.7	778	6	AX179614 Sequence
10	601.4	53.7	7445	6	AR165227 Sequence
11	601.4	53.7	7445	6	AR201398 Sequence
12	601.4	53.7	7445	6	AX459954 Sequence
13	601.4	53.7	8270	10	MMU294727 Sequence
14	555.2	49.6	5935	6	AR165234 Sequence
15	555.2	49.6	5935	6	AR201417 Sequence
16	555.2	49.6	5935	6	AX459988 Sequence
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ALIGNMENTS

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LOCUS AR165226 1119 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 7 from patent US 6274710.
ACCESSION AR165226
VERSION AR165226.1 GI:16238719
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1119)
AUTHORS Dumoutier, L., Loubet, J. and Renaud, J.-C.
TITLE Antibodies which specifically bind T cell inducible factors (Tifs)
JOURNAL Patent: US 6274710-A 7 14-AUG-2001;
FEATURES Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

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BASE COUNT 352 a 233 c 232 g 302 t
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Query Match 100.0%; Score 1119; DB 6; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1.6e-215;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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BASE COUNT 352 a 233 c 232 g 302 t
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Query Match 100.0%; Score 1119; DB 6; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1.6e-215;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Sequence 7 from Patent W00210393.
DEFINITION AX459953
ACCESSION AX459953
VERSION AX459953.1 GI:21725689
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutelestom; Chordata; Craniata; Vertebrata; Eutelestom; Eukaryota; Eutelestia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Dimoutier, L. and Renaud, J.C.
TITLE Isolated nucleic acid molecules which encode c cell inducible factors, or interleukin-21, the proteins encoded, and uses thereof
JOURNAL Patent: WO 0210393-A 7-07-FEB-2002.
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source location/Qualifiers
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BASE COUNT 352 a 233 c 232 g 302 t
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Best Local Similarity 100.0%; Pred. 1.6e-215;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Mus musculus mRNA for TIF alpha protein (IL-22 gene).
DEFINITION AJ249491
ACCESSION AJ249491.1 GI:6996553
VERSION IL-2 gene; IL-Tifa gene; TIF alpha protein.
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1121)
AUTHORS Dumoutier, L., Louahed, J. and Renauld, J.C.
TITLE Cloning and characterization of IL-10-related T cell-derived inducible factor (IL-TIF), a novel cytokine structurally related to IL-10 and inducible by IL-9
JOURNAL Immunology 164, 1814-1819 (2000)
REFERENCES 2 (bases 1 to 1121)
AUTHORS Renauld, J.C.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-1999) Renauld J.C., Cytokine group, Ludwig Institute for Cancer Research, 74, Avenue Hippocrate, Brussels, B-1200, BELGIUM

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BASE COUNT 352 a 235 c 232 g 302 f
ORIGIN

Query Match 100.0%; Score 1119; DB 10; Length 1121;
Best Local Similarity 100.0%; Pred. No. 1.6e-215;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 903 AGCTATGTAACCTCATTCATTCATCAATATTTATATATGTAAGTTATTTATTA 962
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DB 963 GTATACATTTTATTTATGTCAGTTTATTAATATGATTTATTTATGAAACATTA 1022
QY 1021 TATTGATATTTAGTATTAAGGCAATATTTATTAATGACATATCAATGAAACAT 1080
DB 1023 TATTGATATTTAGTATTAAGGCAATATTTATTAATGACATATCAATGAAACAT 1082
QY 1081 TTAGGCTTAAATAACCATGATATCAATAAAAAAA 1119
DB 1083 TTAGGCTTAAATAACCATGATATCAATAAAAAAA 1121

RESULT 5
NMU249492 1118 bp mRNA linear ROD 16-FEB-2000
LOCUS Mus musculus mRNA for TIF beta protein (IL-Tif gene).
DEFINITION AJ249492
ACCESSION AJ249492.1 GI:6996555
VERSION IL-Tif gene; TIF beta protein.
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1118)
AUTHORS Dumoutier, L., Louahed, J. and Renauld, J.C.
TITLE Cloning and characterization of TIF, a new IL-10-related cytokine induced by IL-9
JOURNAL Immunology 164, 1814-1819 (2000)
REFERENCES 2 (bases 1 to 1118)
AUTHORS Renauld, J.C.
TITLE Direct Submission

JOURNAL, Submitted (14-SEP-1999) Renaud J.C., Cytochrome group, Ludwig
Institute for Cancer Research, 74, Avenue Hippocrate, Brussels,
B-1200, BELGIUM

FEATURES
source Location/Qualifiers

1. 1118
/organism="Mus musculus"
/strain="129"
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50.589
/gene="IL-TiPb"
50.589
/function="cytokine"
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/product="TiP beta protein"
/protein_id="CA87547.1"
/db_xref="GI:6996556"
/translation="MAVLQKSMFSLWGLTASCLLIILALMAQANALPIINRCKLEV
SNFOPIVIRTFMLAKKASLADNNDVRLIGKLPQVAKDQCYIMKQVLPETED
ILIPSDRPRPQVPEVPLFTKLSNQLSSCHISGDDONIQNVRRLKETVKKLGESE
IKALGELDLFMSLRNACV"

BASE COUNT 353 a 233 c 235 g 297 t
ORIGIN

Query Match 94.4%; Score 1056.4; DB 10; Length 1118;
Best Local Similarity 97.1%; Pred. No. 6.9e-203;
Matches 1086; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

QY 3 AACAGGCTCTCTCTCACTTATCAAGTGTGACACTTGTGCGATCTCTGATGGCTGCT 62
DB 1 AAGAGGCTCTCTCTCACTTATCAAGTGTGACACTTGTGCGATCTCTGATGGCTGCT 60
QY 63 GCAGAAATCTAGAGTTTTCCTTATGGGAGCTTTGGCCGAGCTGCTGCTTCTCAT 122
DB 61 GCAGAAATCTAGAGTTTTCCTTATGGGAGCTTTGGCCGAGCTGCTGCTTCTCAT 120
QY 123 TGGCCCTGTGGGCCAGAGGCAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182
DB 121 TGGCCCTGTGGGCCAGAGGCAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 183 GTCCAACTTCCAGACGCGCTACATCGTCAACGCGACCTTATGCTGACCAAGAGGCGAG 242
DB 181 GTCCAACTTCCAGACGCGCTACATCGTCAACGCGACCTTATGCTGACCAAGAGGCGAG 240
QY 243 CCTTGAGATTAACAACAACAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
DB 241 CCTTGAGATTAACAACAACAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 303 TGTCTAAGATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 362
DB 301 TGTCTAAGATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 363 GCTCCCGCCAGTGAAGAGGCTTCCAGGCTTACATGACGAGGAGTGTGCTTCTGACCA 422
DB 361 GCTCCCGCCAGTGAAGAGGCTTCCAGGCTTACATGACGAGGAGTGTGCTTCTGACCA 420
QY 423 ACTCAGCAATCAAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
DB 421 ACTCAGCAATCAAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 483 TGTCAAGAGGCTGAAGAGCACTGTAAGAAAGCTTTGAGAGAGTGAAGATCAAGGCGAT 542
DB 481 TGTCAAGAGGCTGAAGAGCACTGTAAGAAAGCTTTGAGAGAGTGAAGATCAAGGCGAT 540
QY 543 TGGGGAAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
DB 541 CGGGGAAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 603 CTAGAAAAAGAAAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 662
DB 601 CTAGAAAAAGAAAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 663 GACTTTTTTACTAAGAAAGTGAAGGCTAAGCTCATCATCTTTAGAAAGATTTTCAT 722

DB 661 GACTTTTTTACTAAGAAAGTGAAGGCTAAGCTAAGCTCATCATCTTTAGAAAGATTTTCAT 720
QY 723 GAAACCTGGCTCAGTTGAAAAAGAAATATGTCGCAAGTTGTCATGAGACCAAGAGTAGA 782
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QY 783 CTGATTAACCAACAAGATTCATGACAAATTTTATGTCACGATGATTAACAAGAAAA 842
DB 781 CTGATTAACCAACAAGATTCATGACAAATTTTATGTCATGATTAACAAGAAAA 840
QY 843 ATATGATCTTTAAAAAATGTTGAAAGAGGTTACCTCTCATTCCTTTAGAAAAAAG 902
DB 841 AGTATGATCTTTAAAAAATGTTGAAAGAGGTTACCTCTCATTCCTCTAGAAAAAAG 900
QY 903 CTATGATTAACCTGATTTCCATATCAATATTTTATATATGATTAAGTTATTTATTAAGT 962
DB 901 CCTATGATTAACCTGATTTCCATATCAATATTTTATATATGATTAAGTTATTTATTAAGT 960
QY 963 ATATGATTTTATTTATGTCAGTTTATTAATATGATTTTATTAAGAAACATTATCTGCTA 1022
DB 961 ATATGATTTTATTTATGTCAGTTTATTAATATGATTTTATTAAGAAAAATTTATCTGATG 1020
QY 1023 TTGATATTTT-AGTATAGGCAATATATTTATTAAGCAATACATGAAACAGATATCT 1081
DB 1021 TTGATATTTT-AGTATAGGCAATATATTTATTAAGCAATACATGAAACAGATATCT 1080
QY 1082 TAGGCTTTAATAACAACATGATATCATTAATAAAAAA 1119
DB 1081 TAGGCTTTAATAACAACATGATATCATTAATAAAAAA 1118

RESULT 6
LOCUS AR165228 1111 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 9 from patent US 6274710.
ACCESSION AR165228
VERSION AR165228.1 GI:16238721
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1111)
AUTHORS Dumoutier, L., Louned, J. and Renaud, J.-C.
TITLES Antibodies which specifically bind T cell inducible factors (TIFs)
JOURNAL Patent: US 6274710-A 9 14-AUG-2001;
FEATURES Location/Qualifiers

source 1. 1111
BASE COUNT 346 a 232 c 236 g 297 t
ORIGIN

Query Match 93.6%; Score 1047.8; DB 6; Length 1111;
Best Local Similarity 97.0%; Pred. No. 3.8e-201;
Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 3 AACAGGCTCTCTCTCACTTATCAAGTGTGACACTTGTGCGATCTCTGATGGCTGCT 62
DB 1 AAGAGGCTCTCTCTCACTTATCAAGTGTGACACTTGTGCGATCTCTGATGGCTGCT 60
QY 63 GCAGAAATCTAGAGTTTTCCTTATGGGAGCTTTGGCCGAGCTGCTGCTTCTCAT 122
DB 61 GCAGAAATCTAGAGTTTTCCTTATGGGAGCTTTGGCCGAGCTGCTGCTTCTCAT 120
QY 123 TGGCCCTGTGGGCCAGAGGCAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182
DB 121 TGGCCCTGTGGGCCAGAGGCAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 183 GTCCAACTTCCAGACGCGTACATCGTCAACGCGACCTTATGCTGCGCAAGAGGCGAG 242
DB 181 GTCCAACTTCCAGACGCGTACATCGTCAACGCGACCTTATGCTGCGCAAGAGGCGAG 240
QY 243 CCTTGAGATTAACAACAACAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302

Db 241 CCTTGGAGATACACACAGACGTCGGCTCATCGGGAGAACTGTTCCGAGAGTCAG 300
 Qy 303 TGCTTAAGATCAGTGCACCTGATGAAAGAGGTCCTCACTTCACCTCGAAGACGTCCT 362
 Db 301 TGCTTAAGATCAGTGCACCTGATGAAAGAGGTCCTCACTTCACCTCGAAGACGTCCT 360
 Qy 363 GCTCCCCAGTCAGACAGGTTCCAGCCCTCATGCAAGAGGTGATCCTTTCCTGACCA 422
 Db 361 GCTCCCCAGTCAGACAGGTTCCGGCCCTCATGCAAGAGGTGTCCTTTCCTGACCA 420
 Qy 423 ACTCAGCAATCAGTGCCTGCTGCTCATGACGCGGTGACGACCAACATCCAGAAAG 482
 Db 421 ACTCAGCAATCAGTGCCTGCTGCTCATGACGCGGTGACGACCAACATCCAGAAAG 480
 Qy 483 TGTCAAGAGGCTGAGAGGACAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGGGAT 542
 Db 481 TGTCAAGAGGCTGAGAGGACAGTGAAGAAAGCTTGAGAGAGCGAGAGATCAAGGGAT 540
 Qy 543 TGGGAACTGAGACCTGCTGTTTATGCTCTGAGAAATGCTTGCTGAGCGAGAAAG 602
 Db 541 CGGGAACTGAGACCTGCTGTTTATGCTCTGAGAAATGCTTGCTGAGCGAGAAAG 600
 Qy 603 CTAGAAACGAGAGACTGCTCTCTGCTCTTCAAAAAGACATTAAGATCCCTGAATG 662
 Db 601 CTAGAAACGAGAGACTGCTCTCTGCTCTTCAAAAAGACATTAAGATCCCTGAATG 660
 Qy 663 GACTTTTCTAAGAAAGTGAAGCTAAGCTCATCATCTTGAAGATTCAT 722
 Db 661 GACTTTTCTAAGAAAGTGAAGCTAAGCTCATCATCTTGAAGATTCAT 720
 Qy 723 GAAACCTGCTCAGTGAAGAAAGTGAAGCTGCAATGCTGAGACGAGAGTAGA 782
 Db 721 GAAACCTGCTCAGTGAAGAAAGTGAAGCTGCAATGCTGAGACGAGAGTAGA 780
 Qy 783 CTGATACCAACAAAGATTCATGACAAATTTTATGTCATGATGATACACAGAAA 842
 Db 781 CTGATACCAACAAAGATTCATGACAAATTTTATGTCATGATGATACACAGAAA 840
 Qy 843 ATATGTAATTAATAAATGTTGAAAGAGTTCCTCATCTCTTGAAGAAAG 902
 Db 841 ATATGTAATTAATAAATGTTGAAAGAGTTCCTCATCTCTTGAAGAAAG 900
 Qy 903 CTTATGTAATTAATAAATGTTGAAAGAGTTCCTCATCTCTTGAAGAAAG 962
 Db 901 CTTATGTAATTAATAAATGTTGAAAGAGTTCCTCATCTCTTGAAGAAAG 960
 Qy 963 ATACATTTTATTAATGTCAGTTTATTAATGATGATTTATTAAGAAACATTAATCTGCTA 1022
 Db 961 ATACATTTTATTAATGTCAGTTTATTAATGATGATTTATTAAGAAACATTAATCTGCTA 1020
 Qy 1023 TTGATATTTT-AGTAAAGGCAAAATTAATTAATGACAAATACTAGGAAACAAATATCT 1081
 Db 1021 TTGATATTTT-AGTAAAGGCAAAATTAATTAATGATTAATTAATTAATTAATTAATCT 1080
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 Db 1081 TAGCCTTAATAACACATGATGATCAATAA 1111

RESULT 7
 AR201399 1111 bp DNA linear PAT 20-APR-2002
 LOCUS AR201399 Sequence 9 from patent US 6359117.
 DEFINITION AR201399
 ACCESSION AR201399
 VERSION AR201399.1 GI:20252287
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 1111)
 Dumoutier, L., Louhed, J. and Renault, J.-C.
 TITLE Isolated nucleic acid molecules which encode T cell inducible

JOURNAL Factors (Tifs), the proteins encoded, and uses therefor
 Patent: US 6359117-A 9 19-MAR-2002;
 FEATURES Location/Qualifiers
 source 1..1111
 BASE COUNT 346 a 232 c 236 g 297 t
 ORIGIN
 Query Match 93.6%; Score 1047.8; DB 6; Length 1111;
 Best Local Similarity 97.0%; Pred. No. 3.8e-201;
 Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

Qy 3 AACAGGCTCTCTCTACTTATCACTGTTGACACTTGGCCATCTCTGATGGCTTCTCT 62
 Db 1 AACAGGCTCTCTCTACTTATCACTTGTGACACTTGGCCATCTCTGATGGCTTCTCT 60
 Qy 63 GCAGAAATCTATGAGTTTTTCCCTTATGGGGACTTTGGCGGAGCTGCTGCTCTCAT 122
 Db 61 GCAGAAATCTATGAGTTTTTCCCTTATGGGGACTTTGGCGGAGCTGCTGCTCTCAT 120
 Qy 123 TGCCCTGTGGGCCAGAGGCAAAATGCGCTGCCCTCAACACCCGGTGCAAGCTTGAAGT 182
 Db 121 TGCCCTGTGGGCCAGAGGCAAAATGCGCTGCCCTCAACACCCGGTGCAAGCTTGAAGT 180
 Qy 183 GTCCAACTTCAGACAGCCGTAATGCTCAACCGCACCTTTATGCTGGCCAAAGAGCCAG 242
 Db 181 GTCCAACTTCAGACAGCCGTAATGCTCAACCGCACCTTTATGCTGGCCAAAGAGCCAG 240
 Qy 243 CTTTGAAGATTAACAACAGAGGTCGGGCTCATCGGGGAGAACTGTTCCGAGAGTCAG 302
 Db 241 CTTTGAAGATTAACAACAGAGGTCGGGCTCATCGGGGAGAACTGTTCCGAGAGTCAG 300
 Qy 303 TGCTTAAGATCAGTGCACCTGATGAAAGAGTGTCTCACTTCACCTGGAAGACGTTCT 362
 Db 301 TGCTTAAGATCAGTGCACCTGATGAAAGAGTGTCTCACTTCACCTGGAAGACGTTCT 360
 Qy 363 GCTCCCCAGTCAGACAGGTTCCAGCCCTCATGCAAGAGAGTGTACTTTCCTGACCA 422
 Db 361 GCTCCCCAGTCAGACAGGTTCCAGCCCTCATGCAAGAGAGTGTACTTTCCTGACCA 420
 Qy 423 ACTCAGCAATCAGTGCCTGCTGCTGCTCATGACGCGGTGACGACCAACATCCAGAAAG 482
 Db 421 ACTCAGCAATCAGTGCCTGCTGCTGCTCATGACGCGGTGACGACCAACATCCAGAAAG 480
 Qy 483 TGTCAAGAGGCTGAGAGGACAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGGGAT 542
 Db 481 TGTCAAGAGGCTGAGAGGACAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGGGAT 540
 Qy 543 TGGGAACTGAGACCTGCTGTTTATGCTCTGAGAAATGCTTGCTGAGCGAGAAAG 602
 Db 541 TGGGAACTGAGACCTGCTGTTTATGCTCTGAGAAATGCTTGCTGAGCGAGAAAG 600
 Qy 603 CTAGAAACGAGAGACTGCTCTCTGCTCTTCAAAAAGACATTAAGATCCCTGAATG 662
 Db 601 CTAGAAACGAGAGACTGCTCTCTGCTCTTCAAAAAGACATTAAGATCCCTGAATG 660
 Qy 663 GACTTTTCTAAGAAAGTGAAGCTAAGCTCATCATCTTGAAGATTCAT 722
 Db 661 GACTTTTCTAAGAAAGTGAAGCTAAGCTCATCATCTTGAAGATTCAT 720
 Qy 723 GAAACCTGCTCAGTGAAGAAAGTGAAGCTGCAATGCTGAGACGAGAGTAGA 782
 Db 721 GAAACCTGCTCAGTGAAGAAAGTGAAGCTGCAATGCTGAGACGAGAGTAGA 780
 Qy 783 CTGATACCAACAAAGATTCATGACAAATTTTATGTCATGATGATTAATGCAACAGAAA 842
 Db 781 CTGATACCAACAAAGATTCATGACAAATTTTATGTCATGATTAATGCAACAGAAA 840
 Qy 843 ATATGTAATTAATAAATGTTGAAAGAGGTTACTCTCATCTTGAAGAAAG 902
 Db 841 ATATGTAATTAATAAATGTTGAAAGAGGTTACTCTCATCTTGAAGAAAG 900
 Qy 903 CTTATGTAATTAATAAATGTTGAAAGAGTTCCTCATCTCTTGAAGAAAG 962

Db	421	ACTGAGCATATGCTCAGCTTCCTGTCACATCAGTGGGACGACCAAGAACATCCGAAAGAA	483	TGTGAGAAAGCTGAGAGAGACAGTGAAGAAAGCTTGAGAGAGATGAGAGATCAAGGCGAT	481	TGTGAGAAAGCTGAGAGAGACAGTGAAGAAAGCTTGAGAGAGAGCGAGAGATCAAGGCGAT	543	TGGGAACTGAGACCTGCTGTTATGTCCTTGAGAAATGCTTGGCTTGAGCGAGAGAGAG	541	CGGGAACTGAGACCTGCTGTTATGTCCTTGAGAAATGCTTGGCTTGAGCGAGAGAGAG	603	CTAAGAAACGAAAGAACTGCTCCTTCCTGCGCTTCTAAGAAAGAAATTAAGATCCCTGAATG	601	CTAAGAAACGAAAGAACTGCTCCTTCCTGCGCTTCTAAGAAAGAAATTAAGATCCCTGAATG	663	GACCTTTTACTAAGGAAAGTGAAGAGCTAACGCTCACTCATTCATTTAGAAATTTACAT	661	GACCTTTTACTAAGGAAAGTGAAGAGCTAACGCTCACTCATTCATTTAGAAATTTACAT	723	GAAACCTGCGCTCAGTTGAAAAAGAAAAATAGTGTCAAGTTGTCCATGAGACCGAGAGTGA	721	GAAACCTGCGCTCAGTTGAAAAAGAAAAATAGTGTCAAGTTGTCCATGAGACCGAGAGTGA	783	CTTGATTAACCGAAAGATTCATTGACAAATATTTATTTGTCACCTGATGATACACAGAAAA	781	CTTGATTAACCGAAAGATTCATTGACAAATATTTATTTGTCATTAATATGCAACAGAAAA	843	ATAATGTACTTAAATAAATGTTTGAAGAGAGGTACCTCTCATTCCTTTGAAAAAAAAG	841	AGTATGTACTTAAATAAATGTTTGAAGAGAGGTACCTCTCATTCCTTTGAAAAAAAAG	903	CTTATGTACTTCAATTCATATCCAAATATTTATATATGTAATGATTTATTTATATAGT	901	CCATATGATCCTTCAATTCATATCCAAATATTTATATATGTAATGATTTATTTATATAGT	963	ATACATTTTATTTATGTCAGTTTATTAATATGATTTATTTATGAAACATTTATCTGCTA	961	ATACATTTTATTTATGTCAGTTTATTAATATGATTTATTTATGAAAAATTTATCTGATG	1023	TTGATATTTT-AGTATAAGGCAAAATATATTTATGACATTAACATGAGAAACAAATATCT	1021	TTGATATTTTAGATTAAGGCAAAATATATTTATGATTAATTAATTAATTAATTAATCT	1082	TAGGCTTTAATTAACACATGATGATATCATATAA	1081	TAGGCTTTAATTAACACATGATGATATCATATAA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
RESULT 9	AX179614	Sequence 37 from Patent WO0164422.	AX179614	778 bp	DNA	linear	PAT 06-AUG-2001																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															</

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IKAIQELDLLEFMSLENACV"

BASE COUNT
ORIGIN

213 a 193 c 197 g 175 t

Query Match 68.7%; Score 768.4; DB 6; Length 778;
Best Local Similarity 99.2%; Pred. No. 7.9e-145;
Matches 772; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 AGGCTCTCTCTCACTTATCAACTGTGACACTTGTGGATCTTGATGGCTGCTTCA 65
DB 1 AGGCTCTCTCTCACTTATCAACTGTGACACTTGTGGATCTTGATGGCTGCTTCA 60
QY 66 GAAATCTATAGATTTTTCCTATATGGGGACTTGGCCGACGTCGCTTCTCATGGC 125
DB 61 GAAATCTATAGATTTTTCCTATATGGGGACTTGGCCGACGTCGCTTCTCATGGC 120
QY 126 CCGTGGGCGCCAGAGGCAATGCGCTGCGCTCAACACCCGCTGCAAGCTTGAAGTGC 185
DB 121 CCGTGGGCGCCAGAGGCAATGCGCTGCGCTCAACACCCGCTGCAAGCTTGAAGTGC 180
QY 186 CAAGTTCAGAGCGCTGATGTCATCCGCACTTTATGCTGGCCAGAGGCGCAAGCTT 245
DB 181 CAAGTTCAGAGCGCTGATGTCATCCGCACTTTATGCTGGCCAGAGGCGCAAGCTT 240
QY 246 TGCAGATTAACAACACAGAGCGTGGGCTCATGGGGAGAACTGTTCCAGAGGTCAGTGC 305
DB 241 TGCAGATTAACAACACAGAGCGTGGGCTCATGGGGAGAACTGTTCCAGAGGTCAGTGC 300
QY 306 TAAAGATCAGTCTACCTGATGAGCAGGTCGCTCACTTCACTTCACTGAAAGCTTCTGCT 365
DB 301 TAAAGATCAGTCTACCTGATGAGCAGGTCGCTCACTTCACTTCACTGAAAGCTTCTGCT 360
QY 366 CCCCCAGTACAGAGGTCACGCCCTCACTGACAGAGGTCGTAACCTTCTGACCAACT 425
DB 361 CCCCCAGTACAGAGGTCACGCCCTCACTGACAGAGGTCGTAACCTTCTGACCAACT 420
QY 426 CAGCAATCAGCTCAGCTCTGTCATACAGAGGTCGTAACCAATCAGCAAGAACT 485
DB 421 CAGCAATCAGCTCAGCTCTGTCATACAGAGGTCGTAACCAATCAGCAAGAACT 480
QY 486 CAGAGGCTGAGAGAGACAGTGAAGAAAGCTTGAAGAGAGTGAAGATCAAGCGCATGG 545
DB 481 CAGAGGCTGAGAGAGACAGTGAAGAAAGCTTGAAGAGAGTGAAGATCAAGCGCATGG 540
QY 546 GGAATCTGACCTGCTGTTTATGTCTCTGAGAAATGCTTGGTCTGAGCGAGAAAGCTA 605
DB 541 GGAATCTGACCTGCTGTTTATGTCTCTGAGAAATGCTTGGTCTGAGCGAGAAAGCTA 600
QY 606 GAAACGAGAAAGCTGCTCTGCTCTCTAATAAAGAACATTAAGATCCCTGAATGGAC 665
DB 601 GAAACGAGAAAGCTGCTCTGCTCTCTAATAAAGAACATTAAGATCCCTGAATGGAC 660
QY 666 TTTTCTTAAAGAGAGTGAAGAGTAACTGTCATCATCATTTAGAGATTTTCAATGAA 725
DB 661 TTTTCTTAAAGAGAGTGAAGAGTAACTGTCATCATCATTTAGAGATTTTCAATGAA 720
QY 726 ACCTGGCTTAAAGAGAGTGAAGAGTAACTGTCATCATCATTTAGAGATTTTCAATGAA 783
DB 721 ACCTGGCTTAAAGAGAGTGAAGAGTAACTGTCATCATCATTTAGAGATTTTCAATGAA 778

RESULT 10

LOCUS AR165227 7445 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6274710.
ACCESSION AR165227
VERSION AR165227.1 GI:16238720
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 7445)
AUTHORS Dumoutier, L., Louhed, J., and Renaud, J.-C.
TITLE Antibodies which specifically bind T cell inducible factors (TIFs)
JOURNAL Patent: US 6274710-A 8 14-Aug-2001;
FEATURES Location/Qualifiers
SOURCE 1..7445
/organism="unknown"

BASE COUNT 2058 a 1570 c 1597 g 2220 t
ORIGIN

Query Match 53.7%; Score 601.4; DB 6; Length 7445;
Best Local Similarity 99.8%; Pred. No. 5.3e-111;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 510 AAAGCTGAGAGAGTGAAGATCAAGGCAATTTGGGGAAGTGAAGCTGCTGTTATGTC 569
DB 6535 ATAGCTTGAAGAGTGAAGATCAAGGCAATTTGGGGAAGTGAAGCTGCTGTTATGTC 6594
QY 570 TCTGAGAAATGCTTGGCTGAGGAGAGAGAGTGAAGAAAGTGAAGAACTGCTTCT 629
DB 6595 TCTGAGAAATGCTTGGCTGAGGAGAGAGAGTGAAGAAAGTGAAGAACTGCTTCT 6654
QY 630 GCCTTCTTAAAGAAACAATTAAGTCCCTGATGAGTGAAGTGAAGTGAAGTGAAG 689
DB 6655 GCCTTCTTAAAGAAACAATTAAGTCCCTGATGAGTGAAGTGAAGTGAAGTGAAG 6714
QY 690 GCTAAGCTCAATCAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 749
DB 6715 GCTAAGCTCAATCAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 6774
QY 750 TAGTGTCAAGTGTCAATGAGACAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 809
DB 6775 TAGTGTCAAGTGTCAATGAGACAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 6834
QY 810 ATATTTTATTTGTCACTGATGATACACAGAAATAATATGTAATTTTAAATTTGTTGA 869
DB 6835 ATATTTTATTTGTCACTGATGATGATACACAGAAATAATATGTAATTTTAAATTTGTTGA 6894
QY 870 AGAGAGTACCTCATCTCTTGAAGAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 929
DB 6895 AGAGAGTACCTCATCTCTTGAAGAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 6954
QY 930 TATTTTATATATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 989
DB 6955 TATTTTATATATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 7014
QY 990 ATATGAGATTTTATATGAAACATTTATGCTATGATGATTTAGTATAGGCAATATTA 1049
DB 7015 ATATGAGATTTTATATGAAACATTTATGCTATGATGATTTAGTATAGGCAATATTA 7074
QY 1050 TTTATGACAAATTAATGAGAAACAAGATATCTTATGAGCTTATATTAACAACATGATATCAT 1109
DB 7075 TTTATGACAAATTAATGAGAAACAAGATATCTTATGAGCTTATATTAACAACATGATATCAT 7134
QY 1110 AAA 1112
DB 7135 AAA 7137

RESULT 11

LOCUS AR201398 7445 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 8 from patent US 6359117.
ACCESSION AR201398
VERSION AR201398.1 GI:20252286
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7445)
AUTHORS Dumoutier, L., Louhed, J., and Renaud, J.-C.
TITLE Isolated nucleic acid molecules which encode T cell inducible

Factors (Tifs), the proteins encoded, and uses therefor
JOURNAL Patent: US 6359117-A 8-19-MAR-2002;
FEATURES Location/Qualifiers

SOURCE

1.7445

/organism="unknown"

BASE COUNT 2058 a 1570 c 1597 g 2220 t

ORIGIN

Query Match 53.7%; Score 601.4; DB 6; Length 7445;

Best Local Similarity 99.8%; Pred. No. 5.3e-111;

Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

510 AAAGCTTGAGAGAGTGGAGATCAAGGCGATTGGGGAACCTGGACCTGCTGTTATGTC 569

5535 ATAGCTTGAGAGAGTGGAGATCAAGGCGATTGGGGAACCTGGACCTGCTGTTATGTC 6594

570 TCTGAGAAATGCTTGGCTGAGCGAGAGAGAGTAAAGAAACGAGAACTGCTCTTCT 629

6595 TCTGAGAAATGCTTGGCTGAGCGAGAGAGAGTAAAGAAACGAGAACTGCTCTTCT 6654

630 GCCCTTCTAAAAGAACATTAAGATCCCTGAATGACCTTTTCTAAAGAGAGTGA 689

6655 GCCCTTCTAAAAGAACATTAAGATCCCTGAATGACCTTTTCTAAAGAGAGTGA 6714

690 GCTAACCTCCATCATCTATTAGAAAGATTTCACATGAAACCTGGCTCACTGAAAAAGAAA 749

6715 GCTAACCTCCATCATCTATTAGAAAGATTTCACATGAAACCTGGCTCACTGAAAAAGAAA 6774

750 TAGTGCAAGTTGTCATGAGACGAGAGGATGATTAACCAAGAGATTCATTGACA 809

6775 TAGTGCAAGTTGTCATGAGACGAGAGGATGATTAACCAAGAGATTCATTGACA 6834

810 ATATTTATTTGTCATGATGATATCAAGAGAAATTAATGACTTTAAATAATGTTGAA 869

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870 AGAGAGTTACCTCTCATCTCTTTAGAAAAAGCTTATGTAATTCATTCCATATCCA 929

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1110 AAA 1112

7135 AAA 7137

RESULT 12
AX459954 7445 bp DNA linear PAT 08-JUL-2002
LOCUS
DEFINITION
SEQUENCE 8 from Patent W00210393.
VERSION
AX459954.1 GI:21725690
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
1 Dumoulier, L. and Renaud, J.C.
Isolated nucleic acid molecules which encode t cell inducible factors, or interleukin-21, the proteins encoded, and uses thereof
Patent: WO 0210393-A 8-07-FEB-2002;

LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES Location/Qualifiers

SOURCE

1.7445

/organism="Mus musculus"

/db_xref="taxon:10090"

BASE COUNT 2059 a 1568 c 1597 g 2221 t

ORIGIN

Query Match 53.7%; Score 601.4; DB 6; Length 7445;

Best Local Similarity 99.8%; Pred. No. 5.3e-111;

Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

510 AAAGCTTGAGAGAGTGGAGATCAAGGCGATTGGGGAACCTGGACCTGCTGTTATGTC 569

5535 ATAGCTTGAGAGAGTGGAGATCAAGGCGATTGGGGAACCTGGACCTGCTGTTATGTC 6594

570 TCTGAGAAATGCTTGGCTGAGCGAGAGAGAGTAAAGAAACGAGAACTGCTCTTCT 629

6595 TCTGAGAAATGCTTGGCTGAGCGAGAGAGAGTAAAGAAACGAGAACTGCTCTTCT 6654

630 GCCCTTCTAAAAGAACATTAAGATCCCTGAATGACCTTTTCTAAAGAGAGTGA 689

6655 GCCCTTCTAAAAGAACATTAAGATCCCTGAATGACCTTTTCTAAAGAGAGTGA 6714

690 GCTAACCTCCATCATCTATTAGAAAGATTTCACATGAAACCTGGCTCACTGAAAAAGAAA 749

6715 GCTAACCTCCATCATCTATTAGAAAGATTTCACATGAAACCTGGCTCACTGAAAAAGAAA 6774

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6775 TAGTGCAAGTTGTCATGAGACGAGAGGATGATTAACCAAGAGATTCATTGACA 6834

810 ATATTTATTTGTCATGATGATATCAAGAGAAATTAATGACTTTAAATAATGTTGAA 869

6835 ATATTTATTTGTCATGATGATATCAAGAGAAATTAATGACTTTAAATAATGTTGAA 6894

870 AGAGAGTTACCTCTCATCTCTTTAGAAAAAGCTTATGTAATTCATTCCATATCCA 929

6895 AGAGAGTTACCTCTCATCTCTTTAGAAAAAGCTTATGTAATTCATTCCATATCCA 6954

930 TATTTATATATGATGATTTATTTATATATAGTATATTTATTTATGTCAGTTATTA 989

6955 TATTTATATATGATGATTTATTTATATATAGTATATTTATTTATGTCAGTTATTA 7014

990 ATATGATTTATTTATATGAAACATTAATCTGCTATTTAGTATTTAGTAAAGCAATATA 1049

7015 ATATGATTTATTTATATGAAACATTAATCTGCTATTTAGTATTTAGTAAAGCAATATA 7074

1050 TTTATGCAATTAATCTATGAAACAGATATCTTGGCTTTATATTAACACATGATATCAT 1109

7075 TTTATGCAATTAATCTATGAAACAGATATCTTGGCTTTATATTAACACATGATATCAT 7134

1110 AAA 1112

7135 AAA 7137

RESULT 13
MMU294727 8270 bp DNA linear ROD 30-MAY-2001
LOCUS
DEFINITION
SEQUENCE 1 from Patent W00210393.
VERSION
MMU294727.1 GI:11967892
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
1 Dumoulier, L., Van Roost, B., Amey, G., Michaux, L. and Renaud, J.C.
IL-TIF/IL-22: genomic organization and mapping of the human and mouse genes

JOURNAL Genes Immun. 1 (8), 488-494 (2000)
MEDLINE 21069354
PUBMED 1197690
REFERENCE 2 (bases 1 to 8270)
AUTHORS Renaud,J.C.
JOURNAL Direct Submission
Submitted (18-SEP-2000) Renaud J.C., UCL 74.59, Ludwig Institute
for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels,
BELGIUM

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BASE COUNT 2324 a 1743 c 1722 g 2481 t
ORIGIN

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Best Local Similarity 99.8%; Pred. No. 5,4e-11;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 510 AAACCTTGAGAGAGTGAAGATCAAGGCGATTGGGAACTGGACCTGCTTTATGTC 569
DB 7360 ATACTTGAGAGAGTGAAGATCAAGGCGATTGGGAACTGGACCTGCTTTATGTC 7419
QY 570 TCTGAAGAAAGCTTGCCTTGAAGGAGAAAGAGTAAAGAGAAAGTCTCTCT 629
DB 7420 TCTGAAGAAAGCTTGCCTTGAAGGAGAAAGAGTAAAGAGAAAGTCTCTCT 7479
QY 630 GCCTTTAAAGAAAGATAGATCCTGATGAGCTTTTAAAGAAAGTGAAG 689
DB 7480 GCCTTTAAAGAAAGATAGATCCTGATGAGCTTTTAAAGAAAGTGAAG 7539
QY 690 GCTAACGTCATCATCTTGAAGATTCACATGAACTGGCTCAGTTGAAAAAGAAA 749
DB 7540 GCTAACGTCATCATCTTGAAGATTCACATGAACTGGCTCAGTTGAAAAAGAAA 7539
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DB 7600 TAGGTCAAGTTGCTCCATGAGACCAAGAGTGAAGTGAAGCAAGATTCATGACA 7659
QY 810 ATATTTATGTCAGTATGATGATACAGAAAAATATGACTTAAAGAAATGTTGCA 869
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DB 7960 AAA 7962

RESULT 14
ARI65234
LOCUS ARI65234 5935 bp DNA linear PAT 17-OCT-2001

DEFINITION Sequence 17 from patent US 6274710.
ACCESSION ARI65234
VERSION ARI65234.1 GI:16238731

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5935)
AUTHORS Dumoutier,L., Louhed,J., and Renaud,J.C.
TITLE Antibodies which specifically bind T Cell inducible factors (TIFs)
JOURNAL Patent: US 6274710-A 17-14-AUG-2001;
FEATURES Location/Qualifiers
1..5935
/organism="unknown"

BASE COUNT 1732 a 1174 c 1346 g 1603 t
ORIGIN
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Best Local Similarity 96.0%; Pred. No. 1,1e-101;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

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QY	570	TCGAGAAATGCTTGCGTCTGAGGAGAAAGCTAGAAAACGAAAGACTGCTCTCT	629
Db	5281	TCGAGAAATGCTTGCGTCTGAGGAGAAAGCTAGAAAACGAAAGACTGCTCTCT	5340
QY	630	GCCCTCTAAAAAACAATAGATCCCTGATGAGCTTTTACTTAAAGAAAGTGAA	689
Db	5341	GCCCTCTAAAAAACAATAGATCCCTGATGAGCTTTTACTTAAAGAAAGTGAA	5400
QY	690	GCTAACGTCATCATCTAGATGAGATTCATGAAACCTGGCTCAGTTGAAAAAGAA	749
Db	5401	GCTAACGTCATCATCTAGATGAGATTCATGAAACCTGGCTCAGTTGAAAAAGAA	5460
QY	750	TAGTCAAGTTGTCATGAGACCAAGAGTACCTGATTAACCAAGAAATTCATTGAC	809
Db	5461	TAGTCAAGTTGTCATGAGACCAAGAGTACCTGATTAACCAAGAAATTCATTGAC	5520
QY	810	ATATTTATGTCATGATGATACAGAGAAATTAATGTAATTTAAATTTGTTGAA	869
Db	5521	ATATTTATGTCATGATGATACAGAGAAATTAATGTAATTTAAATTTGTTGAA	5580
QY	870	AGGAGTTACCTCATCTCTTTAGAAAAAAGCTATGTAATTCATTTCCATATCCAA	929
Db	5581	AGGAGTTACCTCATCTCTTTAGAAAAAAGCTATGTAATTCATTTCCATATCCAA	5640
QY	930	TATTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	989
Db	5641	TATTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	5700
QY	990	ATATGATTTATTTATGAAACATTATCTGCTATGATATTT-AGTATAGGCAATAT	1048
Db	5701	ATATGATTTATTTATGAAACATTATCTGCTATGATATTT-AGTATAGGCAATAT	5760
QY	1049	ATTATGACAAATACATGATGAAACAGATATCTTAGGCTTAATTAACACATGATATCA	1108
Db	5761	ATTATGATATATACATGATGAAACAGATATCTTAGGCTTAATTAACACATGATATCA	5820
QY	1109	TAAA 1112	
Db	5821	TAAA 5824	

RESULT 15

AR201417
LOCUS AR201417 5935 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 29 from patent US 6359117.
ACCESSION AR201417
VERSION AR201417.1 GI:20252305
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5935)
AUTHORS Dumoutier, L., Louhed, J. and Renaud, J.-C.
TITLE Isolated nucleic acid molecules which encode T cell inducible factors (Tlfs), the proteins encoded, and uses therefor
JOURNAL Patent: US 6359117-A 29 19-MAR-2002;
FEATURES
Location/Qualifiers
1..5935
BASE COUNT 1732 a 1174 c 1346 g 1683 t
ORIGIN

Query Match 49.6%; Score 555.2; DB 6; Length 5935;
Best Local Similarity 96.0%; Pred. No. 1,1e-101;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY	510	AAAGCTTGAGAGAGAGATCAAGCGATTGGGAACTGGACCTGCTGTTATGTC	569
Db	5221	ATAGCTTGAGAGAGAGAGATCAAGCGATTGGGAACTGGACCTGCTGTTATGTC	5280
QY	570	TCGAGAAATGCTTGCGTCTGAGGAGAAAGCTAGAAAACGAAAGACTGCTCTCT	629
Db	5281	TCGAGAAATGCTTGCGTCTGAGGAGAAAGCTAGAAAACGAAAGACTGCTCTCT	5340
QY	630	GCCCTCTAAAAAACAATAGATCCCTGATGAGCTTTTACTTAAAGAAAGTGAA	689
Db	5341	GCCCTCTAAAAAACAATAGATCCCTGATGAGCTTTTACTTAAAGAAAGTGAA	5400
QY	690	GCTAACGTCATCATCTAGATGAGATTCATGAAACCTGGCTCAGTTGAAAAAGAA	749
Db	5401	GCTAACGTCATCATCTAGATGAGATTCATGAAACCTGGCTCAGTTGAAAAAGAA	5460
QY	750	TAGTCAAGTTGTCATGAGACCAAGAGTACCTGATTAACCAAGAAATTCATTGAC	809
Db	5461	TAGTCAAGTTGTCATGAGACCAAGAGTACCTGATTAACCAAGAAATTCATTGAC	5520
QY	810	ATATTTATGTCATGATGATACAGAGAAATTAATGTAATTTAAATTTGTTGAA	869
Db	5521	ATATTTATGTCATGATGATACAGAGAAATTAATGTAATTTAAATTTGTTGAA	5580
QY	870	AGGAGTTACCTCATCTCTTTAGAAAAAAGCTATGTAATTCATTTCCATATCCAA	929
Db	5581	AGGAGTTACCTCATCTCTTTAGAAAAAAGCTATGTAATTCATTTCCATATCCAA	5640
QY	930	TATTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	989
Db	5641	TATTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	5700
QY	990	ATATGATTTATTTATGAAACATTATCTGCTATGATATTT-AGTATAGGCAATAT	1048
Db	5701	ATATGATTTATTTATGAAACATTATCTGCTATGATATTT-AGTATAGGCAATAT	5760
QY	1049	ATTATGACAAATACATGATGAAACAGATATCTTAGGCTTAATTAACACATGATATCA	1108
Db	5761	ATTATGATATATACATGATGAAACAGATATCTTAGGCTTAATTAACACATGATATCA	5820
QY	1109	TAAA 1112	
Db	5821	TAAA 5824	

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Job time : 1877.61 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 16:17:16 ; Search time 158.321 Seconds
(without alignments)
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Title: US-09-751-797-7

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Scoring table: IDENTITY NUC
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Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	993.2	88.8	1050	15	US-10-090-365-40
5	993.2	88.8	1050	15	US-10-104-919-42
6	601.4	53.7	7445	10	US-09-751-797-8
7	555.2	49.6	5935	10	US-09-751-797-29
8	535.2	47.8	1191	15	US-10-084-298-1
9	524.8	46.9	1152	11	US-09-870-574-1
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11	524.8	46.9	1152	15	US-10-066-867-153
12	524.8	46.9	1152	15	US-10-066-500-125
13	524.8	46.9	1152	15	US-10-063-547-153
14	524.8	46.9	1152	15	US-10-063-616-153
15	524.8	46.9	1152	15	US-10-063-502-153
16	524.8	46.9	1152	15	US-10-227-884-243

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45	524.8	46.9	1152	15	US-10-230-260-243	Sequence 243, App

ALIGNMENTS

RESULT 1
US-09-751-797-7
Sequence 7, Application US/09751797
Patent No. US20010024652A1
GENERAL INFORMATION:
APPLICANT: Dumontier, Laure
APPLICANT: Renaldi, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible 1
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/751, 797
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 09/419, 568
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/178, 973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-751-797-7
Query Match 100.0%; Score 1119; DB 10; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1.5e-222;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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661 TGGAGCTTTTACTAAG 720
721 ATGAAACCTGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
721 ATGAAACCTGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
781 GACTTGATTAACAAG 840
781 GACTTGATTAACAAG 840
841 AAATTAAGTACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
841 AAATTAAGTACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
841 AAATTAAGTACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
901 AGCTTAAGTACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
901 AGCTTAAGTACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
961 GTATACATTTATTTATGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
961 GTATACATTTATTTATGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
1021 TATGATATTTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1021 TATGATATTTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
1081 TTAGGCTTTAATAAACAATGATATCAATAAAGAGAGAGAGAGAGAGAGAGAGAG 1119
1081 TTAGGCTTTAATAAACAATGATATCAATAAAGAGAGAGAGAGAGAGAGAGAGAG 1119
1081 TTAGGCTTTAATAAACAATGATATCAATAAAGAGAGAGAGAGAGAGAGAGAGAG 1119

RESULT 2
US-10-084-298-3
; Sequence 3, Application US/10084298
; Publication No. US20030099649A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth

APPLICANT: Pitman, Debra
APPLICANT: Fouser, Lynette
APPLICANT: Spaulding, Vikki
APPLICANT: Xuan, Dejun
TITLE OF INVENTION: Composition and Method for Treating Inflammatory
FILE REFERENCE: G1538 CIP
CURRENT APPLICATION NUMBER: US/10/084,298
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/270,823
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/281,353
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/131,473
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/561,811
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 1166
TYPE: DNA
ORGANISM: Murine
US-10-084-298-3

Query Match 99.0%; Score 1107.8; DB 15; Length 1166;
Best Local Similarity 99.4%; Pred. No. 3.2e-220;
Matches 1112; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

1 TAAACAGGCTCTCTCTCACTTATCACTGTGACACTTGGAGTCTGATGGCTGTC 60
24 TAAACAGGCTCTCTCTCACTTATCACTGTGACACTTGGAGTCTGATGGCTGTC 83
61 CTGAGAAATCTATGAGTTTTCCTTATGGGACCTTGGCCGACCTGCTCTC 120
84 CTGAGAAATCTATGAGTTTTCCTTATGGGACCTTGGCCGACCTGCTCTC 143
121 ATTGCCCTGTGGGCCGAGGAGCAATGCGCTGCCCTCAACACCCGGTGAAGCTTGAG 180
144 ATTGCCCTGTGGGCCGAGGAGCAATGCGCTGCCCTCAACACCCGGTGAAGCTTGAG 203
181 GTGTCCAACTTCCAGCAGCCGTACATGTCACACCGACCTTTATGTGGCCCAAGAGGCC 240
204 GTGTCCAACTTCCAGCAGCCGTACATGTCACACCGACCTTTATGTGGCCCAAGAGGCC 263
241 AGCCTTGCAATTAACAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
264 AGCCTTGCAATTAACAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323
301 AGTCTAAAGATCAGTGTACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
324 AGTCTAAAGATCAGTGTACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 383
361 CTGCTCCCCAGTCAGACAGGTTCCAGCCCTACATGAGAGAGGTGAGACCTTCTGACC 420
384 CTGCTCCCCAGTCAGACAGGTTCCAGCCCTACATGAGAGAGGTGAGACCTTCTGACC 443
421 AAATCTGACATCAGCTCAGCTCCTGTCAATCAGCGGTGACGACCAAGATCCAGAG 480
444 AAATCTGACATCAGCTCAGCTCCTGTCAATCAGCGGTGACGACCAAGATCCAGAG 503
481 AATGTCAAGAGCTGAG 540
504 AATGTCAAGAGCTGAG 563
541 ATTGGGAACTGAGACCTGCTGTTATGTCTGAGAAATGCTTGCCTGAGCAAGAGAG 600
564 ATTGGGAACTGAGACCTGCTGTTATGTCTGAGAAATGCTTGCCTGAGCAAGAGAG 623
601 AGCTAGAAAGAGAAAG 660
624 AGCTAGAAAGAGAAAG 683

QY 661 TGGACCTTTTACTAAAGAAAAGTGAAGGTAACGTCATCATGATTAGAAAGATTGAC 720
DB 684 TGGACCTTTTACTAAAGAAAAGTGAAGGTAACGTCATCATGATTAGAAAGATTGAC 743
QY 721 ATGAAACCTGAGCTCAGTTGAAAAGAAAATAGTGTCAAGTTGCCATGACAGAGGTA 780
DB 744 ATGAAACCTGAGCTCAGTTGAAAAGAAAATAGTGTCAAGTTGCCATGACAGAGGTA 803
QY 781 GACTTGATTAACCAAAATATTCATTGACAAATTTTATTGTGCTGATGATTAACAAGAA 840
DB 804 GACTTGATTAACCAAAATATTCATTGACAAATTTTATTGTGCTGATGATTAACAAGAA 863
QY 841 AAATATGATCTTAAATAAATTTGTTGAAGAGGTTCCCTCATCTCTTTAGAAAAA 900
DB 864 AAATATGATCTTAAATAAATTTGTTGAAGAGGTTCCCTCATCTCTTTAGAAAAA 923
QY 901 AGCTTATGTAATTCATTTCCATATCCAAATTTTATATATGTAAGTTATTTATTTATA 960
DB 924 AGCTTATGTAATTCATTTCCATATCCAAATTTTATATATGTAAGTTATTTATTTATA 983
QY 961 GTATACATTTTATTTATGTCAGTTTATTTAATATGATTTATTTATAGAAACATTATCTGC 1020
DB 984 GTATACATTTTATTTATGTCAGTTTATTTAATATGATTTATTTATAGAAACATTATCTGC 1043
QY 1021 TATGATTTTATGATTAAGCAAAATATTTATTTATGACATTAATCTGTAACCAAGATATC 1080
DB 1044 TATGATTTTATGATTAAGCAAAATATTTATTTATGACATTAATCTGTAACCAAGATATC 1103
QY 1081 TTAGGCTTTAATAAACACATGATATCATTAATAAAAAA 1119
DB 1104 TTAGGCTTTAATAAACACATGATATCATTAATAAAAAA 1142

RESULT 3
US-09-751-797-9
; Sequence 9, Application US/09751797
; Patent No. US20010024652A1
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louchet, Jamila
; APPLICANT: Renaud, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
; TITLE OF INVENTION: (Tfirs) The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.2
; CURRENT FILING DATE: US/09/751.797
; PRIOR FILING DATE: 2000-12-29
; PRIOR FILING DATE: 1999-10-18
; PRIOR FILING DATE: 1998-10-26
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 9
; LENGTH: 1111
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
US-09-751-797-9

Query Match 93.6%; Score 1047.8; DB 10; Length 1111;
Best Local Similarity 97.0%; Pred. No. 9e-208;
Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 3 AACAGGCTCTCTCTCACTTATCACTGTGACACTTGTGCGATCTGTAGTGGCTGTCT 62
DB 1 AACAGGCTCTCTCTCACTTATCACTTTTGACACTTGTGCGATGTGAGATGGCTGTCT 60
QY 63 GCAGAAATCTATGAGTTTTCCTTATGAGGACTTTGGCCGCGAGCTGCTGCTTCTCAT 122
DB 61 GCAGAAATCTATGAGTTTTCCTTATGAGGACTTTGGCCGCGAGCTGCTGCTTCTCAT 120
QY 123 TGGCCTGTGGGCGCCGAGAGCAAAATGCGCTGCGGTCAACACCGGGTGCAGAGCTTGAGCT 182
DB 121 TGGCCTGTGGGCGCCGAGAGCAAAATGCGCTGCGGTCAACACCGGGTGCAGAGCTTGAGCT 180

QY 183 GTCCAACTTCCAGAGCCGTTACATGCTCAACCGGACCTTTATGCTGGCCAAAGAGGCCAG 242
DB 181 GTCCAACTTCCAGAGCCGTTACATGCTCAACCGGACCTTTATGCTGGCCAAAGAGGCCAG 240
QY 243 CCTTGAGATTAACAACAGAGCGTCCGGCTCATGCGGAGAGAACTGTTCCGAGAGTCCAG 302
DB 241 CCTTGAGATTAACAACAGAGCGTCCGGCTCATGCGGAGAGAACTGTTCCGAGAGTCCAG 300
QY 303 TGGTAAAGATCACTGCTACCTGATGAAGCAGGTGCTCACTTCAACCTGGAAGAGCTTCT 362
DB 301 TGGTAAAGATCACTGCTACCTGATGAAGCAGGTGCTCACTTCAACCTGGAAGAGCTTCT 360
QY 363 GCTCCCCAGTCAACAGAGTTCAGCCCTTACATGACAGAGGTGTACTTCTTGACCAA 422
DB 361 GCTCCCCAGTCAACAGAGTTCAGCCCTTACATGACAGAGGTGTACTTCTTGACCAA 420
QY 423 ACTGAGCAATGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
DB 421 ACTGAGCAATGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 483 TGTGAGAGGCTGAG 542
DB 481 TGTGAGAGGCTGAG 540
QY 543 TGGGGAACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
DB 541 TGGGGAACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 603 CTAGAAACGAG 662
DB 601 CTAGAAACGAG 660
QY 663 GACTTTTCTTAAAG 722
DB 661 GACTTTTCTTAAAG 720
QY 723 GAAACCTGCTCAGTTGAAAAAGAAAATAGTGTCAAGTTGTCCATGAGACCAAGAGTGA 782
DB 721 GAAACCTGCTCAGTTGAAAAAGAAAATAGTGTCAAGTTGTCCATGAGACCAAGAGTGA 780
QY 783 CTGATTAACCAAG 842
DB 781 CTGATTAACCAAG 840
QY 843 ATATGACTTTTAAAG 902
DB 841 ATATGACTTTTAAAG 900
QY 903 CTATGTAACCTTCACTTCAATATCAATATTTATATATGATTAAGTTATTTATTTATTAAGT 962
DB 901 CTATGTAACCTTCACTTCAATATCAATATTTATATATGATTAAGTTATTTATTTATTAAGT 960
QY 963 ATATATTTTATTTATGAG 1022
DB 961 ATATATTTTATTTATGAG 1020
QY 1023 TTGATATTTT-AGTAAAGCAAAATATATTTATTTATGACATTAAGTGAAGCAAGATATCT 1081
DB 1021 TTGATATTTT-AGTAAAGCAAAATATATTTATTTATGATTAAGTGAAGCAAGATATCT 1080
QY 1082 TAGGCTTTAATAAACACATGATATCATTA 1112
DB 1081 TAGGCTTTAATAAACACATGATATCATTA 1111

RESULT 4
US-10-090-365-40
; Sequence 40, Application US/10090365
; Publication No. US2003007706A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng

APPLICANT: Kindsvogel, Wayne
 APPLICANT: Chen, Zhi
 TITLE OF INVENTION: Mouse Cytokine Receptor
 FILE REFERENCE: 01-08
 CURRENT APPLICATION NUMBER: US/10/090,365
 PRIOR FILING DATE: 2002-03-04
 PRIOR APPLICATION NUMBER: US 60/273,035
 PRIOR FILING DATE: 2001-03-02
 PRIOR APPLICATION NUMBER: US 60/279,232
 PRIOR FILING DATE: 2001-03-27
 NUMBER OF SEQ ID NOS: 49
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 40
 LENGTH: 1050
 TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (50) ... (589)
 US-10-090-365-40

Query Match 88.8%; Score 993.2; DB 15; Length 1050;
 Best Local Similarity 97.2%; Pred. No. 1.9e-196;
 Matches 1021; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

QY 3 AACAGGCTCTCTCTCACTTATCACTGTGACACTTGTGCGATCTCTGATGGCTGCT 62
 DB 1 AACAGGCTCTCTCTCACTTATCACTTGTGACACTTGTGCGATCTCTGATGGCTGCT 60
 QY 63 GCAGAAATCTATGATTTTTCCTTATGCGGACCTTGTGCGGACGCTGCTCTCTCAT 122
 DB 61 GCAGAAATCTATGATTTTTCCTTATGCGGACCTTGTGCGGACGCTGCTCTCTCAT 120
 QY 123 TGGCTGTGGGCGCCAGAGGCAAAATGCGCTGCGCCGCAACCCCGGTGAAGCTTGAAGT 182
 DB 121 TGGCTGTGGGCGCCAGAGGCAAAATGCGCTGCGCCGCAACCCCGGTGAAGCTTGAAGT 180
 QY 183 GTCCAACTTCCAGACGCGTACATCGTCAACCGCACTTATGCTGGCCAGAGGCGCAG 242
 DB 181 GTCCAACTTCCAGACGCGTACATCGTCAACCGCACTTATGCTGGCCAGAGGCGCAG 240
 QY 243 CCTTGAGATTAACAACACAGACGCTCGGCTCATCGGGAGAAACCTGTTCCGAGAGTCAG 302
 DB 241 CCTTGAGATTAACAACACAGACGCTCGGCTCATCGGGAGAAACCTGTTCCGAGAGTCAG 300
 QY 303 TGGTAAAGTCACTGCTACCTGATGAGAGAGGCTCACTTCAACCTGGAAGAGCTTCT 362
 DB 301 TGGTAAAGTCACTGCTACCTGATGAGAGAGGCTCACTTCAACCTGGAAGAGCTTCT 360
 QY 363 GCTCCCCAGTCAGACGAGTTCAGGCGCTACATGACAGAGGTGGTACCTTCTCTGACCA 422
 DB 361 GCTCCCCAGTCAGACGAGTTCAGGCGCTACATGACAGAGGTGGTACCTTCTCTGACCA 420
 QY 423 ACTGACCAATCACTGCTGCTGTCATCATGACGCGGTGACGACAGAGCAATCCAGAGAA 482
 DB 421 ACTGACCAATCACTGCTGCTGTCATCATGACGCGGTGACGACAGAGCAATCCAGAGAA 480
 QY 483 TGTCAAGAGTGAAGAGAGAGAGTGAAGAACTTGAAGAGAGTGAAGAGTCAAGGCGAT 542
 DB 481 TGTCAAGAGTGAAGAGAGAGAGTGAAGAACTTGAAGAGAGTGAAGAGTCAAGGCGAT 540
 QY 543 TGGGAACTGACCTGCTGTTATGCTCTGAGAAATGCTTGGCTGAGCGAGAGAG 602
 DB 541 CGGGGAATGACCTGCTGTTATGCTCTGAGAAATGCTTGGCTGAGCGAGAGAG 600
 QY 603 CTAGAAAAGAGAACTGCTCTTCTGCTTCTTAAAGAAAGCAATTAAGATCCCTGAATG 662
 DB 601 CTAGAAAAGAGAACTGCTCTTCTGCTTCTTAAAGAAAGCAATTAAGATCCCTGAATG 660
 QY 663 GACTTTTATCTAAGAGAAAGTGAAGAGTGAAGTCAATGATCATTTAGAGAGATTTGACAT 722
 DB 661 GACTTTTATCTAAGAGAAAGTGAAGAGTGAAGTCAATGATCATTTAGAGAGATTTGACAT 720

QY 723 GAAACTGGCTCACTTGAAAAAGAAATAGTGTCAAGTTGCTCCATGAGACCGAGAGTGA 782
 DB 721 GAAACTGGCTCACTTGAAAAAGAAATAGTGTCAAGTTGCTCCATGAGACCGAGAGTGA 780
 QY 783 CTGTATACCAACCAAGAGTTCATGCAATATTTATGTCATGATGATACAGAGAAA 842
 DB 781 CTGTATACCAACCAAGAGTTCATGCAATATTTATGTCATGATGATACAGAGAAA 840
 QY 843 ATATGACTTTAAAAATTTGTTGAAAGAGTTACCTCTCATCTCTTGAAGAAAAAG 902
 DB 841 AGTATGACTTTAAAAATTTGTTGAAAGAGTTACCTCTCATCTCTGAAGAAAAAG 900
 QY 903 CTATGTAATCTTCACTTCCATATCCATATTTTATATATGTAAGTTATTTATTAAGT 962
 DB 901 CCTATGTAATCTTCACTTCCATATCCATATTTTATATATGTAAGTTATTTATTAAGT 960
 QY 963 ATACATTTATTTATGATGAGTTATTTATGATGATTTATTTATGAAACATTAATGCTGA 1022
 DB 961 ATACATTTATTTATGATGAGTTATTTATGATGATTTATTTATGAAACATTAATGCTGA 1020
 QY 1023 TTGATATTT-AGTATTAAGCAAAATATATTT 1051
 DB 1021 TTGATATTTGAGTATTAAGCAAAATATATTT 1050

RESULT 5
 US-10-104-919-42
 Sequence 42, Application US/10104919
 Publication NO. US20030099608A1
 GENERAL INFORMATION:
 APPLICANT: Presnell, Scott R.
 APPLICANT: Xu, Wenfeng
 APPLICANT: Kindsvogel, Wayne
 APPLICANT: Chen, Zhi
 APPLICANT: Hughes, Steven D.
 TITLE OF INVENTION: Human Cytokine Receptor
 FILE REFERENCE: 01-12
 CURRENT APPLICATION NUMBER: US/10/104,919
 PRIOR FILING DATE: 2002-03-23
 PRIOR APPLICATION NUMBER: US 60/279,222
 PRIOR FILING DATE: 2001-03-27
 NUMBER OF SEQ ID NOS: 62
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 42
 LENGTH: 1050
 TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (5) ... (589)
 US-10-104-919-42

Query Match 88.8%; Score 993.2; DB 15; Length 1050;
 Best Local Similarity 97.2%; Pred. No. 1.9e-196;
 Matches 1021; Conservative 0; Mismatches 28; Indels 1; Gaps 1;

QY 3 AACAGGCTCTCTCTCACTTATCACTGTGACACTTGTGCGATCTCTGATGGCTGCT 62
 DB 1 AACAGGCTCTCTCTCACTTATCACTTGTGACACTTGTGCGATCTCTGATGGCTGCT 60
 QY 63 GCAGAAATCTATGATTTTTCCTTATGCGGACCTTGTGCGGACGCTGCTCTCTCAT 122
 DB 61 GCAGAAATCTATGATTTTTCCTTATGCGGACCTTGTGCGGACGCTGCTCTCTCAT 120
 QY 123 TGGCTGTGGGCGCCAGAGGCAAAATGCGCTGCGCCGCAACCCCGGTGAAGCTTGAAGT 182
 DB 121 TGGCTGTGGGCGCCAGAGGCAAAATGCGCTGCGCCGCAACCCCGGTGAAGCTTGAAGT 180
 QY 183 GTCCAACTTCCAGACGCGTACATCGTCAACCGCACTTATGCTGGCCAGAGGCGCAG 242
 DB 181 GTCCAACTTCCAGACGCGTACATCGTCAACCGCACTTATGCTGGCCAGAGGCGCAG 240
 QY 243 CCTTGAGATTAACAACACAGACGCTCGGCTCATCGGGAGAAACCTGTTCCGAGAGTCAG 302

RESULT 6
 US-09-751-797-8
 ; Sequence 8, Application US/09751797
 ; Patent No. US20010024652A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumoutier, Laure
 ; APPLICANT: Louboud, Jamila
 ; APPLICANT: Renaud, Jean-Christophe
 ; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
 ; TITLE OF INVENTION: (Tlrs) The Proteins Encoded, and Uses Thereof
 ; FILE REFERENCE: LUD 5543.2
 ; CURRENT APPLICATION NUMBER: US/09/751,797
 ; PRIORITY FILING DATE: 2000-12-29
 ; PRIOR APPLICATION NUMBER: 09/419,568
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: US09/178,973
 ; PRIOR FILING DATE: 1998-10-26

Query Match	53.7%	Score 601.4;	DB 10;	Length 7445;
Best Local Similarity	99.8%;	Pred. No. 1.1e-114;		
Matches 602; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	510	AAACCTTGAGAGAGTGGAGAGATCAAGGCGATTGGGAACTGGACCTGCTGTTTATATGTC	569
Db	6535	ATACCTTGGAAGAGTGGAGAGATCAAGGCGATTGGGAACTGGACCTGCTGTTTATATGTC	6594
QY	570	TCTGAGAAATCTTGCGCTGACGCGAGAAAGCTAGAAAAACGAAGACCTGCTCTTCTCT	629
Db	6595	TCTGAGAAATGCTTGCGCTGACGCGAGAAAGCTAGAAAAACGAAGACCTGCTCTTCTCT	6655
QY	630	GCCCTTCTPAAAAAGAACATTAAGATCCCTGAATGGACTTTTCTTAAAGAAAGTGAGAA	689
Db	6655	GCCCTTCTPAAAAAGAACATTAAGATCCCTGAATGGACTTTTCTTAAAGAAAGTGAGAA	6714
QY	690	GCTAAGCTCCATCATCTTGAAGAATTCCATGAACCTGGCTCAGTTGAAAAAGAAA	749
Db	6715	GCTAAGCTCCATCATCTTGAAGAATTCCATGAACCTGGCTCAGTTGAAAAAGAAA	6774
QY	750	TAGTGTCAAGTTGTCCATGAGACGAGAGGTAGACTTGATTAACAAGATTCATTGACA	809
Db	6775	TAGTGTCAAGTTGTCCATGAGACGAGAGGTAGACTTGATTAACAAGATTCATTGACA	6833
QY	810	ATATTTTATGTGCACTGATGATTAACAAGAAAAATAATGTACTTTAAAAAATTTGTTTGA	869
Db	6835	ATATTTTATGTGCACTGATGATTAACAAGAAAAATAATGTACTTTAAAAAATTTGTTTGA	6894
QY	870	AGAGAGTTACCTCATCTTCCTTTGAAAAAAAAGCTTAATGTACTTCATTTCCATATCCA	929
Db	6895	AGAGAGTTACCTCATCTTCCTTTGAAAAAAAAGCTTAATGTACTTCATTTCCATATCCA	6955
QY	930	TATTTTATATATGTAAGTTATTTATTAATAAGTATACATTTTATTTATGTCAGTTATTA	989
Db	6955	TATTTTATATATGTAAGTTATTTATTAATAAGTATACATTTTATTTATTTATGTCAGTTATTA	7014
QY	990	ATATGATTTATTTATTAAGAAACCTATCTGTATGTAATTTAGTATTAAGGCAATATA	1049
Db	7015	ATATGATTTATTTATTAAGAAACCTATCTGTATGTAATTTAGTATTAAGGCAATATA	7074
QY	1050	TTTATGACAAATTAATGAGAAACAAAGATATCTTAGGCTTTAATTAACACATGATATCAT	1109
Db	7075	TTTATGACAAATTAATGAGAAACAAAGATATCTTAGGCTTTAATTAACACATGATATCAT	7134
QY	1110	AAA 1112	
Db	7135	AAA 7137	

```

US-09-751-797-29
: Sequence 29, Application US/09751797
: Patent No. US20010024652A1
: GENERAL INFORMATION:
: APPLICANT: Dumontier, Laure
: APPLICANT: Louhed, Jamila
: APPLICANT: Renaud, Jean-Christophe
: TITLE OF INVENTION: Isolated Nucleic Acid Molecules which
: TITLE OF INVENTION: (TIFs) The Proteins Encoded, and r
: FILE REFERENCE: LUD 5543.2
: CURRENT APPLICATION NUMBER: US/09/751,797
: CURRENT FILING DATE: 2000-12-29
: PRIOR APPLICATION NUMBER: 09/419, 568
: PRIOR FILING DATE: 1999-10-18
: PRIOR APPLICATION NUMBER: US09/178, 973

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us-09-751-797-7.rnpb

Query Match	49.6%;	Score 555.2;	DB 10;	Length 5935;
Best Local Similarity	96.0%;	Pred. No. 3.6e-105;		
Matches 580;	Conservative 0;	Mismatches 23;	Indels 1;	Gaps 1;

QY	510	AAACCTTGAGAGAGTGGAGAGATCAAGCCATTGGGGAACTGGACCTGCTTTATATGC	569
Db	5221	ATAGCTTGAGAGAGCCGAGAGATCAAAAGCCATCCGGGAACTGGACCTGCTTTATATGC	5288
QY	570	TCGTGAAATGCTTCGCTGCTTGAAGCGAGAAAGACTTGAAGAACTGCTCTCTCT	629
Db	5281	TCGTGAAATGCTTCGCTGCTTGAAGCGAGAAAGACTTGAAGAACTGCTCTCTCT	5340
QY	630	GCCTTCTTAAAGAAACAATAAGATCCCTGAATGCACTTTTACTTAAGAAAGAGAGAA	689
Db	5341	GCCTTCTTAAAGAAACAATAAGATCCCTGAATGCACTTTTACTTAAGAAAGAGAGAA	5400
QY	690	GCTAACGTCACATCATATTAGAAAGATTCAACATGAAACCTGGCTCAGTTGAAAAAGAAA	749
Db	5401	GCTAACGTCACACATCATATTAGAAAGATTCAACATGAAACCTGGCTCAGTTGAAAAAGAAA	5466
QY	750	TAGTGTCAAGTTGTCATGAGACCAAGAGTGAATTGATTAACCAAAAGATTCAATTGCA	809
Db	5461	TAGTGTCAAGTTGTCATGAGACCAAGAGTGAATTGATTAACCAAAAGATTCAATTGCA	5522
QY	810	ATATTTTATGTCACGTGATGATACACAGAAAAAATAAGTACTTTAAAAAATTGTTGAA	869
Db	5521	ATATTTTATGTCACGTGATGATTAATGCAACAGAAAAAATAAGTACTTTAAAAAATTGTTGAA	5580
QY	870	AGGAGGTACCTCATCATCTCTTGAAGAAAAAAGCTTATGTAACCTCATTTCCATATCCAA	929
Db	5581	AGGAGGTACCTCATCATCTCTCTTGAAGAAAAAAGCTTATGTAACCTCATTTCCATATCCAA	5644
QY	930	TATTTTATATAAGTAAGTTTATTTATTAATAAGATATACATTTTATTTATGTCAGTTATTA	989
Db	5641	TATTTTATATAAGTAAGTTTATTTATTAATAAGATATATTTATTTATGTCAGTTATTA	5700
QY	990	ATATGATTTTATTTATTAAGAAACATATCTGATATGATATTT-AGTATTAAGCAATAT	1044
Db	5701	ATATGATTTTATTTATTAAGAAATTTATCTGATATGTAATTTAGATATTAAGCAATATAT	5766
QY	1049	ATTATGACATTAACCTATGAGAAACAAGATATCTTAGGCTTATTAATAACACATGATATCA	1108
Db	5761	ATTATGATTAATTAACCTATGAGAAACAAGATATCTTAGGCTTATTAATAACACATGATATCA	5822
QY	1109	TAAA 1112	
Db	5821	TAAA 5824	
RESULT 8			
US-10-084-298-1			
; Sequence 1, Application US/10084298			
; Publication No. US20030099649A1			
; GENERAL INFORMATION:			
; APPLICANT: Jacobs, Kenneth			
; APPLICANT: Pittman, Debra			
; APPLICANT: Fouser, Lynette			
; APPLICANT: Spaulding, Vikki			
; APPLICANT: Xuan, Dejun			
; TITLE OF INVENTION: Composition and Method for Treating Inflammatory			
; FILE REFERENCE: G1538 CIP			
; CURRENT APPLICATION NUMBER: US/10/084,298			
; CURRENT FILING DATE: 2002-09-10			

Query Match	47.8%;	Score 535.2;	DB 15;	Length 119;
Best Local Similarity	73.4%;	Pred. NO. 2.3e-101;		
Matches 843;	Conservative 0;	Mismatches 268;	Indels 37;	Gaps 11

OY	9	CTCTCCCTCACTTATCAACGTTTGACACCTGTGGATCTGTGATGGCTGCTGCACAAA	68
Db	28	CTCCCTCCCAAGTCAACAGTGTCTCGAATTGTCTCGAATGGCCGCCCTGCAGAA	87
OY	69	ATCTAATAGATTTTCCCTTATGGGAGCTTGGCCGACAGTGCCTGCTTCTCATTCGCCCT	128
Db	88	ATCTGTAGAGCTCTTCTTATGGGGAACCTGAGCACAGCTGCCCTTCTCTTGGCCCT	147
OY	129	GTGGGCCCAAGAGCAAATGCGCTGCGCCGTCAACACCCGGTGCAGAGCTTGAAGTCCAA	188
Db	148	CTTGGTACAGGAGAGAGAGAGCGTGGGCCATCAGCTCCACATGCAAGCTTGACMAATCCAA	207
OY	189	CTTCAGAGAGCGGTACATCTGTCAACCCGACCTTTATGCTGGCAAGAGGACAGCCTTGC	248
Db	208	CTTCAGAGAGCGCTTATATACCAACCGACCTTCACTGTGGCTAAGAGGCTAAGCTTGGC	267
OY	249	AGATTAACAACAAGACGTCGCGGCTCATGGGAGAGAACTGTTCCAGAGAGTCAAGTCTAA	308
Db	268	TGATTAACAACAAGACGTTGCTGTCAATTGGGAGAGAACTGTTCCAGGAGTCAATATAG	327
OY	309	AGATCAGTGTCTAAGTGAAGACAGGTGCTCACTTCAACCTGGAAGAGCTTGTCTCCC	368
Db	328	TGACGCGTGTATGTGAAGACAGGTGCTCACTTCAACCTTGAAGAGGTGCTTCTCCC	387
OY	369	CCAGTCAAGACAGGTTCCAGCCCTCATGACAGAGGTGTACCTTCTGTACCAAACTCAG	428
Db	388	TCAATCTGTATGTTTCCAGCTTATATGCAAGAGGTGTGCTTCTTCTGCGCAAGCTCAG	447
OY	429	CAATCAGCTCAGCTCCTGTCAATCAGCGGTGACGACCAAGAACATCCAGAAATGTCCAG	488
Db	448	CAACAGGTAAGACATGTCTATTTGAAGTGTGATGACCTGTCAATCCAGAGAAATGTGA	507
OY	489	AAGCTGAAGAGACAGTGAAGAAAGCTTGGAGAGATGGAAGATCAAGCGCATTTGGGGA	548
Db	508	AAACGTGAAGACACAGTGAAGAAAGCTTGGAGAGTGAAGATCAAAAGCAATTGGAGA	567
OY	549	ACTGGAAGCTGTGTTATATGCTCGAGAAATGCTTGGCTGAGCGGAAGAAGAGCTAGAA	608
Db	568	ACTGGAATTTGCTGTTTATGTCTCTGAGAAATGCTCTGACTTTGGACCAAGCAAGCTGAAA	627
OY	609	AACGAGAAGTGTCTCTCTCTCTTAAAGAACATATAGATCCTGAAATGGACTTT	668
Db	628	AATGATATATACACCCCTTCCCTGCTAAGAAATACATATAGATGCCCAAGAGGATTT	687
OY	669	TTTA-----CTTAAAGAAAGTGAAGAGCTAACGTCTCATATCATTTAAGAAATTTTCAATGA	724
Db	688	TTTTTAAACAAAAGAAAGATGGGAAGCCMAACTCATCATATATGGGTGATTTCCAAATGA	747
OY	725	AACGTGGCTAGTTGAAGAAAGAAATATGTCAA--GTTGTCCATGAGACAG--AGTAG	781
Db	748	ACCCTGCTTATGTTACAAAGAAACCAATGCCACTTTTGTTTATTAAGACCAAGAGGTAG	807
OY	782	ACTGTATTAACAACAAGATTCATTGACAAATATTTATATTGTCACTGAG-----ATTAACA	837

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Db      808 ACTTCCAGACGATGATTTATGATACATTTTCATGTAAGTGTTCTATACACAG 867
Qy      838 GAAAAATATGACTTTAAAAATTTT-----GAAGAGGTTACTTCTCATTTCT 890
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Qy      891 TTA---GAAAAAGCTATGTAAGTCA--TTTCCATATCCATATTTTATATATGTA 945
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Qy      946 GTTATTTATATATAGATA-----CATTTATTTATGTCAGTTTATATATAGATTT 999
Db      988 ATGATTTATATATATATATAGATGATGATTTTATTTATATATATATATAGATTT 1047
Qy      1000 ATTATAGAAACATTATCTGCTATGATA--TTAGATATAGGCAATA--ATATTTATG 1055
Db      1048 ATTATAGAAACATTCATTCATGATTTGCTACTGATGATGATGATGATGATGATG 1107
Qy      1056 ACAATTAATATAGCTATATACATGTTATTTGACCTCAATATAACATTTGATATCTTA 1167
Db      1108 ACAATTAATATAGCTATATACATGTTATTTGACCTCAATATAACATTTGATATCTTA 1167
Qy      1112 AAAAAAA 1119
Db      1168 AAAAAAA 1175

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RESULT 9

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US-09-870-574-1
; Sequence 1, Application US/09870574
; Patent No. US2002010273A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Austen L.
; APPLICANT: Aggarwal, Sudeepa
; APPLICANT: Xie, Ming-Hong
; APPLICANT: Maruoka, Ellen M.
; APPLICANT: Foster, Jessica S.
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: INTERLEUKIN-22 POLYPEPTIDES, NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: THE SAME AND METHODS FOR THE TREATMENT OF PANCREATIC DISORDERS
; FILE REFERENCE: P2806-1(US)
; CURRENT APPLICATION NUMBER: US/09/870, 574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/169,495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 1
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-870-574-1

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Query Match      46.9%; Score 524.8; DB 11; Length 1152;
Best Local Similarity 73.2%; Pred. No. 3.3e-99;
Matches 832; Conservative 0; Mismatches 267; Indels 37; Gaps 11;

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Qy      9 CTCTCTCTCACTATCAACTGTGACACTGTGAGATCTGATGGCTGTCTGACAGAA 68
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Qy      69 ATCTATGATTTTTCCTTATAGGAGACTTTGGCCGCAAGCTGCTGCTTCTCATTTGCCCT 128
Db      75 ATCTGTGAGCTCTTCTTATAGGAGACCTTGGCCACCAAGCTGCTTCTTCTTGGGCGCT 134
Qy      129 GTGGGCGGAGAGGAAATGCGTGGCCGCTCAACACCGGCGGAAGCTTGAAGGTGCA 188
Db      135 CTGTGTACAGGAGAGAGAGCTGCGCCCATACGCTCCCACTGACAGGCTTGAAGTCA 194

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Qy      189 CTTCAGAGCGGACATGATGCAACGACACCTTTATGCTGAGCCAGAGGCGACGCTTGC 248
Db      195 CTTCAGAGCGGACATGATGCAACGACACCTTTATGCTGAGCCAGAGGCGACGCTTGC 254
Qy      249 AGATAACAACAAGACGCTCGGCTCATCGGAGAGAACTGCTTCCGAGAGTCAAGTGTAA 308
Db      255 TGATTAACAACAAGACGCTCGGCTCATCGGAGAGAACTGCTTCCGAGAGTCAAGTGTAA 314
Qy      309 AGATCACTGCTACCTGATGAGAGAGGTCCTCAACCTTCAACCTGAGAGGCTTGTCTCC 368
Db      315 TGAGCGCTGCTATGATGAGAGAGGTCCTCAACCTTCAACCTGAGAGGCTTGTCTCC 374
Qy      369 CCACTGACAGAGGTCCTGACGCTTCAATGACAGAGGTCCTTCTTCTGACCAACCTGAC 428
Db      375 TCATCTGAATAGGTCCTGACGCTTCAATGACAGAGGTCCTTCTTCTGACGCTGAC 434
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Qy      489 AAGCTGAAGAGAGACAGTGAAGAAAGCTTGAAGAGAGTGAAGATCAAGGCGATTTGGGA 548
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Db      615 AATGAATTAATCAACCCCTTCTGCTGAAGAAATTAAGTCCCTGAATGACCTT 674
Qy      669 TTTA---CTAAGAGAAAGTGAAGTAAAGTCAATGCTCATCATATAGAAATTTCAATGA 724
Db      675 TTTTAAACCAAGAGAGAGAGAGAGGCAATCTCATCATATGATGATGATGATGATGATG 734
Qy      725 AACCTGCTGATGAAAAAGAAATATGTCAT--GTTGTCATGAGACAG--AGGTAG 781
Db      735 ACCCTGCTGATGAAAAAGAAATATGTCAT--GTTGTCATGAGACAG--AGGTAG 794
Qy      782 ACTGATTAACCAAAATTCATGACAAATTTTATGTCACGAG---ATACACA 837
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Qy      838 GAAAAATATGATTAATAAAATTTGTT-----GAAAGAGGTTACCTGATTCCT 890
Db      855 AAAACAATTTATTTTAAATTAATGCTTTTCCATTAATAAAAGATTAATTCATTCCT 914
Qy      891 TTA---GAAAAAGCTTATGTAAGTCA--TTTCCATATCCATATTTATATATGTA 945
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RESULT 10

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US-10-063-588-153
; Sequence 153, Application US/10063588
; Publication No. US20030130483A1
; GENERAL INFORMATION:
; APPLICANT: Bacon, Dan L.
; APPLICANT: Filvaroff, Ellen

```

APPLICANT: Gettisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT FILING DATE: 2002-05-03
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-588-153

Query Match 46.9%; Score 524.8; DB 14; Length 1152;
Best Local Similarity 73.2%; Pred. No. 3.3e-99;
Matches 832; Conservative 0; Mismatches 267; Indels 37; Gaps 11;

QY 9 CTCCTCTCTCACTATATCACTGTGACACTGTGGGATCTCTGATGCTGTCTGACAGAA 68
DB 15 CTCCTCTCTCACTATATCACTGTGACACTGTGGGATCTCTGATGCTGTCTGACAGAA 74
QY 69 ATCTATGATTTTCCCTTATGAGGACCTTGGCCGCCAGCTGCTCTTCTCATTTGCCCT 128
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QY 129 GTGGGCCAGAGAGGAAAGCGCTGCGCCGTCACACCCGCGTCAAGCTTGAAGTGTCCAA 188
DB 135 CTGTGTACAG 194
QY 189 CTTCAGAGAGCGGTACATCTGTCACCGGACCTTTATGCTGCGCAAGAGAGAGAGAG 248
DB 195 CTTCAGAGAGCGGTATATCACCAACCGGACCTTTATGCTGCGCTAAGAGAGAGAGAG 254
QY 249 AGATTAACAACAAG 308
DB 255 TGATTAACAACAAG 314
QY 309 AGATCAGTCTACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368
DB 315 TGAAGGCTGTATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
QY 369 CCACTCAGACAG 428
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QY 1056 ACAATTAATGAG 1107
DB 1095 ACAATTAATTAAG 1150

RESULT 11
US-10-006-867-153
Sequence 153, Application US/10006867
Publication No. US20020119130A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gettisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/063435
PRIOR FILING DATE: 1997-10-29
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 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: PCT/US98/19093
 PRIOR FILING DATE: 1998-09-14
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: PCT/US98/19437
 PRIOR FILING DATE: 1998-09-17
 PRIOR APPLICATION NUMBER: PCT/US98/24855
 PRIOR FILING DATE: 1998-11-20
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: 1998-12-01
 PRIOR APPLICATION NUMBER: PCT/US98/25130
 PRIOR FILING DATE: 1998-11-25
 PRIOR APPLICATION NUMBER: PCT/US99/05028
 PRIOR FILING DATE: 1999-03-08
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: 1999-06-02
 PRIOR APPLICATION NUMBER: PCT/US99/20111
 PRIOR FILING DATE: 1999-09-01
 PRIOR APPLICATION NUMBER: PCT/US99/20594
 PRIOR FILING DATE: 1999-09-08

;; PRIOR APPLICATION NUMBER: PCT/US99/210900
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/215477

Query Match	46.9%	Score 524.8;	DB 15;	Length 1152;
Best Local Similarity	73.2%	Pred. No. 3.3e-99;		
Matches 832;	Conservative	0;	Mismatches 267;	Indels 37;
				Gaps 11;

QY	9	CTCTCCCTCTCACTTATCAACGTTTACACTGTGGATCTCTGAATGGCTCTCCAGAA	68
Db	15	CTCCCTCCCAAGTCAACGATGCTCGAGTTAGAAATTGCTTGCAAATGGCCGCTCAGAA	74
QY	69	ATCTATGAGTTTTTCCCTTATGGGACCTTTGGCCGCGACGCTGCTTCTATGTCCT	128
Db	75	ATCTGTGAGCTCTTTCCTTATGGGAGCCCTGGCCACAGCTGCTCTCTTCTTGGCCCT	134
QY	129	GTGGGCCAGGAGGCGAAATGGCGCTCCCGTCAACACCCGGTGCAGCTTGAGTGGCAA	188
Db	135	CTTGGTACAGGGAGGAGCAGCTGGCCCAATACGCTTCCACTGAGGCTTGACAAAGTCCA	194
QY	189	CTTCAGAGAGCGGTACATCTGTCAACCGCACCTTTATGTCTGGCCAAAGAGCCGCTTGC	248
Db	195	CTTCAGAGAGCCCTTATATCAACCGCACCTTCAATGCTGGCTTAAGAGGCTATGCTGGC	254
QY	249	AGATAACAACACACAGCTCGGCTCATCGGGAGAACTGTTCCGAGAGTCACTGCTTAA	308
Db	255	TGATATAACAACACAGCTGCTCTCATTTGGGAGAACTGTTCCACGAGTCAATATGAG	314
QY	309	AGATACAGTCTACCTGATGAGACAGGTGCTCACTTCAACCGTGGAAAGGTTCTGTGCC	368
Db	315	TGAGGCGTGTATCTGATGAGACAGGTGCTGAATTCACCTTGAAGAGTGTGTTCC	374
QY	359	CCAGTCAAGCAGGTTCCAGCCCTCAATGACAGAGGTGTACTTCTCTGACCAAACTCAG	428
Db	375	TCAATCTGATAGGTTCCAGCTTATATGACAGAGGTGTGCTCTCTCTGCGACGCTCAG	434
QY	429	CAATCAGCTCAGCTCCTGTACATCAGCGGTGACGACCAAAATCCAGAAAGATGTCA	488
Db	435	CAACAGGCTTAACACATGTCATATTTGAAAGTATGACTGCTCATATCCAGAGGATGTGA	494
QY	489	AAGGCTGAAGGAGACAGTGA AAAAGCTTGGAGAGATGGAGAGATCAAGCCATTGGGA	548
Db	495	AAAGCTGAAGGAGACAGTGA AAAAGCTTGGAGAGATGGAGAGATCAAGCAATTTGGA	554
QY	549	ACTGGACGCTGTTATGCTCTGTGAAGATGCTTGTGCTGACGAGAAAGAAAGTATGAA	608
Db	555	ACTGGAATTTGCTGTTTATGCTCTGTGAAGATGCTTGTGCTGACGAGAAAGTATGAA	614
QY	609	AAAGAAATGCTGCTCTGCTTCTTAAAAAGAACATATAGATCCCTGAATGACTTT	668
Db	615	AAAGAAATGCTGCTCTCTGCTTCTTAAAAAGAACATATAGATCCCTGAATGACTTT	674
QY	669	TTTA---CTTAAAGAAAGTGAAGCTTACGTCATCATTAAGAATTTCAATGA	724
Db	675	TTTTTAAACCAAAAGGAATGGGAACCAATCCATCAAGATGGGATTCCTCAATGA	734
QY	725	AACTGGCTCAGTTGAAAAAGAAATAGTCA--GTGTCCATGAGACCA--AGGTAG	781
Db	735	ACCCCTGCGTTAGTTACAAAGAAACCAATGCCACTTTGTTTATTAAGACCAAGGTAG	794
QY	782	ACTGATTAACCAAAAGATTCATGACAATATTTTATGTCACTGATG---ATACACA	837
Db	795	ACTTCTAAGCATATGATTTATTTGATTAACATTTCAATTTGAATGGGTGCTCTATACAG	854
QY	838	GAAATTAATGTACTTTAAAAATTTGTT-----GAAAGAGGTACTCTCATCTCT	890
Db	855	AAAAACAATTAATTTTAAAAATATGTCTTTTCCATAAAAAGATTAATCTTCATTTCT	914
QY	891	TTA---GAAAAAAGCTTATGTAATCTCA--TTTCCATATCCAAATTTTATATATGTA	945
Db	915	TTAGGGGAAAAAACCCCTAATATGCTTCAAGTTTCCAAATATCAGTACTTTATATTTATA	974
QY	946	GTTTATTTATTAATAGATA-----CAITTTATTAATGACGTTTATTAATATGATTT	999

Db 975 ATGATTTATTTATTTATTAAGACTGATTTTATTTATTAACATTTTATTTATTAATGATTT 1034
 QY 1000 ATTATAGAAACATTATCTGCTATGTGTA TTTAGTAAAGGCAATA--ATATTTATG 1055
 Db 1035 ATTATATGAAACATTCATTCATATTTGCTACTGTGCTTAAGGCTTAATTTGATATTTATG 1094
 QY 1056 ACATTAAGCTATGCTTAATTAACACATGATATC 1107
 Db 1095 ACATTAATTAAGCTATTAACATGTTATTTATTTGACCTCAATTAACACATGATATC 1150

RESULT 13
US-10-063

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: Sequence 153, Application US/10063547
: Publication No. US2002018268A1
: GENERAL INFORMATION:
: APPLICANT: Eaton, Dan L.
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerltsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3230R1C1
: CURRENT APPLICATION NUMBER: US/10/063,547
: CURRENT FILING DATE: 2002-05-02
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 170
: SEQ ID NO 153
: LENGTH: 1152
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-063-547-153

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Query Match	46.9%	Score 524.8;	DB 15;	Length 1152;
Best Local Similarity	73.2%;	Pred. No. 3.3e-99;		
Matches 832;	Conservative 0;	Mismatches 267;	Indels 37;	Gaps 11

0Y	9	CTCTCTCTCACTTATCAACTGTTGACACTGTGGATCTCTGAAGGCTGTCACAGA	68
Db	15	CTCTCTCCCAAGTACCAAGTGTGCTGGAATTGAATGTCTGCAATGGCCGCTCAGAA	74
0Y	69	ATCTATGAGTTTTCCTTTATGGGACTTTGGCCGCCAGCTGCTTCTCATTTGCCCT	128
Db	75	ATCTGTGAGCTCTTCTTTATGGGACCTTGCCACAGACTGCTCTCTCTTTGGCCCT	134
0Y	129	GTGGGCCCCAGAGGCAAAATGCGCTGCCCCGTCAACAACCCGGTCCAGCTTGAGGTGCCAA	188
Db	135	CTTGTGTACAGGAGGAGGACGCTGCCCATCAGCTCCCATGCAAGCTTGACAAATGTC	194
0Y	189	CTTCAGAGCCGCTACATCGTCAACCGCAACCTTTATGGGCCAAGAGGAGCCTTGC	248
Db	195	CTTCAGAGCCCTTATATCACCAACCGACCTTCACTGTGGCTTAAAGAGGCTAAGCTTGGC	254
0Y	249	AGATTAACAACACAGACGTCGCGGCTCATCGGGAGGAACTGTTCGAGGAGTCACTGCTAA	308
Db	255	TGATTAACAACACAGACGTTTCGTTCTATTGGGGAGAACTGTTCCACGAGTCAGTATGAG	314
0Y	309	AGATCAAGTCTACTCTGATGAACAGAGTGTCTCAACTTCAACCTGGAAGACGTTTGTGCTCC	368
Db	315	TGAGGCGTCTATCTGATGAACAGAGTGTGAACCTTCAACCTTGAAGAAAGCTGTGCTCC	374
0Y	369	CCAGTCAAGACAGGTTCCAGCCCTCAATGACAGAGGTGTGTAACCTTTCTGACCAAACTCG	428
Db	375	TCAATCTGATAGGTTCCAGCCTTATATGAGGAGGAGGTGGCCCTTCTGGCCAGGCTCAG	434
0Y	429	CAATCAGCTCAGTCTCTGTCAATCAGCGGTGACCAAGAACCTCCAAAGAAATGTGAG	488

Db 425 CAACAGGCTAGACATGTCATATTGAAGTGATGACCTGCATATCCAGGAATGTGCA 494
 QY 489 AAGGCTGAAGGAGACAGTGAAGAAAGCTTGGAGAGATGAGATCAAGCGATGGGGA 548
 Db 495 AAACGTGAAGGACACAGTGAAGAAAGCTTGGAGAGATGAGATCAAGCAATTGGAGA 554
 QY 549 ACTGACCTGCTGTTTATGCTCTGAGAAATGCTTGGCTGAGCGAAGAAAGAGTAA 608
 Db 555 ACTGATTTGCTGTTTATGCTCTGAGAAATGCTTGGCTGAGCGAAGAAAGCTGAAA 614
 QY 609 AACGAGACAGTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 668
 Db 615 AATGAATACCTAACCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 674
 QY 669 TTTA---CTAAGAGAAAGTGAAGAGCTAACGCTCATCATCATTAAGAAATTCACATGA 724
 Db 675 TTTTAAACCAAG 734
 QY 725 AACCTGCTCAGTTGAAAAGAAAATAGTTCAA--GTTGTCATGAGAACAG--AGGTAG 781
 Db 735 ACCCTGCTGTTAGTTACAAAGAAAACAAATGCCACTTTGTTTATTAAGACAGAAAGGTAG 794
 QY 782 ACTGATTAACCAAG 837
 Db 795 ACTTCTTAGCATAGATATTATTTGATTAACATTTGATTTGATTTGATTTGATTTGAT 854
 QY 838 GAAAAATATGTAATTTTAAAAATTTT-----GAAAGAGGTTACCTCTCATTCCT 890
 Db 855 AAAACAATTTATTTTAAATTAATTTGCTTTTCCATAAAAAGATTACTTTCCATTCCT 914
 QY 891 TTA---GAAAAAGCTTATGTACTGA--TTTCCATATCCATATTTTATATATGTA 945
 Db 915 TTAGGGGAAAAAAGCCCTAAATAGCTCATGTTTCCATATCAGTACTTTATTTATTA 974
 QY 946 GTTATTTATATATAGTATA-----CATTTATTTATGAGTTATTAATATAGATTT 999
 Db 975 ATGTAATTTATTTATTTATTAAGACTGCATTTATTTATTAATCAATTTATTAATATGATTT 1034
 QY 1000 ATTTATGAACATTAATCTGCTATTTGATA--TTTAGTATAGGCAATA---ATATTTATG 1055
 Db 1035 ATTTATGAACATTAATCTGCTATTTGATA--TTTAGTATAGGCTATATTTGATTTATG 1094
 QY 1056 ACAATTAATATG---AACCAAGATATCTTAGGCTTTAATTAACATGATATC 1107
 Db 1095 ACAATTAATATAGAGCTATTAACATGTTTATTTGACCTCAATTAACATTTGATATC 1150
 RESULT 14
 US-10-063-616-153
 ; Sequence 153, Application US/10063616
 ; Publication No. US20030013855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gettisen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Matanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,616
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 153
 ; LENGTH: 1152
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-063-616-153

Query Match 46.94; Score 524.8; DB 15; Length 1152;
 Best Local Similarity 73.24; Pred. No. 3.3e-99;
 Matches 832; Conservative 0; Mismatches 267; Indels 37; Gaps 11;
 9 CTCCTCTCTCACTATCAACTGTGACACTGTGCGATCTCTGATGGCTGCTGCAAGA 68
 15 CTCCTCTCTCACTATCAACTGTGACACTGTGCGATCTCTGATGGCTGCTGCAAGA 74
 QY 69 ATCTATAGATTTTCCCTTATGGGACCTTTGGCCGACGCTGCTCTCTCATTCGCT 128
 Db 75 ATCTGATAGCTCTTCTCTTATGGGACCTTTGGCCGACGCTGCTCTCTCTGCTGCT 134
 QY 129 GTGGGCCGAGAGCAAAATGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 188
 Db 135 CTGTGTACAG 194
 QY 189 CTTCAGAGCGCTATATCTGCAACCGACCTTATGCTGGCCAGAGAGCGCTGCTGCT 248
 Db 195 CTTCAGAGCGCTATATCTGCAACCGACCTTATGCTGGCCAGAGAGCGCTGCTGCT 254
 QY 249 AGATTAACAACAG 308
 Db 255 TGATTAACAACAG 314
 QY 309 AGATCAAGTCTACCTGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368
 Db 315 TGAGCGCTGCTATCTGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
 QY 369 CCACTGACAG 428
 Db 375 TCAATCTGATGAG 434
 QY 429 CAATCAGCTCAGCTCTCTGATCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 488
 Db 435 CAACAGCTGACAG 494
 QY 489 AAGCTGAAGGAGACAGTGAAGAAAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 548
 Db 495 AAACGTGAAGGACACAGTGAAGAAAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAG 554
 QY 549 ACTGACCTGCTGTTTATGCTCTGAGAAATGCTTGGCTGAGCGAAGAAAGAGTAA 608
 Db 555 ACTGATTTGCTGTTTATGCTCTGAGAAATGCTTGGCTGAGCGAAGAAAGAGTAA 614
 QY 609 AACGAGACAGTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 668
 Db 615 AATGAATACCTAACCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 674
 QY 669 TTTA---CTAAGAGAAAGTGAAGAGCTAACGCTCATCATCATTAAGAAATTCACATGA 724
 Db 675 TTTTAAACCAAG 734
 QY 725 AACCTGCTCAGTTGAAAAGAAAATAGTTCAA--GTTGTCATGAGAACAG--AGGTAG 781
 Db 735 ACCCTGCTGTTAGTTACAAAGAAAACAAATGCCACTTTGTTTATTAAGACAGAAAGGTAG 794
 QY 782 ACTGATTAACCAAG 837
 Db 795 ACTTCTTAGCATAGATATTATTTGATTAACATTTGATTTGATTTGATTTGATTTGAT 854
 QY 838 GAAAAATATGTAATTTTAAAAATTTT-----GAAAGAGGTTACCTCTCATTCCT 890
 Db 855 AAAACAATTTATTTTAAATTAATTTGCTTTTCCATAAAAAGATTACTTTCCATTCCT 914
 QY 891 TTA---GAAAAAGCTTATGTACTGA--TTTCCATATCCATATTTTATATATGTA 945
 Db 915 TTAGGGGAAAAAAGCCCTAAATAGCTCATGTTTCCATATCAGTACTTTATATTA 974
 QY 946 GTTATTTATATATAGTATA-----CATTTATTTATGAGTTATTAATATAGATTT 999
 Db 975 ATGTAATTTATTTATTTATTAAGACTGCATTTTATTTATTAATCAATTTATTAATATGATTT 1034

```

QY      1000  TTTTAAACAATATCTGCGATTTGAA-ATTACTAAAGCAAAAT---ATATTG 1055
Db      1035  ATTATTAACAATCATTCGATTCGATTTGCGTACTGATGTGAAGCTAATATGATATTATG 1094
QY      1056  ACAATTAATCTAG---AAACAAGATCTTAGGCTTAAATTAACAACATGATATAC 1107
Db      1095  ACAATTAATTTAGAGCTATTAACATGTTTATTATTGACCTCAATTAACACTTGGATATC 1150

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RESULT 15

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US-10-063-502-153
; Sequence 153, Application US/10063502
; Publication No. US20030023042A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Macanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,502
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-502-153

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Query Match	46.9%	Score 524.8	DB 15	Length 1152
Best Local Similarity	73.2%	Pred. NO. 3.3e-99		
Matches 833	Conservative	0	Mismatches 267	Indels 37
				Gaps 11

Qy 69 ATCTATGAGTTTTCCTTATGGGACTTTGCGCCGACGTGCTCTCAATGCCCC 128

Db 75 ATCTGAGAGCTTTCTCTTATGGGACCTGGCCACACAGTGCCTCTTCTTTGGCCCT 134

QY 129 GTGGGCCAGGAGGCATAATGCGCTGCGCCGTCAACACCCCGTGCAGCTTGAGGTGTCCA 188

Db 135 CTTGTATCAGGGAGGACAGCTGCGCCCATCAGCTCCACATGCAAGGCTTGACAAATGCCA 1944

QY	189	CTTCCAGCAGCGCCGTACATCGTAAACCGCACCTTTATGCTGGCCAGAGAGGCCAGCCCTTGC	248
Db	195	CTTCCAGCAGCGCCCTATATCACCAACCGCACCTTCATGCTGGCGTAAAGAGGCTAGCTTGGC	254

QY 249 AGATAACAACAAGACGCTCCGGCTCATTCGGGAGAAACTGTCGAGAGTCAGTGTCTAA 308
Db 255 TGATAACAACAAGACGCTTCCTCATTTGGGGAGAACTGTTCCACGAGTCAGTATCAG 314

Qy 309 AGATCACTGCTACCTGATGAAGCAGGTCTCAACTTACCCCTGGAAAGCTTGCTGCC 368
315 TGAGCGCTGCTACTCTGATGAAAGCAGGTCTGAACTTACCCCTGGAAAGTGTGTTGCC 374

Qy 369 CCAGTCGACAGAGTTCCAGCCCTACATGACAGAGTGGTACCTTTCGACCAACCTCAG 428
Db 375 TCATCTGATAGTTCACAGCCTTATATCCAGAGAGTGGTCCCTTCCTGCGCAGGCTCAG 434

Dd
QY
435

CAACAGCTAAGCACAATGTCATTGTGAAGGTGATGACTGCATATCCGAGCATGTGCA

494

489 TACGCTGAGAGACAGCTGAAAGCTTGAGAGAGTGGAGAGATCAAGGCGATTGGGA 548

D	b	495	AAAGCTAAGACACACATGAAAAAGCTTGGAGAGAGTGGAGAGATCAAAAGCAATTGGAGA	554
O	y	549	ACTGACCTGCTGTTTATGTCTCTGAGAAATGCTTGGCTCTGACCGAGAAAGCTAGAA	608
D	b	555	ACTGATTTGGTGTTTATGTCTCGAAGAAATGCTCGATTGGACCAAGCAAACTGAAA	614
O	y	609	AACGAGAACTGCCTCTTCGCTTCTTAAAAAAGAACATATAGATTCCTCGATGACATT	668
D	b	615	AATGAATTAACATAACCCCTTTCCTGCTAGAAATTAACATTAAGATGCCCAAGATTT	674
O	y	669	TTTA---CTAAGGAAAGTGAAGAGCTAACGTCATCATCATTAAGAAGATTTCACTGA	724
D	b	675	TTTTTAACCAAAAGAAAGATGGGAAGCCAACTCATCATATATGGTGGATTCAAAAGA	734
O	y	725	AACCTGGCTAGTGAAGAAAGAAATATGTGCA--GTGGCATAGACCCAG--AGGTAG	781
D	b	735	ACCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTGTTTAAAGCAAGAGGTAG	794
O	y	782	ACTTGATTAACCAAGAAGTCATTGACAAATATTTATTTGTCAGTGAG---ATPACA	837
D	b	795	ACTTCTAAGCATGATATTTATTTGAATAACATTCATATGTATACGTGGTTCATATACAG	854
O	y	838	GAAATTAATGACTTTAAAAAATTTGTT-----GAAAGAGTTACCTCTCATTCCT	890
D	b	855	AAAACAATTATTTTTTAATTAATGTCTTTTTCGATTAATAAAGATTCTTCCATTCCT	914
O	y	891	TTA---GAAAAAAGCTTATGTAACTTCA--TTTCCATATCCAAATATTTATATATGTA	945
D	b	915	TTAGGGGAAAAAACCCTTAATPACTCTCATGTTCCATATACAGTACTTATATTTATA	974
O	y	946	GTTATTTATTAATAGATA-----CATTTATTTATGTCAGTTATTAATATGAGATT	999
D	b	975	ATGATTTATTTATTTATTAAGACTGCATTTATTTATTAATCAATTTATTAATATGATTT	1033
O	y	1000	ATTATTAAGAAACATTATCTGCTATTGATA--TTTAGATAAGCAAAATA--ATATTTAG	1055
D	b	1035	ATTATTAAGAAACATCATTCATGATTTGCTACTGTAGTGAAGCTAATTTGATTTATG	1094
O	y	1056	ACATTAACATAGG---AAACAAGTATCTAGAGCTTTAATAAACAATGATATAC	1107
D	b	1095	ACAATTAATTAAGAGCTATAACATGTTTATTTATGACTCAATTAACACTTGGATATC	1150

Search completed: July 20, 2003, 03:45:26
Job time : 163.321 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:07:55 ; Search time 35.2798 Seconds
(without alignments)
9727.122 Million cell updates/sec

Title:	US-09-751-797-7
Perfect score:	1119
Sequence:	1 taacacgctctcctccac.....tggatatcataaaaaaaaa 1119

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database :
Issued Patents NA:*
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3: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
4: /cgn2_6/prodata/1/ina/5S_COMB.seq.*
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	1119	100.0	1119	4	US-09-178-973B-7	Sequence 7, Appl1
	2	1119	100.0	1119	4	US-09-419-568F-7	Sequence 7, Appl1
	3	1119	100.0	1119	4	US-09-354-243B-9	Sequence 7, Appl1
	4	1047.8	93.6	1111	4	US-09-178-973B-9	Sequence 9, Appl1
	5	1047.8	93.6	1111	4	US-09-419-568F-9	Sequence 9, Appl1
	6	1047.8	93.6	1111	4	US-09-354-243B-9	Sequence 9, Appl1
	7	601.4	53.7	7445	4	US-09-178-973B-8	Sequence 8, Appl1
	8	601.4	53.7	7445	4	US-09-419-568F-8	Sequence 8, Appl1
	9	601.4	53.7	7445	4	US-09-354-243B-8	Sequence 8, Appl1
	10	555.2	49.6	5935	4	US-09-178-973B-17	Sequence 17, Appl1
	11	555.2	49.6	5935	4	US-09-419-568F-17	Sequence 17, Appl1
	12	555.2	49.6	5935	4	US-09-354-243B-29	Sequence 29, Appl1
	13	409.2	36.6	690	4	US-09-419-568F-24	Sequence 24, Appl1
	14	409.2	36.6	690	4	US-09-354-243B-24	Sequence 24, Appl1
	15	126	11.3	4797	4	US-09-419-568F-25	Sequence 25, Appl1
	16	126	11.3	4797	4	US-09-354-243B-25	Sequence 25, Appl1
	17	59.4	5.3	5852	1	US-07-867-106-2	Sequence 2, Appl1
	18	51.8	4.6	678	1	US-07-991-867B-23	Sequence 23, Appl1
	19	51.8	4.6	678	1	US-08-107-755A-23	Sequence 23, Appl1
	20	51.8	4.6	678	2	US-08-544-312-23	Sequence 23, Appl1
	21	51.8	4.6	678	4	US-09-370-861A-23	Sequence 23, Appl1
	22	51.8	4.6	6768	1	US-08-107-755A-1	Sequence 1, Appl1
	23	51.8	4.6	8457	1	US-07-991-867B-1	Sequence 1, Appl1
	24	51.8	4.6	8457	2	US-08-544-312-1	Sequence 1, Appl1
	25	51.8	4.6	8457	4	US-09-370-861A-1	Sequence 1, Appl1
	26	51.4	4.6	168575	4	US-09-412-280-1	Sequence 1, Appl1
	27	51.2	4.6	20674	4	US-09-641-638-651	Sequence 651, Appl1

C 28	50.8	837	1	US-08-232-416-18	Sequence 288, Appl
C 29	50.8	4.5	7218	1	US-08-232-463-21
C 30	50.6	4.5	4526	1	US-07-855-412B-4
C 31	50.6	4.5	4526	2	US-08-308-887A-4
C 32	50.6	4.5	4526	3	US-08-981-094-4
C 33	49.6	4.4	636	1	US-08-998-416-1137
C 34	49.2	4.4	731	1	US-08-451-405A-2
C 35	49.2	4.4	8920	2	US-08-446-855A-1
C 36	49.2	4.4	8920	4	US-09-150-741-1
C 37	48.2	4.3	615	4	US-08-998-416-186
C 38	48.2	4.3	636	4	US-08-998-416-1137
C 39	48.2	4.3	837	4	US-08-998-416-288
C 40	47.2	4.2	1689	1	US-07-991-867B-41
C 41	47.2	4.2	1689	2	US-08-544-33-41
C 42	47.2	4.2	1689	4	US-09-370-861A-41
C 43	47.2	4.2	1947	4	US-09-370-861A-74
C 44	47	4.2	665	2	US-08-883-795A-36
C 45	47	4.2	12793	4	US-09-004-836-124
C 46					Sequence 124, Appl

ALIGNMENTS

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RESULT 1
US-09-178-973B-7
/ Sequence 7, Application US/09178973B
/ Patent No. 6274710
/ GENERAL INFORMATION:
/ APPLICANT: Dumoutier, Laure
/ APPLICANT: Louhe, Jukka
/ APPLICANT: Renaud, Jean-Christophe
/ TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
/ TITLE OF INVENTION: (ribs)
/ TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
/ FILE REFERENCE: LUD 5543
/ CURRENT APPLICATION NUMBER: US/09/178,973B
/ CURRENT FILING DATE: 1998-10-26
/ NUMBER OF SEQ ID NOS: 17
/ SEQ ID NO 7
/ LENGTH: 1119
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ US-09-178-973B-7

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Query Match	100.0 %	Score 1119	DB 4.9	Length 1119
Best Local Similarity	100.0 %	Pred. No. 1.8e-273		
Matches 1119	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	TAAACAGGCTCCTCTCACTTATCAACTGTGTACATTGTGCATCTCTGATGGCTGTC	60	
Db	1	TAAACAGGCTCCTCTCACTTATCAACTGTGTACATTGTGCATCTCTGATGGCTGTC	60	
QY	61	CTGCAGAAATCTATGATGATTTTCCCTTATGGGGACTTTGGCCGACGTGCTGCTTCTC	120	
Db	61	CTGCAGAAATCTATGATGATTTTCCCTTATGGGGACTTTGGCCGACGTGCTGCTTCTC	120	
QY	121	ATTGCCCTGTGGGCCACGAGAGGCAAAATGCGCTGCCCTTCAACACCCGGTGCAGCTTGAG	180	
Db	121	ATTGCCCTGTGGGCCACGAGAGGCAAAATGCGCTGCCCTTCAACACCCGGTGCAGCTTGAG	180	
QY	181	GTTGTCAACTTCCAGCAGCCGTACATCGTCAACCGCACCTTTATGCTGGCCAAAGAGGCC	240	
Db	181	GTTGTCAACTTCCAGCAGCCGTACATCGTCAACCGCACCTTTATGCTGGCCAAAGAGGCC	240	
QY	241	AGCCTTGCAGATTAACAACACAGACGTCGCGCTCATCGGGGAGAAACTGTTCCGAGAGTC	300	
Db	241	AGCCTTGCAGATTAACAACACAGACGTCGCGCTCATCGGGGAGAAACTGTTCCGAGAGATC	300	
QY	301	AGTGTCTAAAGATCAGTGTCTACTCTGATGTAAGCAGGTGCTCAACTTCAACCTTGGAAACGTT	360	
Db	301	AGTGTCTAAAGATCAGTGTCTACTCTGATGTAAGCAGGTGCTCAACTTCAACCTTGGAAACGTT	360	
QY	361	CTGTCTCCCCCAGTACAGACAGGTTCCAGCCCTACATGACAGAGGTGTACTTTTCCGTACC	420	

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Db      361  CTGCTCCCCAGTCAGACAGGTTCCAGCCCTACATGACGAGGAGTGATCTTTCTTGACC 420
Qy      421  AAACACAGCAATCAGCTCAGCTCCTGTACATCAGCGGTGACGACAGACATCCAGAG 480
Db      421  AAATCAGACATCAGCTCAGCTCCTGTACATCAGCGGTGACGACAGACATCCAGAG 480
Qy      481  AATGTCAAGAGCTGAGAGACAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGCG 540
Db      481  AATGTCAAGAGCTGAGAGACAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGCG 540
Qy      541  ATTGGGAACTGAGACTGCTGTATATGTCTGAGAAATGCTGGCTGAGCGGAGAA 600
Db      541  ATTGGGAACTGAGACTGCTGTATATGTCTGAGAAATGCTGGCTGAGCGGAGAA 600
Qy      601  AGCTAGAAAACGAGAACCTGCTCTCTGCTCTTAAAGAAACATTAAGATCCCTGAA 660
Db      601  AGCTAGAAAACGAGAACCTGCTCTCTGCTCTTAAAGAAACATTAAGATCCCTGAA 660
Qy      661  TGGACTTTTCTTAAAGAAAGTGAAGAGCTAACGTCATCATCATTTAGAAATTTGAC 720
Db      661  TGGACTTTTCTTAAAGAAAGTGAAGAGCTAACGTCATCATCATTTAGAAATTTGAC 720
Qy      721  ATGAAACCTGGCTCACTGAAAGAAATAGTGCAGAGTTGCTCATGAGACGAGGTA 780
Db      721  ATGAAACCTGGCTCACTGAAAGAAATAGTGCAGAGTTGCTCATGAGACGAGGTA 780
Qy      781  GACTTGATTAACCAAAAGATTCATGACAAATTTTATGTCAGTATGATACAAAGAA 840
Db      781  GACTTGATTAACCAAAAGATTCATGACAAATTTTATGTCAGTATGATACAAAGAA 840
Qy      841  AAATATGTAATTTTAAAGAAATGTTGAAAGAGGTTACCTCTCATCTTTAGAAAAA 900
Db      841  AAATATGTAATTTTAAAGAAATGTTGAAAGAGGTTACCTCTCATCTTTAGAAAAA 900
Qy      901  AGCTTAGTAATCTTATTCATATCCAAATTTTATATATGTAAGTTATTTATTAATA 960
Db      901  AGCTTAGTAATCTTATTCATATCCAAATTTTATATATGTAAGTTATTTATTAATA 960
Qy      961  GTATACATTTTATTTATGTCAGTTATTAATATGATTTATTAATAGAAATTAATCTGC 1020
Db      961  GTATACATTTTATTTATGTCAGTTATTAATATGATTTATTAATAGAAATTAATCTGC 1020
Qy      1021  TATTGATATTTAGTATTAAGCAATATATTTATGACAAATTAATGAGAAACAGATATC 1080
Db      1021  TATTGATATTTAGTATTAAGCAATATATTTATGACAAATTAATGAGAAACAGATATC 1080
Qy      1081  TTAGGCTTAAATTAACATGATATTCATTAATAAAAAAA 1119
Db      1081  TTAGGCTTAAATTAACATGATATTCATTAATAAAAAAA 1119

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RESULT 2 US-09-419-568F-7

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; Sequence 7, Application US/09419568F
; Patent No. 6331613
; GENERAL INFORMATION:
; APPLICANT: Dumoulier, Laure
; APPLICANT: Loubet, Jamila
; APPLICANT: Renaud, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
; TITLE OF INVENTION: (Title) The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.2
; CURRENT APPLICATION NUMBER: US/09/419,568F
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US09/354,243
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 7
; LENGTH: 1119
; TYPE: DNA

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; ORGANISM: Mus musculus
; FEATURE:
; US-09-419-568F-7
Query Match      100.0%; Score 1119; DB 4; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1,8e-273;
Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TAAACAGGCTCTCTCTCACTTATCAACTGTGACATCTGTGATCTGTGATGCTGTC 60
1 TAAACAGGCTCTCTCTCACTTATCAACTGTGACATCTGTGATCTGTGATGCTGTC 60
1 TAAACAGGCTCTCTCTCACTTATCAACTGTGACATCTGTGATCTGTGATGCTGTC 60
61 CTGAGAAATCTATGAGTTTTCCTTATGAGGAGCTTGGCCGAGCTGCTCTCTC 120
61 CTGAGAAATCTATGAGTTTTCCTTATGAGGAGCTTGGCCGAGCTGCTCTCTC 120
121 ATTGCCCTGTGGGCCGAGAGGCAATAGCCCTGCTCAACACCCGGTGCACCTTGAG 180
121 ATTGCCCTGTGGGCCGAGAGGCAATAGCCCTGCTCAACACCCGGTGCACCTTGAG 180
181 GTGTCAACTTCCAGACGCGTACATGCTCAACCGCACTTTATGCTGGCCAGAGGCC 240
181 GTGTCAACTTCCAGACGCGTACATGCTCAACCGCACTTTATGCTGGCCAGAGGCC 240
241 AGCTTGCAATTAACCAACAGAGCTCCGCTCATGCGGAGAACTGTTCCGAGAGTC 300
241 AGCTTGCAATTAACCAACAGAGCTCCGCTCATGCGGAGAACTGTTCCGAGAGTC 300
301 AGCTTGAAGTCACTGCTACCTGATGAAGAGGCTGCTCAACTTCACTGGAAGAGCTT 360
301 AGCTTGAAGTCACTGCTACCTGATGAAGAGGCTGCTCAACTTCACTGGAAGAGCTT 360
361 CTGCTCCCCAGTCAGACAGGTTCCAGCCCTCAATGACAGAGGTTGTAACCTTTCTGACC 420
361 CTGCTCCCCAGTCAGACAGGTTCCAGCCCTCAATGACAGAGGTTGTAACCTTTCTGACC 420
421 AAATCAGCAATCAGCTCAGCTCCTGTCAATCAGCGGTGACGACCAAGATCCAGAG 480
421 AAATCAGCAATCAGCTCAGCTCCTGTCAATCAGCGGTGACGACCAAGATCCAGAG 480
481 AATGTCAAGAGCTGAGAGACAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGCG 540
481 AATGTCAAGAGCTGAGAGACAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGCG 540
541 ATTGGGAACTGAGACTGCTGTATATGTCTGAGAAATGCTTGCCTGAGCGAAGAA 600
541 ATTGGGAACTGAGACTGCTGTATATGTCTGAGAAATGCTTGCCTGAGCGAAGAA 600
601 AGCTAGAAAACGAGAACTGCTCTCTGCTCTTAAAGAAACATTAAGATCCCTGAA 660
601 AGCTAGAAAACGAGAACTGCTCTCTGCTCTTAAAGAAACATTAAGATCCCTGAA 660
661 TGGACTTTTCTTAAAGAAAGTGAAGAGTGAAGTCAATCATCATTAAGAAATTTGAC 720
661 TGGACTTTTCTTAAAGAAAGTGAAGAGTGAAGTCAATCATCATTAAGAAATTTGAC 720
721 ATGAAACCTGGCTCACTGAAAGAAATAGTGCAGAGTTGCTCATGAGACGAGGTA 780
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781 GACTTGATTAACCAAAAGATTCATGACAAATTTTATGTCAGTATGATACAAAGAA 840
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841 AAATATGTAATTTTAAAGAAATGTTGAAAGAGGTTACCTCTCATCTTTAGAAAAA 900
841 AAATATGTAATTTTAAAGAAATGTTGAAAGAGGTTACCTCTCATCTTTAGAAAAA 900
901 AGCTTAGTAATCTTATTCATATCCAAATTTTATATATGTAAGTTATTTATTAATA 960
901 AGCTTAGTAATCTTATTCATATCCAAATTTTATATATGTAAGTTATTTATTAATA 960
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Db 961 GATACATTATTTATGAGTTATATATGATTTATTTATGAAACATTAATCTGC 1020

Qy 1021 TATTGATATTAGTATTAAGGCAAAATATATTTATGACATTAATGAAACAGATATC 1080

Db 1021 TATTGATATTAGTATTAAGGCAAAATATTTATGACATTAATGAAACAGATATC 1080

Qy 1081 TTAGGCTTTAATTAACACATGATATCATTAATAAAAAA 1119

Db 1081 TTAGGCTTTAATTAACACATGATATCATTAATAAAAAA 1119

RESULT 3

US-09-354-243B-7

Sequence 7, Application US/09354243B

Patent No. 6359117

GENERAL INFORMATION:

APPLICANT: Dumoutier, Laure

APPLICANT: Louhed, Jamila

APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides

TITLE OF INVENTION: (TIPS)

FILE REFERENCE: LUD 5543.1

CURRENT APPLICATION NUMBER: US/09/354,243B

CURRENT FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US09/178,973

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 7

LENGTH: 1119

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

US-09-354-243B-7

Query Match 100.0%; Score 1119; DB 4; Length 1119;

Best Local Similarity 100.0%; Pred. No. 1,8e-273;

Matches 1119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAAACAGGCTCTCTCTCACTTATCAACTGTGACACTGTGAGATCTGATGGCTGTC 60

Db 1 TAAACAGGCTCTCTCTCACTTATCAACTGTGACACTGTGAGATCTGATGGCTGTC 60

Qy 61 CTGCAGAAATCTATGAGTTTTCCTATGAGGACTTTGCGCGACGCTGCTCTC 120

Db 61 CTGCAGAAATCTATGAGTTTTCCTATGAGGACTTTGCGCGACGCTGCTCTC 120

Qy 121 ATTGCGCTGTGGGCGCCAGAGGCAATGCGCTGCGCTCAACACCCGCTGCAAGCTTGAG 180

Db 121 ATTGCGCTGTGGGCGCCAGAGGCAATGCGCTGCGCTCAACACCCGCTGCAAGCTTGAG 180

Qy 181 GTGTCCAACTTCAGAGAGCGGTACATGTCACCGACCTTTATGCTGGGCAAGAGGCC 240

Db 181 GTGTCCAACTTCAGAGAGCGGTACATGTCACCGACCTTTATGCTGGGCAAGAGGCC 240

Qy 241 AGCTTGCAGATTAACAACAACAAGCTGCGCTCATCGGAGAACTGTTCCAGAGATC 300

Db 241 AGCTTGCAGATTAACAACAACAAGCTGCGCTCATCGGAGAACTGTTCCAGAGATC 300

Qy 301 AGTGTAAAGATCAGTGTCTCTGATGTAAGCAAGGTGCTCAACTTCAGAGAGATC 360

Db 301 AGTGTAAAGATCAGTGTCTCTGATGTAAGCAAGGTGCTCAACTTCAGAGAGATC 360

Qy 361 CTGCTCCCCAGTCAAGACAGGTTCCAGCTTCACTGAGAGAGGTGATACCTTTCTGACC 420

Db 361 CTGCTCCCCAGTCAAGACAGGTTCCAGCTTCACTGAGAGAGGTGATACCTTTCTGACC 420

Qy 421 AAATCTGCAATGAGCTCAGCTCTCTGATCAATGAGCGGTGACGACAAATCAGAGAG 480

Db 421 AAATCTGCAATGAGCTCAGCTCTCTGATCAATGAGCGGTGACGACAAATCAGAGAG 480

Qy 481 AATGTCAAGAGGCTGAAAGAGACAGTGAATAAAAGCTTGAGAGAGATGAGATCAAGCG 540

Db 481 AATGTCAAGAGGCTGAAAGAGACAGTGAATAAAAGCTTGAGAGAGATGAGATCAAGCG 540

Qy 541 ATTGGGGAACGTGACCTGCTGTTATGTCCTGAGAAATGCTTGGCTCTGACGAGAA 600

Db 541 ATTGGGGAACGTGACCTGCTGTTATGTCCTGAGAAATGCTTGGCTCTGACGAGAA 600

Qy 601 AGCTGAAACAGAAAGACGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

Db 601 AGCTGAAACAGAAAGACGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

Qy 661 TGGACTTTTCTAAGAGAAAGTGAAGTCACTGATCATCTGATGAGATTTGAC 720

Db 661 TGGACTTTTCTAAGAGAAAGTGAAGTCACTGATCATCTGATGAGATTTGAC 720

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Db 721 ATGAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

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Db 781 GACTGATTAACCAAAAGATTCATGCAATATTTATGCTGATGATGATGATGATGAT 840

Qy 841 AAATATGACTTTAAAAAATGTTGAAAGAGGTACCTGCTGCTGCTGCTGCTGCTGCT 900

Db 841 AAATATGACTTTAAAAAATGTTGAAAGAGGTACCTGCTGCTGCTGCTGCTGCTGCT 900

Qy 901 AGCTTATGATCTTCAATTCATATCAATATTTATATATGATGATGATGATGATGAT 960

Db 901 AGCTTATGATCTTCAATTCATATCAATATTTATATATGATGATGATGATGATGAT 960

Qy 961 GTATACATTTATTTATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1020

Db 961 GTATACATTTATTTATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1020

Qy 1021 TATTGATTTTATGATTAAGGCAAAATATATTTATGACATTAATGAAACAGATATC 1080

Db 1021 TATTGATTTTATGATTAAGGCAAAATATATTTATGACATTAATGAAACAGATATC 1080

Qy 1081 TTAGGCTTTAATTAACACATGATATCATTAATAAAAAA 1119

Db 1081 TTAGGCTTTAATTAACACATGATATCATTAATAAAAAA 1119

RESULT 4

US-09-178-973B-9

Sequence 9, Application US/09178973B

Patent No. 6274710

GENERAL INFORMATION:

APPLICANT: Dumoutier, Laure

APPLICANT: Louhed, Jamila

APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides

TITLE OF INVENTION: (TIPS)

FILE REFERENCE: LUD 5543

CURRENT APPLICATION NUMBER: US/09/178,973B

CURRENT FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 17

SEQ ID NO 9

LENGTH: 1111

TYPE: DNA

ORGANISM: Mus musculus

US-09-178-973B-9

Query Match 93.6%; Score 1047.8; DB 4; Length 1111;

Best Local Similarity 97.0%; Pred. No. 1.7e-255;

Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

Qy 3 AACAGGCTCTCTCTCACTTATCACTGATGACATGTCGATCTCTGATGCTGCTCT 62

Db 1 AACAGGCTCTCTCTCACTTATCACTGATGACATGTCGATGCTGATGCTGCTCTCT 60

QY 63 GCAGAAATCTATGAGTTTTCCTTATGAGGGACTTTGCGCCGACGCTGCTGCTCTCAT 122
 DB 61 GCAGAAATCTATGAGTTTTCCTTATGAGGGACTTTGCGCCGACGCTGCTGCTCTCAT 120
 QY 123 TGCCTGTGAGGCGCCGAGGAGCAAAATGCGCTGCGCCGCAACACCCGGTGCAGCTTGAAGT 182
 DB 121 TGCCTGTGAGGCGCCGAGGAGCAAAATGCGCTGCGCCGCAACACCCGGTGCAGCTTGAAGT 180
 QY 183 GTCCAACTTCCAGCAGCCGTAACATCGTCAACCGCACCTTATGCTGGCCAGAGAGCCAG 242
 DB 181 GTCCAACTTCCAGCAGCCGTAACATCGTCAACCGCACCTTATGCTGGCCAGAGAGCCAG 240
 QY 243 CCTTGCAATTAACAACACAGACGTCGCGCTCATCGGGAGAAACCTGTTCCGAGAGTCAAG 302
 DB 241 CCTTGCAATTAACAACACAGACGTCGCGCTCATCGGGAGAAACCTGTTCCGAGAGTCAAG 300
 QY 303 TCGTAAAGTCAAGTCTACCTGATGAAGAGAGTCTCAACCTTCCAGAGAGCTTCT 362
 DB 301 TCGTAAAGTCAAGTCTACCTGATGAAGAGAGTCTCAACCTTCCAGAGAGCTTCT 360
 QY 363 GCTCCCCCAGTCAAGACAGGTTCCAGCCCTACATGACAGAGTGTGTAACCTTCCAGCA 422
 DB 361 GCTCCCCCAGTCAAGACAGGTTCCAGCCCTACATGACAGAGTGTGTAACCTTCCAGCA 420
 QY 423 ACTCAGCAATCAGCTCAGCTCCTGTCAATCAGCGGTGACGACAGAACATCCAGAGAA 482
 DB 421 ACTCAGCAATCAGCTCAGCTCCTGTCAATCAGCGGTGACGACAGAACATCCAGAGAA 480
 QY 483 TGTCAAGAGCTGAAGAGAGACAGTGAAGAAAGCTTGAGAGAGTGAAGAGATCAAGCGCAT 542
 DB 481 TGTCAAGAGCTGAAGAGAGACAGTGAAGAAAGCTTGAGAGAGTGAAGAGATCAAGCGCAT 540
 QY 543 TGGGGAACAGTGAACCTGTTATGTCTCGAGAAATGCTGCGTGAAGCGAGAGAG 602
 DB 541 TGGGGAACAGTGAACCTGTTATGTCTCGAGAAATGCTGCGTGAAGCGAGAGAG 600
 QY 603 CTAGAAAGAGAAAGTGTCTCTTCTGCTCTTAAAGAAAGCAATTAAGTCCCTGAATG 662
 DB 601 CTAGAAAGAGAAAGTGTCTCTTCTGCTCTTAAAGAAAGCAATTAAGTCCCTGAATG 660
 QY 663 GACTTTTATCTTAAAGAAAGTGAAGAGTCAAGTCAATCATATTAAGAAAGTTTACAT 722
 DB 661 GACTTTTATCTTAAAGAAAGTGAAGAGTCAAGTCAATCATATTAAGAAAGTTTACAT 720
 QY 723 GAAACCTGGCTAGTGAAGAAAGAAATAGTCAAGTGTCCATGAGAGACAGAGGTAGA 782
 DB 721 GAAACCTGGCTAGTGAAGAAAGAAATAGTCAAGTGTCCATGAGAGACAGAGGTAGA 780
 QY 783 CTTGATTAACCAAGAAATTCATTGACAAATTTTATGTCATGATGATCAACAGAGAA 842
 DB 781 CTTGATTAACCAAGAAATTCATTGACAAATTTTATGTCATGATGATCAACAGAGAA 840
 QY 843 ATATAGTACTTAAAGAAATTTGTTGAAGAGAGTCACTCTCATCTCTTGAAGAAAG 902
 DB 841 ATATAGTACTTAAAGAAATTTGTTGAAGAGAGTCACTCTCATCTCTTGAAGAAAG 900
 QY 903 CTATAGTAATCATTTCCATCAATCAATTTTATATATATAGATTAATTAATTAAGT 962
 DB 901 CTATAGTAATCATTTCCATCAATCAATTTTATATATATAGATTAATTAATTAAGT 960
 QY 963 ATACATTTTATTTATGTCAGTTTATTAATATGAGATTTATTAAGAAACATTAATCTGCTA 1022
 DB 961 ATACATTTTATTTATGTCAGTTTATTAATATGAGATTTATTAAGAAACATTAATCTGATG 1020
 QY 1023 TTGATATTT-AGTATAGGCAATTAATTTATGACAAATTAATGAGAAACAGATATCT 1081
 DB 1021 TTGATATTTAGATATAGGCAATTAATTTATGATTAATTAATTAAGAAACAGATATCT 1080
 QY 1082 TAGGCTTATTAACACATGATATCATAA 1112
 DB 1081 TAGGCTTATTAACACATGATATCATAA 1111

RESULT 5
 US-09-419-568F-9
 ; Sequence 9, Application US/09419568F
 ; Patent No. 6331613
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumoulier, Laure
 ; APPLICANT: Lomouler, Jamila
 ; APPLICANT: Renaud, Jean-Christophe
 ; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
 ; FILE REFERENCE: LUD 5543.2
 ; CURRENT APPLICATION NUMBER: US/09/419,568F
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: US09/354,243
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: US09/178,973
 ; PRIOR FILING DATE: 1998-10-26
 ; NUMBER OF SEQ ID NOS: 29
 ; SEQ ID NO 9
 ; LENGTH: 1111
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 US-09-419-568F-9
 Query Match 93.6%; Score 1047.8; DB 4; Length 1111;
 Best Local Similarity 97.0%; Pred. No. 1.7e-255;
 Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;
 QY 3 AACAGGCTCTCTCTCACTTATCAACTGTTGACACTTGTGCGATCTTGATGCTGCTCT 62
 DB 1 AACAGGCTCTCTCTCACTTATCAACTTGTGACACTTGTGCGATCTTGATGCTGCTCT 60
 QY 63 GCAGAAATCTATGAGTTTTCCTTATGAGGGACTTTGCGCCGACGCTGCTGCTCTCAT 122
 DB 61 GCAGAAATCTATGAGTTTTCCTTATGAGGGACTTTGCGCCGACGCTGCTGCTCTCAT 120
 QY 123 TGCCTGTGAGGCGCCGAGGAGCAAAATGCGCTGCGCCGCAACACCCGGTGCAGCTTGAAGT 182
 DB 121 TGCCTGTGAGGCGCCGAGGAGCAAAATGCGCTGCGCCGCAACACCCGGTGCAGCTTGAAGT 180
 QY 183 GTCCAACTTCCAGCAGCCGTAACATCGTCAACCGCACCTTATGCTGGCCAGAGAGCCAG 242
 DB 181 GTCCAACTTCCAGCAGCCGTAACATCGTCAACCGCACCTTATGCTGGCCAGAGAGCCAG 240
 QY 243 CCTTGCAATTAACAACAGACGTCGCGCTCATCGGGAGAAACCTGTTCCGAGAGTCAAG 302
 DB 241 CCTTGCAATTAACAACAGACGTCGCGCTCATCGGGAGAAACCTGTTCCGAGAGTCAAG 300
 QY 303 TCGTAAAGTCAAGTCTACCTGATGAAGAGAGTCTCAACCTTCCAGAGAGCTTCT 362
 DB 301 TCGTAAAGTCAAGTCTACCTGATGAAGAGAGTCTCAACCTTCCAGAGAGCTTCT 360
 QY 363 GCTCCCCCAGTCAAGACAGGTTCCAGCCCTACATGACAGAGTGTGTAACCTTCCAGCA 422
 DB 361 GCTCCCCCAGTCAAGACAGGTTCCAGCCCTACATGACAGAGTGTGTAACCTTCCAGCA 420
 QY 423 ACTCAGCAATCAGCTCAGCTCCTGTCAATCAGCGGTGACGACAGAACATCCAGAGAA 482
 DB 421 ACTCAGCAATCAGCTCAGCTCCTGTCAATCAGCGGTGACGACAGAACATCCAGAGAA 480
 QY 483 TGTCAAGAGCTGAAGAGAGACAGTGAAGAAAGCTTGAGAGAGTGAAGAGATCAAGCGCAT 540
 DB 481 TGTCAAGAGCTGAAGAGAGACAGTGAAGAAAGCTTGAGAGAGTGAAGAGATCAAGCGCAT 540
 QY 543 TGGGGAACAGTGAACCTGTTATGTCTCGAGAAATGCTGCGTGAAGCGAGAGAG 602
 DB 541 TGGGGAACAGTGAACCTGTTATGTCTCGAGAAATGCTGCGTGAAGCGAGAGAG 600
 QY 603 CTAGAAAGAGAAAGTGTCTCTGCTCTTAAAGAAAGCAATTAAGTCCCTGAATG 662
 DB 601 CTAGAAAGAGAAAGTGTCTCTGCTCTTAAAGAAAGCAATTAAGTCCCTGAATG 660

QY 663 GACCTTTTACTAAAGAAAGTGAAGCTTAACGTCATCATTAAGAAATTTCACAT 722
DB 661 GACTTTTTTACTAAAGAAAGTGAAGCTTAACGTCATCATTAAGAAATTTCACAT 720
QY 723 GAAACCTGGCTCAGTTGAAAAAGAAATAGTGTCAAGTTGTCATGAGACCAAGAGTGA 782
DB 721 GAAACCTGGCTCAGTTGAAAAAGAAATAGTGTCAAGTTGTCATGAGACCAAGAGTGA 780
QY 783 CTTGATTAACCAACAAGATTCATTGACAAATTTTATTGTCATGATGATACCAAGAAA 842
DB 781 CTTGATTAACCAACAAGATTCATTGACAAATTTTATTGTCATGATGATACCAAGAAA 840
QY 843 ATAACTACTTTAAAAATTTGTTGAAGAGGTTCCCTCAATCCTTTAGAAAAAAG 902
DB 841 AGTATGTACTTTAAAAATTTGTTGAAGAGGTTCCCTCAATCCTTTAGAAAAAAG 900
QY 903 CTTATGTAACTTCAATTCATTCATCAATATTTTATATATATAGTTTATTTATTAAT 962
DB 901 CCTATGTAACTTCAATTCATTCATCAATATTTTATATATATAGTTTATTTATTAAT 960
QY 963 ATACATTTTATTTATGTCAGTTTATTAATATATATATTTATTTATTAAGAAACATTA 1022
DB 961 ATACATTTTATTTATGTCAGTTTATTAATATATATATTTATTTATTAAGAAACATTA 1020
QY 1023 TTGATATTTT-AGTATTAAGCAAAATTAATTTTATGACATTAATGAGAAACAAGATTC 1081
DB 1021 TTGATATTTTGAAGATTAAGCAAAATTAATTTATGATATTAATGAGAAACAAGATTC 1080
QY 1082 TAGGCTTTAATAAACAATGATATCATATA 1112
DB 1081 TAGGCTTTAATAAACAATGATATCATATA 1111

RESULT 6

US-09-354-243B-9
Sequence 9, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louned, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
TITLE OF INVENTION: (Tlfs)
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:

US-09-354-243B-9

Query Match 93.6%; Score 1047.8; DB 4; Length 1111;
Best Local Similarity 97.0%; Pmed. No. 1.7e-255;
Matches 1078; Conservative 0; Mismatches 32; Indels 1; Gaps 1;
QY 3 AACAGGCTCTCTCTCACTTATCAACTGTGACACTTGTGCAGTCTCTGATGCGTGCCT 62
DB 1 AACAGGCTCTCTCTCACTTATCAACTGTGACACTTGTGCAGTCTCTGATGCGTGCCT 60
QY 63 GCAGAAATCTATGAGATTTTCCCTTATGGGAAGCTTTGGCCGCAAGCTGCTGCTTCAT 122
DB 61 GCAGAAATCTATGAGATTTTCCCTTATGGGAAGCTTTGGCCGCAAGCTGCTGCTTCAT 120
QY 123 TGCCCTGTGGGCCCAAGGCAATATGCGTGCCTGCAACACCCGGGTCAGAGCTTGAGT 182
DB 121 TGCCCTGTGGGCCCAAGGCAATATGCGTGCCTGCAACACCCGGGTCAGAGCTTGAGT 180

QY 183 GTCCAACTTCAGACAGCCGTACATCTCAACCCGACCTTATGCTGGCCAGAGGCCAG 242
DB 181 GTCCAACTTCAGACAGCCGTACATCTCAACCCGACCTTATGCTGGCCAGAGGCCAG 240
QY 243 CTTGAGATTAACAACAAGAGTCCGCTCATTCGGGAGAAACTGTTCCGAGAGTCA 302
DB 241 CTTGAGATTAACAACAAGAGTCCGCTCATTCGGGAGAAACTGTTCCGAGAGTCA 300
QY 303 TGTATAAGTCAAGTCTTACCTGATGAAGAGGTGCTCAACTTCACCTCGAAGAGCTTCT 362
DB 301 TGTATAAGTCAAGTCTTACCTGATGAAGAGGTGCTCAACTTCACCTCGAAGAGCTTCT 360
QY 363 GCTCCCCAGTCAAGAGGTCCAGCTCAATGACAGAGGTGATCCTTCTCGACCA 422
DB 361 GCTCCCCAGTCAAGAGGTCCAGCTCAATGACAGAGGTGATCCTTCTCGACCA 420
QY 423 ACTCAGCAATCAAGCTCAGCTCCGTCATCAATCAAGCTGACGACCAAGATCCAGAGAA 482
DB 421 ACTCAGCAATCAAGCTCAGCTCCGTCATCAATCAAGCTGACGACCAAGATCCAGAGAA 480
QY 483 TGTCAAGAGCTGAAGAGACAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGCCAT 542
DB 481 TGTCAAGAGCTGAAGAGACAGTGAAGAAAGCTTGAGAGAGTGAAGATCAAGCCAT 540
QY 543 TGGGGAATCGACCTGCTTTATGCTCTGAGAAATGCTTGCTGTCGACGAGAGAG 602
DB 541 CGGGGAATCGACCTGCTTTATGCTCTGAGAAATGCTTGCTGTCGACGAGAGAG 600
QY 603 CTGAAAAAGAGAAATGCTGCTCTGCTGCTTAAAGAAACATTAAGATCCCTGATG 662
DB 601 CTGAAAAAGAGAAATGCTGCTCTGCTGCTTAAAGAAACATTAAGATCCCTGATG 660
QY 663 GACTTTTCTTAAAGAAAGTGAAGCTTAACGTCATCATTAAGAAATTTCACAT 722
DB 661 GACTTTTCTTAAAGAAAGTGAAGCTTAACGTCATCATTAAGAAATTTCACAT 720
QY 723 GAAACCTGGCTCAGTTGAAAAAGAAATAGTGTCAAGTTGTCATGAGACCAAGAGTGA 782
DB 721 GAAACCTGGCTCAGTTGAAAAAGAAATAGTGTCAAGTTGTCATGAGACCAAGAGTGA 780
QY 783 CTTGATTAACCAACAAGATTCATTGACAAATTTTATTGTCATGATGATACCAAGAAA 842
DB 781 CTTGATTAACCAACAAGATTCATTGACAAATTTTATTGTCATGATGATACCAAGAAA 840
QY 843 ATAACTACTTTAAAAATTTGTTGAAGAGGTTCCCTCAATCCTTTAGAAAAAAG 902
DB 841 AGTATGTACTTTAAAAATTTGTTGAAGAGGTTCCCTCAATCCTTTAGAAAAAAG 900
QY 903 CTTATGTAACTTCAATTCATTCATCAATATTTTATATATATAGTTTATTTATTAAT 962
DB 901 CCTATGTAACTTCAATTCATTCATCAATATTTTATATATATAGTTTATTTATTAAT 960
QY 963 ATACATTTTATTTATGTCAGTTTATTAATATATATTTATTTATTAAGAAACATTA 1022
DB 961 ATACATTTTATTTATGTCAGTTTATTAATATATATTTATTTATTAAGAAACATTA 1020
QY 1023 TTGATATTTT-AGTATTAAGCAAAATTAATTTTATGACATTAATGAGAAACAAGATTC 1081
DB 1021 TTGATATTTTGAAGATTAAGCAAAATTAATTTATGATATTAATGAGAAACAAGATTC 1080
QY 1082 TAGGCTTTAATAAACAATGATATCATATA 1112
DB 1081 TAGGCTTTAATAAACAATGATATCATATA 1111

RESULT 7

US-09-178-973B-8
Sequence 8, Application US/09178973B
Patent No. 6274710
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louned, Jamila
APPLICANT: Renaud, Jean-Christophe


```

1 CURRENT APPLICATION NUMBER: US/09/419,568F
2
3 CURRENT FILING DATE: 1999-10-18
4
5 PRIOR APPLICATION NUMBER: US09/354,243
6
7 PRIOR FILING DATE: 1999-07-16
8
9 PRIOR APPLICATION NUMBER: US09/178,973
10
11 PRIOR FILING DATE: 1998-10-26
12
13 NUMBER OF SEQ ID NOS: 29
14
15 SEQ ID NO: 8
16
17 LENGTH: 7445
18
19 TYPE: DNA
20
21 ORGANISM: Mus musculus
22
23 FEATURE:
24
25 Feature 1

```

Query Match	53.7%	Score 601.4	DB 4	Length 7445
Best Local Similarity	99.8%	Pred. No. 2,4e-142		
Matches 602	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY 510	AAAGCTTGAGAGAGTGGAGAGATCAAGCGAATTGGGAACTGGACCTGCTGTTATATGTC			569
Db 6535	ATAGCTTGAGAGAGTGGAGAGATCAAGCGAATTGGGAACTGGACCTGCTGTTATATGTC			6594
QY 570	TCGAGAAATNGCTTGGCTGCTGACGAGAAAGAACTGAAACGAAAGACGCTCCCTCT			629
Db 6595	TCGAGAAATNGCTTGGCTGCTGACGAGAAAGAACTGAAACGAAAGACGCTCCCTCT			6654
QY 630	GCCCTCTAAAAAAGAACATTAAGATCCCTGATAGACTTTTCTAAAGAGAAAGTGAGAA			689
Db 6655	GCCCTCTAAAAAAGAACATTAAGATCCCTGATAGACTTTTCTAAAGAGAAAGTGAGAA			6714
QY 690	GCTAAGCTCCATCATCATTTAGAAAGATTCCATGAAACCTGGCTCAGTTGAAAAAGAAA			749
Db 6715	GCTAAGCTCCATCATCATTTAGAAAGATTCCATGAAACCTGGCTCAGTTGAAAAAGAAA			6774
QY 750	TAGTGTCAAGTGTGCCATGAGACCAAGGTAGACTGATATCCAGCAAAAGATTCATTGACA			809
Db 6775	TAGTGTCAAGTGTGCCATGAGACCAAGGTAGACTGATATCCAGCAAAAGATTCATTGACA			6834
QY 810	ATATTTTATATGTCACTGATGATACAAACAGAAAAATATGACTTTAAAAAATTGTTGAA			869
Db 6835	ATATTTTATATGTCACTGATGATACAAACAGAAAAATATGACTTTAAAAAATTGTTGAA			6894
QY 870	AGGAGGTTACCTTCATCTCTTTAGAAAAAAGCTTATGTAACTTCATTTCCATATCCAA			929
Db 6895	AGGAGGTTACCTTCATCTCTTTAGAAAAAAGCTTATGTAACTTCATTTCCATATCCAA			6954
QY 930	TATTTTATATATGTAAGTTATTTATATAGTAATCATTTTATATATGTCAGTTTATTA			989
Db 6955	TATTTTATATATGTAAGTTATTTATATAGTAATCATTTTATATATGTCAGTTTATTA			7014
QY 990	ATATGGATTATTTATATGAAACATTTCTGCTATGATTTTATGTAATGAGCAAAATATA			1049
Db 7015	ATATGGATTATTTATATGAAACATTTCTGCTATGATTTTATGTAATGAGCAAAATATA			7074
QY 1050	TTTATGCAATTAACCTATGAGAAACAGATATCTTAGGCTTTATATPAACACATGATATCAT			1109
Db 7075	TTTATGCAATTAACCTATGAGAAACAGATATCTTAGGCTTTATATPAACACATGATATCAT			7134
QY 1110	AAA 1112			
Db 7135	AAA 7137			

RESULT 9

US-09-354-243B-8

Sequence 8, Application US/09354243B

Patent No. 6359117

GENERAL INFORMATION:

APPLICANT: Dumoulier, Laure

APPLICANT: Louned, Jamila

APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible

TITLE OF INVENTION: (TIFFS)

TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIORITY FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29

SEQ ID NO 8
LENGTH: 7445
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-354-243B-8

Query Match 53.7%; Score 601.4; DB 4; Length 7445;
Best Local Similarity 99.8%; Pred. No. 2,4e-142;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	510	AAAGCTTGAGAGAGATGAGAGATCAAGCGATGGGGAACCTGCTGTTATGTC	569
DB	6535	ATAGCTTGAGAGAGATGAGAGATCAAGCGATGGGGAACCTGCTGTTATGTC	6594
QY	570	TCGAGAAATGCTGCTGCTGAGCGAGAAAGCTGAGAAAGAAAGTGCCTCCT	629
DB	6595	TCGAGAAATGCTGCTGCTGAGCGAGAAAGCTGAGAAAGAAAGTGCCTCCT	6654
QY	630	GCCTCTAAAAAGAAACAATAGATCCCTGATGAGCTTTTAAAGAAAGTGA	689
DB	6655	GCCTCTAAAAAGAAACAATAGATCCCTGATGAGCTTTTAAAGAAAGTGA	6714
QY	690	GCTAACGTCATCATTCATTAAGATTCACATGAACCTGCTGAGTGAAGAAA	749
DB	6715	GCTAACGTCATCATTCATTAAGATTCACATGAACCTGCTGAGTGAAGAAA	6774
QY	750	TAGTCAAGTGTGTCATGAGACGAGGTAGCTGATPACACAAAGATTCATTG	809
DB	6775	TAGTCAAGTGTGTCATGAGACGAGGTAGCTGATPACACAAAGATTCATTG	6834
QY	810	ATATTTTATGTCATGATGATACACAGAAAAATATGATCTTTAAAAATGTTGA	869
DB	6835	ATATTTTATGTCATGATGATACACAGAAAAATATGATCTTTAAAAATGTTGA	6894
QY	870	AGAGGTTACCTCTCATTCCTTTAGAAAAAAGCTTATGTAATCTTCATTCAC	929
DB	6895	AGAGGTTACCTCTCATTCCTTTAGAAAAAAGCTTATGTAATCTTCATTCAC	6954
QY	930	TATTTTATATGATGATTTTATTAAGATTCATTTATTTATGCTGATTTA	989
DB	6955	TATTTTATATGATGATTTTATTAAGATTCATTTATTTATGCTGATTTA	7014
QY	990	ATATGATTTATTTATTAAGAAACATTCATGATTTATTAAGTAAAGCAATATA	1049
DB	7015	ATATGATTTATTTATTAAGAAACATTCATGATTTATTAAGTAAAGCAATATA	7074
QY	1050	TTTATGACAAATACATGAGAAACAGATATCTTAGGCTTTAATAAACATGATAT	1109
DB	7075	TTTATGACAAATACATGAGAAACAGATATCTTAGGCTTTAATAAACATGATAT	7134
QY	1110	AAA 1112	
DB	7135	AAA 7137	

RESULT 10

US-09-178-973B-17
Sequence 17, Application US/09178973B
Patent No. 6274710
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
TITLE OF INVENTION: (Tlfs)

TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543
CURRENT APPLICATION NUMBER: US/09/178,973B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 17
LENGTH: 5935
TYPE: DNA
ORGANISM: Mus musculus
US-09-178-973B-17

Query Match 49.6%; Score 555.2; DB 4; Length 5935;
Best Local Similarity 96.0%; Pred. No. 1e-130;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY	510	AAAGCTTGAGAGAGATGAGAGATCAAGCGATGGGGAACCTGCTGTTATGTC	569
DB	5221	ATAGCTTGAGAGAGATGAGAGATCAAGCGATGGGGAACCTGCTGTTATGTC	5280
QY	570	TCGAGAAATGCTGCTGCTGAGCGAGAAAGCTGAGAAAGAAAGTGCCTCCT	629
DB	5281	TCGAGAAATGCTGCTGCTGAGCGAGAAAGCTGAGAAAGAAAGTGCCTCCT	5340
QY	630	GCCTCTAAAAAGAAACAATAGATCCCTGATGAGCTTTTAAAGAAAGTGA	689
DB	5341	GCCTCTAAAAAGAAACAATAGATCCCTGATGAGCTTTTAAAGAAAGTGA	5400
QY	690	GCTAACGTCATCATTCATTAAGATTCACATGAACCTGCTGAGTGAAGAAA	749
DB	5401	GCTAACGTCATCATTCATTAAGATTCACATGAACCTGCTGAGTGAAGAAA	5460
QY	750	TAGTCAAGTGTGTCATGAGACGAGGTAGCTGATPACACAAAGATTCATTG	809
DB	5461	TAGTCAAGTGTGTCATGAGACGAGGTAGCTGATPACACAAAGATTCATTG	5520
QY	810	ATATTTTATGTCATGATGATACACAGAAAAATATGATCTTTAAAAATGTTGA	869
DB	5521	ATATTTTATGTCATGATGATACACAGAAAAATATGATCTTTAAAAATGTTGA	5580
QY	870	AGAGGTTACCTCTCATTCCTTTAGAAAAAAGCTTATGTAATCTTCATTCAC	929
DB	5581	AGAGGTTACCTCTCATTCCTTTAGAAAAAAGCTTATGTAATCTTCATTCAC	5640
QY	930	TATTTTATATGATGATTTTATTAAGATTCATTTATTTATGCTGATTTA	989
DB	5641	TATTTTATATGATGATTTTATTAAGATTCATTTATTTATGCTGATTTA	5700
QY	990	ATATGATTTATTTATTAAGAAACATTCATGATTTATTAAGTAAAGCAATAT	1048
DB	5701	ATATGATTTATTTATTAAGAAACATTCATGATTTATTAAGTAAAGCAATAT	5760
QY	1049	ATTATGACAAATACATGAGAAACAGATATCTTAGGCTTTAATAAACATGATAT	1108
DB	5761	ATTATGACAAATACATGAGAAACAGATATCTTAGGCTTTAATAAACATGATAT	5820
QY	1109	TAAA 1112	
DB	5821	TAAA 5824	

RESULT 11

US-09-419-568F-29
Sequence 29, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18

```

: PRIOR APPLICATION NUMBER: US09/354,243
: PRIOR FILING DATE: 1999-07-16
: PRIOR APPLICATION NUMBER: US09/178,973
: PRIOR FILING DATE: 1999-10-26
: NUMBER OF SEQ ID NOS: 29
: SEQ ID NO 29
: LENGTH: 5935
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
US-09-419-568F-29

```

Query Match	49.6%	Score	555.2	DB	4	Length	5935
Best Local Similarity	96.0%	Pred.	No. 1e-130				
Matches	580	Conservative	0	Mismatches	23	Indels	1
						Gaps	1

QY	510	AAACCTTGAGAGAGTGGAGATCAAGGCGCATTTGGGGAACCTGAGCTGCTTTATATGTC	569
Db	5221	ATACCTTGGAGAGAGCGGAGATCAAAAGCCATCGGGGAACCTGAGCTGCTTTATATGTC	5280
QY	570	TCTGAGAAATGCTTCGCTCTGAGCGAGAGAAGCTAGAAAAAGAAAGACTGCTTCCT	629
Db	5281	TCTGAGAAATGCTTCGCTCTGAGCGAGAGAAGCTAGAAAAAGAAAGACTGCTTCCT	5340
QY	630	GCCCTTCTAAAAAGAACATAAGATCCCTGAATGSACTTTTACTTAAAGGAAAGTGAGAA	689
Db	5341	GCCCTTCTAAAAAGAACATAAGATCCCTGAATGSACTTTTACTTAAAGGAAAGTGAGAA	5400
QY	690	GCTAACGCTCCATCATCTATTAGAGATTTCAATGAAACCTGGCTCAGTGGAAAAAGAAA	749
Db	5401	GCTAACGCTCCATCATCTATTAGAGATTTCAATGAAACCTGGCTCAGTGGAAAAAGAAA	5460
QY	750	TAGTGTCAAGTTGTTCATGAGACGAGAGTGAAGCTTGATTAACCAAAAGATTCATTGACA	809
Db	5461	TAGTGTCAAGTTGTTCATGAGACGAGAGTGAAGCTTGATTAACCAAAAGATTCATTGACA	5520
QY	810	ATATTTATTTGTCCTGATGATGATACACAGAAAAATATGTACTTTAAAAATTTGTTGAA	869
Db	5521	ATATTTATTTGTCCTGATGATGATACACAGAAAAATATGTACTTTAAAAATTTGTTGAA	5580
QY	870	AGGAGGTACCTCCATCATCTTCCTTTAGAAAAAAGCTTATGTAACTTCATTTCCATATCCAA	929
Db	5581	AGGAGGTACCTCCATCATCTTCCTTTAGAAAAAAGCTTATGTAACTTCATTTCCATATCCAA	5640
QY	930	TATTTTATATATGTAAGTTATTATTATTAACATACATTTTATTATGTCAGTTTATTA	989
Db	5641	TATTTTATATATGTAAGTTATTATTATTAACATACATTTTATTATGTCAGTTTATTA	5700
QY	990	ATATGGAATTTTATATAGAAACATTATCTGCTATGATATTT-AGTATTAAGGCAAAATPAT	1048
Db	5701	ATATGGAATTTTATATAGAAACATTATCTGCTATGATATTT-AGTATTAAGGCAAAATPAT	5760
QY	1049	ATTATATGACATAATCTATGAAACAAAGATATCTTAGGCTTTATATPAAACACATGATATCA	1108
Db	5761	ATTATATGATATAATCTATGAAACAAAGATATCTTAGGCTTTATATPAAACACATGATATCA	5820
QY	1109	TAAA TAAA 1112	
Db	5821	TAAA TAAA 5824	

RESULT 12
 US-09-354-243B-29
 ; Sequence 29, Application US/09354243B
 ; Patent No. 6359117
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumoutier, Laure
 ; APPLICANT: Louhed, Jamila
 ; TITLE OF INVENTION: Renaud, Jean-Christophe
 ; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides
 ; TITLE OF INVENTION: (Tifs)
 ; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
 ; FILE REFERENCE: LUD 5543.1

```

: CURRENT APPLICATION NUMBER: US/09/354,243B
:
: CURRENT FILING DATE: 1999-07-16
:
: PRIOR APPLICATION NUMBER: US09/178,973
:
: PRIOR FILING DATE: 1998-10-26
:
: NUMBER OF SEQ ID NOS: 29
:
: SEQ ID NO 29
:
: LENGTH: 5935
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
US-09-354-243B-29

```

Query Match	49.6%	Score 55.2	DB 4	Length 5935
Best Local Similarity	96.0%	Pred. No. 1e-130		
Matches 580	Conservative 0	Mismatches 23	Indels 1	Gaps 1

Qy	510	AAAGCTTGGAAGAGGTGGAGGATCAAGCCGATTTGGGGAACCTGCTGTTATATGC	569
Db	5221	ATAGCTTGGAAGAGCGGAGGAGATCAAGCCGATTTGGGGAACCTGCTGTTATATGC	5280
Qy	570	TCTGAGAAGTCTTGCGTCTGAGCGAGAAGAAGCTAGAAAAAGAAAGAACTGCTCTTCC	629
Db	5281	TCTGAGAAGTCTTGCGTCTGAGCGAGAAGAAGCTAGAAAAAGAAAGAACTGCTCTTCC	5340
Qy	630	GCCTTCTTAAAAAGAACATTAAGATCCCTGATGAGACTTTTACTTAAAGAAAAGTGA	689
Db	5341	GCCTTCTTAAAAAGAACATTAAGATCCCTGATGAGACTTTTACTTAAAGAAAAGTGA	5400
Qy	690	GCTAACGTCACATCATTTAGAGATTCCACATGAACCTGGCTCAGTTGAAAAAGAAA	749
Db	5401	GCTAACGTCACATCATTTAGAGATTCCACATGAACCTGGCTCAGTTGAAAAAGAAA	5460
Qy	750	TAGTGTCAAGTTGTCATGAAGACAGAGGTAGACTTGATTAACCAAGATTCATTGACA	809
Db	5461	TAGTGTCAAGTTGTCATGAAGACAGAGGTAGACTTGATTAACCAAGATTCATTGACA	5520
Qy	810	ATATTTTATTTCTCACTGATGATACAAACGAAAAAATAAGCTATTTAAAAATGTTGAA	869
Db	5521	ATATTTTATTTCTCACTGATGATACAAACGAAAAAATAAGCTATTTAAAAATGTTGAA	5580
Qy	870	AGAGAGTTACCTCTCATCTCTTTAGAAAAAAAGCTTATGTAACCTTCATTTCCATACCA	929
Db	5581	AGAGAGTTACCTCTCATCTCTTTAGAAAAAAAGCTTATGTAACCTTCATTTCCATACCA	5640
Qy	930	TATTTTATATATGTAAGTTTATTTATATATATATACATTTTATTTATGTCAGTTATTA	989
Db	5641	TATTTTATATATGTAAGTTTATTTATATATATATACATTTTATTTATGTCAGTTATTA	5700
Qy	990	ATATGAGATTTATTTATATAGAAACATATATCGTATGATGATTT-AGATTAAGGCAATTAAT	1048
Db	5701	ATATGAGATTTATTTATATAGAAAAATATATCTGATGTTGATTTTGAGATTAAGCAATTAAT	5760
Qy	1049	ATTATATGCAATTAATCTATAGAAAACAGATATCTTAGAGCTTTATATAAACACATGATATCA	1108
Db	5761	ATTATATGATTAATTAATCTATAGAAAACAGATATCTTAGAGCTTTATATAAACACATGATATCA	5820
Qy	1109	TAAA	
Db	5821	TAAA 5824	

RESULT 13
 US-09-419-568F-24
 Sequence 24 Application US/09419568F
 Patent No. 6331613
 GENERAL INFORMATION:
 APPLICANT: Dumoutier, laurie
 APPLICANT: Louhed, Jamila
 APPLICANT: Renaud, Jean-Christophe
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible P
 TITLE OF INVENTION: (Title) The Proteins Encoded, and Uses Thereof
 FILE REFERENCE: LUD 5543.2
 CURRENT APPLICATION NUMBER: US/09/419,568F

/ CURRENT FILING DATE: 1999-10-18
/ PRIOR APPLICATION NUMBER: US09/354,243
/ PRIOR FILING DATE: 1999-07-16
/ PRIOR APPLICATION NUMBER: US09/178,973
/ PRIOR FILING DATE: 1998-10-26
/ NUMBER OF SEQ ID NOS: 29
/ SEQ ID NO 24
/ LENGTH: 690
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
US-09-419-568F-24

Query Match
Best Local Similarity 36.6%; Score 409.2; DB 4; Length 690;
Pred. No. 3e-94;
Matches 504; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 9 CTCCTCTCACTTATCACTGTTGACACTTGTGCGATCTGTATGGCTGTCTCTGAGAA 68
DB 29 CTCCTTCCCAAGTACAGTGTGCTGAGTTAGATTGTCTGCAATGGCCGCTGAGAA 88
QY 69 ATCTATGATTTTCCCTTATGAGGACCTTGGCCGAGCTGCTGCTTCTCATTTGCCCT 128
DB 89 ATCTGAGACTCTTCTTATGAGGACCTTGGCCGAGCTGCTGCTTCTTCTGAGCCCT 148
QY 129 GTGGGCGCCAGAGGAGAAATGCGCTGCGCTCAACACCCGGTGAAGCTTGAAGTCCAA 188
DB 149 CTGTGATACAGGAGGAGGAGCTGCGCCATCACTGAGCTTGAACAAGTCCAA 208
QY 189 CTTCAGAGCCGATACATGTCACCGACCTTATGCTGGCCAAAGAGCCAGCTTGC 248
DB 209 CTTCAGAGCCGATATATACCAACCGACCTTATGCTGGCTTGAAGAGCTTGTGC 268
QY 249 AGATTAACAACAGACGTCGCGCTCATCGGAGAAATCTTCCGAGAGTCACTGCTAA 308
DB 269 TGAATTAACAACAGACGTCGCTCATCGGAGAAATCTTCCGAGAGTCACTGCTAA 328
QY 309 AGATTAACAACAGACGTCGCGCTCATCGGAGAAATCTTCCGAGAGTCACTGCTAA 368
DB 329 TGAATTAACAACAGACGTCGCTCATCGGAGAAATCTTCCGAGAGTCACTGCTAA 388
QY 369 CAGTACAGAGGTTCCAGCCCTACATGACGAGAGTGTACCTTCTCTGCAAACTCAG 428
DB 389 TCAATTAACAACAGACGTCGCTCATCGGAGAAATCTTCCGAGAGTCACTGCTAA 448
QY 429 CAATCACTCACTCTCTGTCATCAATGACGAGTGAAGCAATCATCAGAGATGTCA 488
DB 449 CAACAGGCTAAGACATGTCTATTTGAAGTGTATGACATCATCAGAGATGTCA 508
QY 489 AAGGCTGAAGAGACAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGGCGATTGGGA 548
DB 509 AAGGCTGAAGAGACAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGGCGATTGGGA 568
QY 549 AAGGCTGAAGAGACAGTGAAGAAAGCTTGAAGAGTGAAGATCAAGGCGATTGGGA 608
DB 569 ACTGAGTTGCTGTTATATCTTGAAGAAATGCTGATTTGACAGAGCAAGCTGAAA 628
QY 609 AAGGAGAACTGCTCTCTGCTCTTCAAAAAGAAATTAAGATCCCTGAATGCACTTT 668
DB 629 AATGAATACTAACCCCTTCTCTGCTGAATAATTAAGATGATGCCCAAGCGATT 688
QY 669 TT 670
DB 689 TT 690

RESULT 14
US-09-354-243B-24
/ Sequence 24, Application US/09354243B
/ Patent No. 6359117
/ GENERAL INFORMATION:
/ APPLICANT: Dumoulier, Laure
/ APPLICANT: Louhed, Tamila

/ APPLICANT: Renaud, Jean-Christophe
/ TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
/ TITLE OF INVENTION: (Tlfe)
/ FILE REFERENCE: LUD 5543.1
/ CURRENT APPLICATION NUMBER: US/09/354,243B
/ PRIOR FILING DATE: 1999-07-16
/ PRIOR APPLICATION NUMBER: US09/178,973
/ PRIOR FILING DATE: 1998-10-26
/ NUMBER OF SEQ ID NOS: 29
/ SEQ ID NO 24
/ LENGTH: 690
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
US-09-354-243B-24

Query Match
Best Local Similarity 36.6%; Score 409.2; DB 4; Length 690;
Pred. No. 3e-94;
Matches 504; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 9 CTCCTCTCACTTATCACTGTTGACACTTGTGCGATCTGTATGGCTGTCTCTGAGAA 68
DB 29 CTCCTTCCCAAGTACAGTGTGCTGAGTTAGATTGTCTGCAATGGCCGCTGAGAA 88
QY 69 ATCTATGATTTTCCCTTATGAGGACCTTGGCCGAGCTGCTGCTTCTCATTTGCCCT 128
DB 89 ATCTGAGACTCTTCTTATGAGGACCTTGGCCGAGCTGCTGCTTCTTCTGAGCCCT 148
QY 129 GTGGGCGCCAGAGGAGAAATGCGCTGCGCTCAACACCCGGTGAAGCTTGAAGTCCAA 188
DB 149 CTGTGATACAGGAGGAGGAGCTGCGCCATCACTGAGCTTGAACAAGTCCAA 208
QY 189 CTTCAGAGCCGATACATGTCACCGACCTTATGCTGGCCAAAGAGCCAGCTTGC 248
DB 209 CTTCAGAGCCGATATATACCAACCGACCTTATGCTGGCTTGAAGAGCTTGTGC 268
QY 249 AGATTAACAACAGACGTCGCGCTCATCGGAGAAATCTTCCGAGAGTCACTGCTAA 308
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RESULT 15
US-09-419-568F-25
/ Sequence 25, Application US/09419568F

Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
TITLE OF INVENTION: (Title) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 25
LENGTH: 4797
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-419-568F-25

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:03:00 ; Search time 12472.3 Seconds

(without alignments)
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Title: US-09-751-797-8

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

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LOCUS AR165227 7445 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6274710.
ACCESSION AR165227
VERSION AR165227.1 GI:16238720
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7445)
AUTHORS Dumontier L., Louhed J. and Renaud J.-C.
TITLE Antibodies which specifically bind T Cell Inducible factors (Tifs)
JOURNAL Patent: US 6274710-A 8 14-AUG-2001;
FEATURES Location/Qualifiers

source 1. 7445
/organism="unknown"
BASE COUNT 2058 a 1570 c 1597 g 2220 t
ORIGIN

Query Match 100.0%; Score 7445; DB 6; Length 7445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4561 TAAATATAGGCTATATATATATTAATTAAGATTAACAACAAGAGTGAATAGCTCCCAAT 4620
QY 4621 TTAATGGCTGCTTCAAAAAGTAAATATATCATGATGATTAATTAATAGTGTATG 4680
DB 4621 TTAATGGCTGCTTCAAAAAGTAAATATATCATGATGATTAATTAATAGTGTATG 4680
QY 4681 AAAGTATAGATGGAACCCCTTCCCTTACTTTTACTTCTTACTTCTTACTTCTTCTTCTTCT 4740
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DB 4741 TTCAACCTGATCAACGCACTAGTAAAGCACTATCTGCTGAGTATTAATAGCTTT 4800
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DB 4921 GCTCTTGCAGATGGGTGTGCTTAAGTAATCAGAAACAGAGAGGCTCCGCTTGAATG 4980
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DB 4981 TATCAGTAAGATATCTACCTTATCTCTTCTATCGAACTTAATGCTCTTCTTCTTCTG 5040
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QY 5161 ATGCAAGGCAACACTTCTGATAGCTGTGTAAGGTTATTAATCATTTACTTTGTG 5220
DB 5161 ATGCAAGGCAACACTTCTGATAGCTGTGTAAGGTTATTAATCATTTACTTTGTG 5220
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DB 5401 GGGGAAAGATGTTTAGCTGAGAAATCTGACCGGAGGAAATCTGCTAGAGCTCCCG 5460
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DB 6121 CTGCTACTTGAACAGATTAAGGAGTGAAGAACTTTTTCACACCCCACTAAATTT 6180
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DB 6301 CAAGTATATAGGTAATGCTGTGCTGCTTGAAGTCAAGAAAGGATGATTTAAGT 6360
QY 6361 TTGGGCAAAATCAT 6420
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QY 6421 AAGAGGCTATATCTTGTGCTCAAGCAAGCAATATGATCAACAGCTTTCTTACTG 6480

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Db      6421 AGAAGCTGATCTGTTTGGTCTCAGCAAGCAAAATGTCACCACTCTTTCTAACTG 6480
Qy      6481 GTCACCTTTAGAAAAATGCTACCTGTGCTCAAAATGGTTGTATTTCTTATTTTCAAGCT 6540
Db      6481 GTACCACTTTAGAAAAATGCTACCTGTGCTCAAAATGGTTGTATTTCTTATTTTCAAGCT 6540
Qy      6541 TGGAGAGAGTGGAGAGATCAAGGAGATTGGGGAACCTGCTGTATTTATGTCCTGAG 6600
Db      6541 TGGAGAGAGTGGAGAGATCAAGGAGATTGGGGAACCTGCTGTATTTATGTCCTGAG 6600
Qy      6601 AAATGCTTGGCTCGAGCGAGAGAGAGCTAGAAAACGAAAGAACTGCTCCCTGCTG 6660
Db      6601 AAATGCTTGGCTCGAGCGAGAGAGAGCTAGAAAACGAAAGAACTGCTCCCTGCTG 6660
Qy      6661 TAAAAAGACAAATAGATCCCTGAATGAACTTTTAACTAAAGGAAAGTGAAGAGCTAAC 6720
Db      6661 TAAAAAGACAAATAGATCCCTGAATGAACTTTTAACTAAAGGAAAGTGAAGAGCTAAC 6720
Qy      6721 GTCCATCATCTTGAAGATTTTCAATGAACCTGCTCACTTGAAGAAAGAAATAGTGT 6780
Db      6721 GTCCATCATCTTGAAGATTTTCAATGAACCTGCTCACTTGAAGAAAGAAATAGTGT 6780
Qy      6781 CAAGTGTCCATGAGCAAGAGGTAGACTTGAATACCAAGAAATTCATTTGACATATTT 6840
Db      6781 CAAGTGTCCATGAGCAAGAGGTAGACTTGAATACCAAGAAATTCATTTGACATATTT 6840
Qy      6841 TATGTCTCATGATATCAACAGAAAAATATGACTTTAAAAAATGTTTGAAGAGAG 6900
Db      6841 TATGTCTCATGATATCAACAGAAAAATATGACTTTAAAAAATGTTTGAAGAGAG 6900
Qy      6901 TTACCTCTCATCTCTTGAAGAAAAAGCTTATGTAACCTTCATTTCCATATCAATATTT 6960
Db      6901 TTACCTCTCATCTCTTGAAGAAAAAGCTTATGTAACCTTCATTTCCATATCAATATTT 6960
Qy      6961 ATATATGTAGTATTTATTTATTAAGATATACATTTTATTTATGTCAGTTTATTAATAG 7020
Db      6961 ATATATGTAGTATTTATTTATTAAGATATACATTTTATTTATGTCAGTTTATTAATAG 7020
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Db      7021 ATTATTTATGAAGAACTTATCTGCTATGATTTTATTAAGATTAAGGCAAAATATTTATG 7080
Qy      7081 ACAATACTATGGAAGAGATATCTTAGGCTTTAATTAACATGATATCATTAATCT 7140
Db      7081 ACAATACTATGGAAGAGATATCTTAGGCTTTAATTAACATGATATCATTAATCT 7140
Qy      7141 TCTGCTTGTATTTTCTCCCTTTAATATCAACAATACATCATCATCATTAACCA 7200
Db      7141 TCTGCTTGTATTTTCTCCCTTTAATATCAACAATACATCATCATCATTAACCA 7200
Qy      7201 ATCATCTCATGATTTTCAAGCTTGAACCATTAATTAACGTTAAAGTTGGTCCGGAAGC 7260
Db      7201 ATCATCTCATGATTTTCAAGCTTGAACCATTAATTAACGTTAAAGTTGGTCCGGAAGC 7260
Qy      7261 CTGAGTTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTG 7320
Db      7261 CTGAGTTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTGTTGTG 7320
Qy      7321 ATATTAAGTGTGTTCTCTATCAAGCTTGTGCTTATTAATTTGAAGACAGGCTGTGCTAG 7380
Db      7321 ATATTAAGTGTGTTCTCTATCAAGCTTGTGCTTATTAATTTGAAGACAGGCTGTGCTAG 7380
Qy      7381 AACCTGATGAGCTGAGCTGAGCAAGCTCTATTAATTTTGAAGATTAATTAATG 7440
Db      7381 AACCTGATGAGCTGAGCTGAGCAAGCTCTATTAATTTTGAAGATTAATTAATG 7440
Qy      7441 TGTAT 7445
Db      7441 TGTAT 7445

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AR201398
LOCUS      AR201398      7445 bp      DNA      linear      PAT 20-Apr-2002
DEFINITION Sequence 8 from patent US 6359117.
ACCESSION AR201398
VERSION    AR201398.1  GI:20252286
KEYWORDS
SOURCE
ORGANISM   Unknown.
REFERENCE   1. (bases 1 to 7445)
AUTHORS    Dumoutier, L., Louhed, J. and Renauld, J.-C.
TITLE       Isolated nucleic acid molecules which encode T cell inducible
FEATURES
JOURNAL     Patent: US 6359117-A 8 19-MAR-2002;
            Location/Qualifiers
            source
            1. 7445
BASE COUNT 2058 a 1570 c 1597 g 2220 t
ORIGIN
Query Match 100.0%; Score 7445; DB 6; Length 7445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 GTCATACCTGCTTAAGATTTCTTAATTTATTAAGAAAACTATTTCTTAATGAAGA 60
Qy      61 GCAACGAGACAGTATTTATAGATGTTCTGACATGACAGAGTGAAGTGAAG 120
Db      61 GCAACGAGACAGTATTTATAGATGTTCTGACATGACAGAGTGAAGTGAAG 120
Qy      121 TAAAGGCGGTATTAATCAGCATTAACCAACATGTTAATGTTTCTTGCAAGAACT 180
Db      121 TAAAGGCGGTATTAATCAGCATTAACCAACATGTTAATGTTTCTTGCAAGAACT 180
Qy      181 TGAATCTATGTTTAAACAATCTCAAGCTCTAAATATGTTGTAACGACTGAGTCG 240
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Qy      241 CTGCTGTCACAGAGCTCTTGAGCAGCTCTCCTGTTGCAATTTATGTTCTTGA 300
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Qy      301 TCGACTCCCAACCTCTCACTTGGCTCTGATGAGCCACCTTCAACTTCTGATTTA 360
Db      301 TCGACTCCCAACCTCTCACTTGGCTCTGATGAGCCACCTTCAACTTCTGATTTA 360
Qy      361 TGAATCTCATGTTTAACTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
Db      361 TGAATCTCATGTTTAACTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
Qy      421 TGTTCACCAACATGATGTTCTGAGCAAGAGCTGCGTGGTGTGAGGAGCAAGGA 480
Db      421 TGTTCACCAACATGATGTTCTGAGCAAGAGCTGCGTGGTGTGAGGAGCAAGGA 480
Qy      481 GCAAGAGAGGAGTGGCTGAGCAGGAGTCAAGATGTTGAGCCACATGAGAGTGT 540
Db      481 GCAAGAGAGGAGTGGCTGAGCAGGAGTCAAGATGTTGAGCCACATGAGAGTGT 540
Qy      541 GGGAGTTAGACCCAGGCTCTCCAGAAATGCAAGCAAAATGCTTTAACACAGCGGCA 600
Db      541 GGGAGTTAGACCCAGGCTCTCCAGAAATGCAAGCAAAATGCTTTAACACAGCGGCA 600
Qy      601 TCTCTCTCCAGCCCAACATGAGTGTGTTAGATTTCACTGATATGAGTGTGAGTGC 660
Db      601 TCTCTCTCCAGCCCAACATGAGTGTGTTAGATTTCACTGATATGAGTGTGAGTGC 660
Qy      661 TTCACTACATGCACTCCCTTGTGATCTTTGCAAGAGAACCAACCAAGAGAGAT 720
Db      661 TTCACTACATGCACTCCCTTGTGATCTTTGCAAGAGAACCAACCAAGAGAGAT 720
Qy      721 CCCCACTGCTTGTGCTCTCAAGTGTGCACTCTCAACAGGTCAAGATTTCTCAAGTGT 780

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D	721	CCCCACACCTCTTGGCTCCTCAAGTCGTGACCTCTCAACAGGTCAAGATTCTCCAGTGT	780
Q	781	CCCTCAACACTTCTCCCGACGTGTCCTCCCTCAACACTTCTCCAGTGTCCCTCAACATT	840
D	781	CCCTCAACACTTCTCCCGACGTGTCCTCCCTCAACACTTCTCCAGTGTCCCTCAACATT	840
Q	841	CTCCAGTGTCCCTCAACACTTCTTGATCTCAATTAAGTCGAGGGGAGAAAGATCTCAACN	900
D	841	CTCCAGTGTCCCTCAACACTTCTTGATCTCAATTAAGTCGAGGGGAGAAAGATCTCAACN	900
Q	901	GTCATTTTCATGACTTGGCGTTCTAGCTTGAGATGTAGGCACTTGGCGTGTACGTAGGGT	960
D	901	GTCATTTTCATGACTTGGCGTTCTAGCTTGAGATGTAGGCACTTGGCGTGTACGTAGGGT	960
Q	961	AGGCGTGTCCCGCGCTGTAGGAAAGACTTTCCTAGTCTAGTGTGACGCTCACTCTG	1020
D	961	AGGCGTGTCCCGCGCTGTAGGAAAGACTTTCCTAGTCTAGTGTGACGCTCACTCTG	1020
Q	1021	GGATTCAAGTCAACATGCAAAATAATCCAGTATTTGTAAATCTCTTCTCACT	1080
D	1021	GGATTCAAGTCAACATGCAAAATAATCCAGTATTTGTAAATCTCTTCTCACT	1080
Q	1081	ATCCATCTAATAGATGTTATGTGTAGGCTCATTTAAATAATATTTTGAAGCTTATGC	1140
D	1081	ATCCATCTAATAGATGTTATGTGTAGGCTCATTTAAATAATATTTTGAAGCTTATGC	1140
Q	1141	TTGACAAAGTAAATGTCAAGAAATTGCAAAATGTAAGATTAATTTTAAAAAAA	1200
D	1141	TTGACAAAGTAAATGTCAAGAAATTGCAAAATGTAAGATTAATTTTAAAAAAA	1200
Q	1201	TCTATGCTTAAATAGTCTATTAGATTGTTCACATCCGATATTTTCAACTTAACCTTGACC	1260
D	1201	TCTATGCTTAAATAGTCTATTAGATTGTTCACATCCGATATTTTCAACTTAACCTTGACC	1260
Q	1261	TTGGCTATGATTTCAACCTTTGTATTTTGACATCTACATPAAACAGTCTCTGAACCAAGCAT	1320
D	1261	TTGGCTATGATTTCAACCTTTGTATTTTGACATCTACATPAAACAGTCTCTGAACCAAGCAT	1320
Q	1321	TCTGTGCAATGGGAGCTGTGGAAGAAAGCCAACTTTCTATTAATAAAAAAAAAACAGCTA	1380
D	1321	TCTGTGCAATGGGAGCTGTGGAAGAAAGCCAACTTTCTATTAATAAAAAAAAAACAGCTA	1380
Q	1381	GTTATAGTTTGAAGATTCATPACTAATTAATAATAATAATAATAATAATAATAATAATAATA	1440
D	1381	GTTATAGTTTGAAGATTCATPACTAATTAATAATAATAATAATAATAATAATAATAATAATA	1440
Q	1441	AATAATCTCCAAAGTTTCAATTATGAGCTTATTTCAAGCAAGAAATATAGACAAGGCTCT	1500
D	1441	AATAATCTCCAAAGTTTCAATTATGAGCTTATTTCAAGCAAGAAATATAGACAAGGCTCT	1500
Q	1501	TTTATTTTGTGTCCTCTTAAGAGATPAGAATCTATGAAGTGTGTGGGAAATGATGCC	1560
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D	1561	GTCACCAAAAGCGTGAATCAATPACTGCGGAGATCAAAAGGCTGCTCACTCAATCAGAA	1620
Q	1621	TCTACTACGCGAAAGCATGTGCTTTCTTGAACCCGTGTTTAGAAGATTTCTGGGATTT	1680
D	1621	TCTACTACGCGAAAGCATGTGCTTTCTTGAACCCGTGTTTAGAAGATTTCTGGGATTT	1680
Q	1681	GTGTGCAAAAGCATGTTGTGGCCCTCAACGTCGACGTTTATGGGAAAGCTTCCATCTCT	1740
D	1681	GTGTGCAAAAGCATGTTGTGGCCCTCAACGTCGACGTTTATGGGAAAGCTTCCATCTCT	1740
Q	1741	CAAGGTGGAAAGGCTTGGAGGTGTCTTGTGGCTCTATGTGGGTGTAGTACTTCTC	1800
D	1741	CAAGGTGGAAAGGCTTGGAGGTGTCTTGTGGCTCTATGTGGGTGTAGTACTTCTC	1800
Q	1801	AGAAACACGACTGGAATTAAGATATGTGATGTCAATCATTTCAATATCCAAAAA	1860

Db	1801	AGAAAGACAGACCTGGAAATTACGATTAAGTGTGATGTGTCATATCAATTCATTCACATACCAAAAA	1868
Qy	1861	ACCCTGTGTCCCGATGGCTATAAAGACCAACTTCGTGCTCTCCCATCAACAAGCAG	1920
Db	1861	ACCCTGTGTCCCGATGGCTATAAAGACCAACTTCGTGCTCTCCCATCAACAAGCAG	1920
Qy	1921	ACACCTAAACAGGTAAAGCATCTCAGACCTCTACAGAAATCATCGCTTGGTACCATGCTA	1980
Db	1921	ACACCTAAACAGGTAAAGCATCTCAGACCTCTACAGAAATCATCGCTTGGTACCATGCTA	1980
Qy	1981	CCGACGAAACATGTGCCCTCGATATGTTTTGGCTTTTACTCTCCTACATCAAGGCTCTCT	2040
Db	1981	CCGACGAAACATGTGCCCTCGATATGTTTTGGCTTTTACTCTCCTACATCAAGGCTCTCT	2040
Qy	2041	CTCACTTATCAACTGTGTGACACTGTGCGATCTCTGATAGCGTGTCTGACAGAAATCTATG	2100
Db	2041	CTCACTTATCAACTGTGTGACACTGTGCGATCTCTGATAGCGTGTCTGACAGAAATCTATG	2100
Qy	2101	AGTTTTTCCCTTATAGGGGACTTTGCGCGCCAGCTGCTGCTTCTCATTTGCCCTGTGGCC	2160
Db	2101	AGTTTTTCCCTTATAGGGGACTTTGCGCGCCAGCTGCTGCTTCTCATTTGCCCTGTGGCC	2160
Qy	2161	CAGGAGGAAATGCGCTGCCCGCTCAACACCCGGGTGCAAGCTTGAAGGTCCAACTTCCAG	2220
Db	2161	CAGGAGGAAATGCGCTGCCCGCTCAACACCCGGGTGCAAGCTTGAAGGTCCAACTTCCAG	2220
Qy	2221	CAGCGGTACATCTGTCAACCCGACCTTTATGTGTGCCCAGAGAGTACAGCTGCATCTCTT	2280
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Qy	2281	CTCTCCATACCGGCTTGCAATTTTCTGTGAAGCACTTGCAAACTCTTTAGGGGGGCTTTA	2340
Db	2281	CTCTCCATACCGGCTTGCAATTTTCTGTGAAGCACTTGCAAACTCTTTAGGGGGGCTTTA	2340
Qy	2341	TCTCCGCAAGGTCTCACTACCTATGTTTTGTGTCTCTTAAAGACCTTTAAGACCTGGGT	2400
Db	2341	TCTCCGCAAGGTCTCACTACCTATGTTTTGTGTCTCTTAAAGACCTTTAAGACCTGGGT	2400
Qy	2401	CTTTTTCATTTCTATTTCAAGGCTCTGAGACCAATTTCCATCTTTGGGCTTCAGGACACA	2460
Db	2401	CTTTTTCATTTCTATTTCAAGGCTCTGAGACCAATTTCCATCTTTGGGCTTCAGGACACA	2460
Qy	2461	TATACGAAATTTATCTACAGAGGCGCAATTTAGAAAGCACCAAGCTGCAATCTTTC	2520
Db	2461	TATACGAAATTTATCTACAGAGGCGCAATTTAGAAAGCACCAAGCTGCAATCTTTC	2520
Qy	2521	CATTTCTGTGTGCTCTCTTCTGAACCTATCTCTTGGCTACATCTGTAGACCACTGGC	2580
Db	2521	CATTTCTGTGTGCTCTCTTCTGAACCTATCTCTTGGCTACATCTGTAGACCACTGGC	2580
Qy	2581	GACATACATCTCTACTTACAGGCTTTTCTCATCTCTCTTACCCAGGACTTAGGGT	2640
Db	2581	GACATACATCTCTACTTACAGGCTTTTCTCATCTCTCTTACCCAGGACTTAGGGT	2640
Qy	2641	TTTCTCTCTTTCAGGCCAGGCTTGAAGATTAACAACAGAGCTCGGGCTCATCGGGAGAGA	2700
Db	2641	TTTCTCTCTTTCAGGCCAGGCTTGAAGATTAACAACAGAGCTCGGGCTCATCGGGAGAGA	2700
Qy	2701	AACTGTTCCGAGAGTCAAGTAAAGTCTTCACTGTGAAGACAGGGCTAGGTGCGGAGC	2760
Db	2701	AACTGTTCCGAGAGTCAAGTAAAGTCTTCACTGTGAAGACAGGGCTAGGTGCGGAGC	2760
Qy	2761	TGGTGGACCCCTGCGGATAGTCTAGCGATACCCCTGCTCTTCTTCTACCTGCGAG	2820
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Qy	2821	CTAAAGATCAGTCTACCTGATGAAGACAGTGTCTCACTTCAACCCTGGAAGAGCTTCTGC	2880
Db	2821	CTAAAGATCAGTCTACCTGATGAAGACAGTGTCTCACTTCAACCCTGGAAGAGCTTCTGC	2880
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DB 3001 CCTCTTATTCAGTAAGAACCCGAGAGTCCGCTCTCTCTCTTCAAGAGTGAAGA 3060
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DB 3061 GGGCTCAGCACCACCAATCATAGGCACTTGAATAGGTCAAAAGGCTTGGCTC 3120
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DB 3721 CAGCTCTTCTGTAAAGGAGGAGCCTGATTTCAAGTCTTCAAGAAACAAATATGCTCAGA 3780
QY 3781 GAATCTAGTCAAGTGAATCTAGTCAACAGCGGCAAAATGACTGAACGCTCTATT 3840
DB 3781 GAATCTAGTCAAGTGAATCTAGTCAACAGCGGCAAAATGACTGAACGCTCTATT 3840
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LOCUS Sequence 8 from Patent M00210393.
DEFINITION AX459954
ACCESSION AX459954
VERSION AX459954.1 GI:21725690
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Dumoutier, L. and Renaud, J.C.
TITLE Isolated nucleic acid molecules which encode a cell inducible
factor, or interleukin-21, the proteins encoded, and uses thereof
JOURNAL Patent: WO 0210393-A 8-07-FEB-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES
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 ACCESSION AR201417
 VERSION AR201417.1 GI:20252305
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 5935)
 AUTHORS Dumoulier, L., Louhed, J., and Renaud, J.-C.
 TITLE Isolated nucleic acid molecules which encode T cell inducible factors (TIFs), the proteins encoded, and uses therefor
 JOURNAL Patent: US 6359117-A 29 19-MAR-2002;
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BASE COUNT 1732 a 1174 c 1346 g 1683 t
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LOCUS AX459988
DEFINITION Sequence 42 from Patent WO0210393.
ACCESSION AX459988
VERSION AX459988.1 GI:21725722
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1

AUTHORS Dumoutier, L. and Renaud, J.C.
TITLE Isolated nucleic acid molecules which encode t cell inducible factors, or interleukin-21, the proteins encoded, and uses thereof
JOURNAL Patent: WO 0210393-A 42 07-FEB-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
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Location/Qualifiers
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RESULT 8
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DEFINITION AJ294728
ACCESSION AJ294728.1 GI:11967894
VERSION IL-TIF beta protein; ILT1Fb gene.
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 5935)
AUTHORS Dumoutier, L., Van Roost, E., Ameye, G., Michaux, L. and Renaud, J.C.
TITLE IL-TIF/ILT-22: genomic organization and mapping of the human and mouse genes
JOURNAL Genes Immun. 1 (8), 488-494 (2000)
MEDLINE 21069354
PUBMED 11197690
REFERENCE 2 (bases 1 to 5935)
AUTHORS Renaud, J.C.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2000) Renaud J.C., UCL 74-59, Ludwig Institute for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels, BELGIUM

FEATURES
source location/Qualifiers
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 LOCUS AC111483
 DEFINITION Rattus norvegicus clone CH230-87D20, *** SEQUENCING IN PROGRESS
 AC111483.2 GI:21736032
 VERSION AC111483.2
 KEYWORDS HTG; HTGS_PHASE1.

SOURCE
 ORGANISM
 Norway rat.
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 133899)
 AUTHORS
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-ouman,F.R., Allen,C.,
 Albrooks,S.L., Amaralunga,H.C., Aye,J.R., Ayele,M., Banks,T.,
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 Williams,G., Williamson,A., Wlezyk,R., Woodson,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G., and Gibbs,R.
 Direct Submission
 Unpublished
 2 (bases 1 to 133899)
 Morley,K.C.
 Direct Submission
 Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 133899)
 Morley,K.C.
 Direct Submission
 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 12, 2002 this sequence version replaced gi:18701248.
 COMMENT
 Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 Project Information
 Center Project name: GNMK
 Center Clone name: CH230-87D20
 Sequencing Statistics
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye 100% of reads
 Assembly program: Phrap; version 0.990329

Consensus quality: 69386 bases at least Q40
 Consensus quality: 74271 bases at least Q30
 Consensus quality: 78120 bases at least Q20

* NOTE: Estimated insect size may differ from sequence length.
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_drafi_delta.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 70 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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AUTHORS     Rieder,M.J., Carrington,D.P., Chung,M.-W., Lee,K.L., Poel,C.L.,
             Yi,Q. and Nickerson,D.A.
TITLE       Submitted (01-JUN-2001) Molecular Biotechnology, University of
             Washington, 1705 NE Pacific, Seattle, WA 98195, USA
             To cite this work please use: SeattleSNPs, NHLBI Program for
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Db	1524	CAG	GA	T	AT	T	AT	GA	CA	T	AG	G	CT	CT	TT	TT	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	1587		
Qy	1538	GAA	TT	G	T	G	G	GA	AAAA	T	AG	AT	CC	G	T	GA	CA	AAAA	GC	T	GA	CT	CA	T	AA	T	AG	CT	CA	GG	GA	AT	CA	1597	
Db	1584	AA	AG	CT	G	T	AG	GA	AAAA	T	AG	AT	CC	G	T	GA	CA	AAAA	T	AG	CT	CA	CT	CA	AG	CA	CT	AT	TA	AG	GA	AT	CA	1644	
Qy	1598	AAG	CT	G	CT	CT	ACT	CA	AT	CAGA	----	T	CT	AT	CA	GG	CA	AA	GC	AT	GA	CG	AT	G	CT	T	T	T	T	T	T	T	T	1655	
Db	1644	AA	CA	T	TT	TA	T	AT	CT	AA	AT	CT	GA	CT	CT	AT	TA	GA	CA	AAAA	CA	AT	T	G	T	T	T	T	T	T	T	T	T	1703	
Qy	1655	----	CC	G	T	T	TA	GA	AA	T	CT	G	GA	AT	T	T	G	T	GC	CA	AAAA	AG	CA	CT	G	T	T	T	T	T	T	T	T	1711	
Db	1704	AT	G	A	G	G	T	T	TA	GA	AA	AT	T	CT	G	GA	AT	T	T	G	AT	TT	G	CT	GT	TA	AA	----	TA	AG	1762				
Qy	1712	TG	AC	G	T	T	T	TA	GG	AA	CA	CT	T	CC	AT	CT	CA	AG	T	GG	GA	AG	CT	T	T	GA	AG	T	G	T	G	T	T	T	1771
Db	1763	TG	AC	G	T	T	T	TA	GG	AA	CA	CT	T	CC	AT	CT	CA	AG	T	GG	GA	AG	CT	T	T	GA	AG	T	G	T	G	T	T	T	1811
Qy	1772	TG</																																	

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Db 2226 CCACGTGAGGCTTGACCAAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTCAT 2285
Qy 2250 GCTGGCCAAAGAGGTACAGCTGACATCTCTTTCTCT-----C 2285
Db 2286 GCTGGCTAAGAGGTATACATCTCAATCTGCTCTTTCTCGTTGATCTACTTGAATCC 2345
Qy 2286 CATACCGGCTTGGCCATTTCTCTGTAAGACACTTGCAAACTCTTGAAGGCGCTTATATCC 2345
Db 2346 AAATAGTCTTAAACTTTCTTCAGAGCATCTTAAGACTTGAAGAACCCACTTTAT 2405
Qy 2346 GCAGGTCTCACTACTATGTTTCTGTCTCTTATAGACTCTTTAAGAGCTGGTCTTT 2405
Db 2406 CCGTGAAG--GTAGTAAATTTTCTGTTTTCAGAGACTCTTTGGGAATCGGCTTTT 2463
Qy 2406 TCTATTTCTATTCAAGGTCTCAGAGCAATTTCTATCTTGGCTTCAAGACATATAC 2465
Db 2464 TTTTCTTGAAGCTTCTCC-----TTCAATTTGGCTTTATGATACATATGA 2513
Qy 2466 TGAATTTATATCAAGAGCGCATTTAAGAACCCACGACTGCATACTTCC--A 2522
Db 2514 TGAATTTTCCAAAGACGCGCATTCAGTATTCATCTGATGATTTTCTTTTCTTTA 2573
Qy 2523 TTTCTGTGCTCTCTGTAATCTATCTCTTGGCTATCC----- 2565
Db 2574 TGCCCTGTGCTATTTCTTAACTATGACACATCTGAATTTCTGCTTTAGTCTTTATG 2633
Qy 2566 -----CTGAGACCCACTGCGGACATATCTCTACTTACAGGCTTTCTTCATCTC 2617
Db 2614 ATGTTGCTCTGGGGAGAGCGGATGGGGACATGTCTATGTATTAATTTTTTCTATTTG 2693
Qy 2618 CTGTACCCCAAGGCACTTAGGGTTTC-TCTCTTCAAGCGAGCCCTTGAGATAACACA 2676
Db 2694 CTCAATGTCCAGACCTTAGTCTTTCTCTCTCCAGGCTAGCTTGGGTGATTAACAACA 2753
Qy 2677 CAGAGTCCGGCTACCGGGGAGAACTGTTCCAGAGGTCACTGTAATCTCTCACTG 2736
Db 2754 CAGAGTTCGTCTCATGGGAGAACTGTCCAGAGGTCACTGTAATCTCACTG 2813
Qy 2737 ATGAGCAGAGG-----TAGCTGCGGAGCTGTGAGACCTCTGGGATG--- 2780
Db 2814 ACGAACGGGGCCGTGTCCGTCAATGGGTACTTGGGGTGTGTATGATGTTTAGTGC 2873
Qy 2781 -TCTGACGTATGACCCCTGTGCTCTTGTCTACTCTGAGGCTAAAGATCACTGCTACT 2839
Db 2874 TTATCCCTTATGACCTTTCTGTTCCTTCCACTGAGATGATGAGACGCTGCTATCT 2933
Qy 2880 GATGAAGCAGGTGCTCAACTTCACTGTAAGAGCTTGTCTCTCCCACTGACAGAGTT 2899
Db 2934 GATGAAGCAGGTGCTCAACTTCACTGTAAGAGAGTGTCTCTCAATCTGATAGTT 2993
Qy 2990 CCAGCCCTAATGAGAGGTGTGTAACCTTCTGACCAAACTCAGAACTCAGCTAGCTC 2959
Db 2994 CCAGCTTATATGAGAGGTGTGTGCTCTTCCAGGCTCAGCTCAGCAAGCTAAAGC 3053
Qy 2960 CTGTGTAGTCTGACTGTGCTACCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3019
Db 3054 ATGTATAGTCTGACTGTGCTACCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3113
Qy 3020 AACCCGAGGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3079
Db 3114 ACCCCCTTAAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3173
Qy 3080 ATCATAGGCACTTGAATATGATCAAAAGCTTTGGCTTCAATTGATGATATCTTGG 3139
Db 3174 TTGGCAGAGGTGTATCAAGAGTCA-----TTTGGGATCATAGATATTTGCTTTGC 3226
Qy 3140 TTTGTATAGTGAAGCTTATTTGTTTATTCATGGAAGAAATCAACTCAATTTCTGTA 3199
Db 3227 TTTGACTAGTCAACTTTGAGTTTATAGTGTGAATGGGTCTGGAATTAAAGTATACA 3286
Qy 3200 GGATGAAAGATGTTGGAGCAAGAAAAGCCCTAGATAGAGAAACAGATCTGCTGAGTA 3259
Db 3287 GAAGCGCATGTGTTGTCTCTGGAAAAAAGCACTCA----- 3325

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Qy 3260 TAGTACTTATGGGGGAGACAGGGGCGATATCCACTGATGATCAAGTACTTG--TGGGAGA 3318
Db 3326 -----GGTTGCTAAGATGAGAAAGGTGTGGGAAAAAATCTAATATGTGGAAA 3374
Qy 3319 GAATTCATGATGATCAAGTACTTGTGGCATGAGAGATCCACTGATCAAGTACTTGTG 3378
Db 3375 TGATCCATTAGTCTAAGTGTGTGAGGGAGGGAGTGGCATGGAGAAATTTGAAGAG 3434
Qy 3379 GGGGAGGGAATGCGACAGACCAAAAGTTGAAGGAGAGAGATGAGAGGCTCATGT 3438
Db 3435 AAAGTGGAAATGGGAAGCTTAA-----GTGCGT 3465
Qy 3439 TGGGGTGTGAAGGTCACTCTTTTCCATGTATGAGAGTGAAGAAAAACA-GTGTG 3497
Db 3466 GGTGGTGGGACAGCTGTGGCCCTGTGTATGTATGTGGAACCAAAATGGAGGCGTG 3525
Qy 3498 TGAATTGATGTCTTCAACACCCCAACTATGAAACATTCACGAGAGCGGCGACAG 3557
Db 3526 TGAATGTATGCGCTGAACATTTGAAACTATGAAAAAAGTTGAGTGAAGTGGGCCA 3585
Qy 3558 TGTGGAGACCTGGCATTTAGGA--AGCGCGCTTTTCAACAGAGAACTTATGCTC 3615
Db 3586 GTAAAGGCCCTTAGACTTACTGAAGAGGCTTAATTTTCAATGAGATGTTTATGTAC 3645
Qy 3616 ATCTGTGTGCTACCTCCACCTTGTATGAGGTTCACTCAGGTTTCTTTCTA---- 3670
Db 3646 ATTTCTTCTTCAAGCATGACATTTTCTGAGATTCAGATGAGTTTATTTCTTACAGA 3705
Qy 3671 -----CGTTCTTCTACTGTGTGAAACTTCAAGTATTTCCCAAGA 3714
Db 3706 ATTTGATTAATCTACTCCGCTCTTCCCAAAATGAACTCAGTAAAGATTTCCAAAGA 3765
Qy 3715 CGAGAGAGCTCTTCTGTATGAGAGAGAGCTGATTTTCACTGATGATGAGAAATAG 3774
Db 3766 TGAAGAGGTCTCTTGAAGAGAGTACTGTGATCTTGGGCTCCAAAGGAATTAAGAG 3825
Qy 3775 CTCAGAGATCTAGGTCAAGTAAATCTAGGTCAAGCGGCAAAATGATGAAGCC 3834
Db 3826 CTCAGGAATCTAGGTCACTGTGAATCTAGGTCACTGTGGGCAAAATTAAGAGCT 3885
Qy 3835 TCTATTCAGGTGAAGGTCACTGCTCAATATATCTGAGTATTTGGCTCCCAAGCA 3894
Db 3886 TTAATTCAGGTGAATTTACTGTATCTCCATGTGGGTGAGGTTCATTAAGTTTCA 3945
Qy 3895 TAAATCTGTATGGA--GTGCGTTTATTTTGGAGACATCAGCGGTGACAGACAGA 3953
Db 3946 CAACATTAAGATGATGCTGTGTATTTATGATATGAAAGTATGATGACTTGCA 4005
Qy 3954 CATCCAGAAAGATGCAAGAGCTGAAGAGACAGTGAAGAAAGTATTTGGCAAGCA 4013
Db 4006 TATCCAGAGATGTCAGAAAGCTGAGAGACAGATGAAGAAAGTATGATATACGT 4065
Qy 4014 CAATCTAAGCCATTCACTAG--GAGAGTGGGATTTCTTCTGCTTCCAGTCTCT 4071
Db 4066 CAATCTAAGTATCATATGAGAGACAAATGTTGTTTCTTCTTCTTCTTCTTCTTCC 4125
Qy 4072 TCTATTTGTATCAATTTATTTGACTGTGTATCTATCTGTGTATCTCTGCTTCTG 4131
Db 4126 ATCACTTTGTATTTTCACTGATTTCTTCAACCAAGGGGATTA---CTTTGGGT 4181
Qy 4132 ACCGTATCTAGCTGGGTCTATAGATCTTTCATGTGTCTTAATTT---GTAAGTAC 4188
Db 4182 CTGTATATGATATATATCTATATCTAGATGTCAATTTCCAAATCTTGCAAAATTGAG 4241
Qy 4189 AATCTGAGCTTACAGAAAGCTTATGCTCAAGCACTCATGAGCATTTGCTGGAGAT 4248
Db 4242 AATCTTAAGACTGTTGGATCTTATGCTTCTATGACATTAACCTCAGATTTCTGGGAT 4301
Qy 4249 GCGTTGTACAGAGTCAATGCTTAAGAGACAGATCCCTGATTTCCAGCTCTGCACTG--C 4307
Db 4302 GGTCAGTGCAAGATGAGGCTTAAGATCAGGTCTCTGAAATCCCAAGCCAGCACTTTTC 4361

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OY	4308	TTACTGGCGCATGTGTAATTA	CTTTGGCTGTGATTAAGTA	TTTGGGAA--	-GGCACTTCCCA	4365		
Db	4362	CCGGTGGGATACAGATTAG	TTTTGGTACCACTTAATCT	TTCGGGAAATTC	CAGATTCCTTA	4421		
OY	4366	CGGACCTTCATAATCTG	TAAGAACCATGCAT	TGAAACATAGAA--	-GCTGGGCAACAAC	4421		
Db	4422	TTGACTCATGTAACTG	TAAGAAAGTACTTGTT	TAAAAACAGAAATATG	CGCTATGGGCAAT	4481		
OY	4422	TTACTAGAGATGATTTTT	TGAGCTCATTAAACGAT	GTCTGAAA	TGTGGCAAAATCAAC	4481		
Db	4482	TTATTTGAAGTCATTTT	TGAAGTCATTAATGAT	CTATGCTTGAAC	CTTGGAAAGATTA	4511		
OY	4482	CAGAAATACACAAAGAG	CTGGAATTGGCAAT	TGAGACAGTATTTAG	AATCACTGGTAT	4541		
Db	4542	CAGAACATAGGAAAGAG	CTGGACCTGCATATAG	GGGTAAATTTCTCGA--	-GTAA	4594		
OY	4542	TAAATAGCATCATCTTA	TATAAATATATGGGCT	ATATATATATTA	TGAATTAACAA	4601		
Db	4595	TAAACACTTATTTTGA	ATTATACATATATCTAT	CAGATATGATTATAT	TATGTTTAAAGCA	4654		
OY	4602	GAGTGGATAGCCTCCCA	TTTACTTGGCTGGTTT	CAAAAGATMAAAATAT	CACTGATG	4661		
Db	4655	GAGCAGACAAC--CGA	ATCTTTTATACAGGTT	CAAAATAGATMAAAAT	TATGTAAGA	4713		
OY	4662	GATTATATTATATGT	CATGAAGATAGATGA	AAACCTTTCTTACTTA	CTTTTCACTTCA	4721		
Db	4714	GATTTATATATGTTAA	TATGAAAGCTGTAAT	TGGTAAGCTTTTTTTT	CTTCTCTCCCA	4773		
OY	4722	-----TTTCTTAGTT	TTTTTTTTTTCTTCA	CACCTTGATTC	AAGCCATAGTACACT	4773		
Db	4774	TCAAGACCTTCATTC	TAGTTTCTTCTCTCA	CTCCCTC	MACAAATCCCTTAGGGAGCA	4833		
OY	4774	ATTCGCTGTAGCTAT	TATATATATGATCTT	TACAGCAACAACAT	TGCTGTGTGGCCTTTGG	4833		
Db	4834	ATCATTGTGGGCTGT	GTATATCTTCTATGT	GAATGATATACAT	CAATGTGGCTTAATTTGG	4893		
OY	4834	GGAAGGGAACGATAG	CAGAGGCTCAGGCTAG	CAAGCTGACTTG	CCCTTAAAGCCAGA	4893		
Db	4894	TGAAGAAGAAC--ACA	TATGAAAGGCTTAGAT	CTAACATATAGTAC	CAACCCCAAAACCGGA	4951		
OY	4894	GGCATGTGTGATAC	AGAGAAATGAGAGCT	CTTGGCAAGTGGGTGT	GCTTAATATACAG	4953		
Db	4952	GGAATGATTAGGAC	AGTGAAGTGAAGCTCTT--	GCAAGCGATACAACT	TAAATATACAG	5010		
OY	4954	AAACAGGAAGGCT	CCGGTGTATGGAAT	TATCAGTAAG--	-----TATCAACCTTA	5003		
Db	5011	AAACATGAAAGGCT	CAAGTATGAAATTTT	TAGTAACAAGCTTA	CACTTAATTTCCCTTT	5070		
OY	5004	TCTCCTTCTATCGA	CACTTAATGCTCTCTTTT	CTTGTGTGTAGGCT	GATTAACACACTT	5063		
Db	5071	TTTCCCTCTTGAC	TTTTTAAAAAAGCGTTT	CTTCTAGACAT	CAATTAATATAGTGTACT	5130		
OY	5064	GTT--TTCTTTGAG	TGTCTATGCGCTTT	TGATTTTTAGTGT	CTGTGCCAGTCTTGT--	5119		
Db	5131	GTTTCTTCTTGTAT	TAAATGAAAGCTTGTAT	GTATTAATGTG	TAAAGCCAGTCTCTCTG	5190		
OY	5120	TAGAGGGTTGTAT	CTTGAACACCTGGGCT	TGATGTATGAC	TGACCAAGGCAACA	CTT	5179	
Db	5191	TTATATGAACTAT	TCTATGACATGAGG	GCTGAATGTATG	ATCATGCACAGACAGG	CATG	5250	
OY	5180	CTGATGCTGTGTAA	AGGTTATATTAATTA	CT-----	TGTCTTTGGAAAGT	5231		
Db	5251	CTTTATACATCTT	GTCTTAAAAAATTA	CTGATTTATCTGT	GTGTGCTTTA	AAAAGT	5310	
OY	5232	GAAGCGTGTGAGAA	AGATCTCACAGAGAT	GTGTCTGTATG	AGAAACTTTTTTTT	5291		
Db	5311	GAAGTGTGAGAGAG	AGATCTCATGTGG-----	-----	-ATCTGTGT	5347		
OY	5292	CCCCCTAAATGCT	ATATATACACTT	TGCTCA-----	ACTTGA	CTTTTATACATG	CGTGC	5348
Db	5348	GATTTTCAAGAC	CTTTATATCAATTTT	TGAAGATATATTT	CAATATTTTGCA	TGGGTTGCC	5407	
OY	5349	ACATGAAAGATG	TTTAGCCCGCTCT	CATGAGCTCT	GTGGAAAGCA	CCATATAGGGAAG	5408	

Db	5408	ATGTGAAGGTGATTAATGCTTTTCTTGCTGTAAGCTTACAGAAACCA-CAGAGGGAGAGC	5466
Oy	5409	AATTTTATGCTGANAATACTGACCCGACAGGAAACTGTCAGAGCTCCCCGA-----	5462
Db	5467	AATTTTGTTCAGANAAGATCAACAGAGAGGAAACTGTGAGAGCTGTCAATTAGGT	5526
Oy	5463	-----GACCAACCAAGGTGTTAAGTAGAAACAGTCCAGGGTGGCTCAT	5506
Db	5527	GGTTTGGGAGCATTAATTCCTCTGCTGGGGGTAAAGCAACAGCAAGTTGGTGTAGT	5586
Oy	5507	GTAATAGAAATGGAACAGAGCGAGGAGATAGTACTAAAGTTTCATAGGGTCC-GGAGT	5585
Db	5587	AAAT-CCATGACAGACATGAGGGACGATTAACCTTAAATTTCTTTATATCTTGGAGT	5645
Oy	5566	CTTAAAGATACAAATATAGCTGC--TTGGGCTTCAATAAAGAAAGTCTGGGAAGGCAGC	5623
Db	5646	CTTTGAGATGAAAAGAAATATCTTTTGGCTTATGTCAAAAGAAAGATATGAAAGGTGAA	5705
Oy	5624	AAGTAGAGGGAATGGAAGGAAAAAACAAGATGTAAGAGACTTGAACCTACATCAAT	5683
Db	5706	AGGCGGAGAAACAGAA-----AAGAAAGAACATGTATTTATATAGAGA	5753
Oy	5684	CCTTACCAACCAATTTTCTTGGAACAATATAGAGTATGATATGATTTGCAG	5744
Db	5754	CAATGTGACACAGGTTTTCTTGAAATATGCAAAATATGATATGATAGAGAAATTCGT	5813
Oy	5744	GGGACTTGCTTGGCATTTGAATCGGGTTTTCTCTCCATTGAGGTTGAAAGCCGCA	5803
Db	5814	AGGGAATGCTTTTCACTGAAATTTGGGTTTCCTT--TCGATTAAGTTTGGATCTTCA	5876
Oy	5804	CCCTTTTACCCCTGCAATGAGAGAGAAAGAGGGTGTATATGACTCTTACCTGAGATT	5863
Db	5871	TCGCAATTAGCT----TGAGAGAGAAAGATAAATGTTAGACCTATATCTGGTTTC	5928
Oy	5864	TACTAGTTTACGCAATGGAACAGACACTCGGAGCTCTCTTGACAAAAAAATGGAAC	5922
Db	5927	TATTAATTAAGCAAGTGAAMAACCTATTTGGTATTTTCCCAAAAGTGAACATT	5986
Oy	5924	CTGTGTTTGTCTGTTGTTGTTCTTTGTAGAAGCAAGCAAGCCGACACATG	5983
Db	5987	TTCTTTTACTGTTGTCAAAAAGGTGGAATAGAAAAAGCTTATATGATTTGGTAATAC	6046
Oy	5984	GTTGAATGTGGGTCTTTGAGTCAAGGCTTTTGAATGAGCACTCATATAGTT-----	6037
Db	6047	ATGTTTCAAGTCAATTGAGTAGAGATGTTTAAATCAGAGTGTCCAAATATTGGCTT	6106
Oy	6038	-----GATCATGTCAAGTGAAGGCTACCTGTCAAGCCGAGCCTG	6079
Db	6107	CCCTGACACACTTGAAGAATGTCTTGTGACACATMAAATACAAAGAACATATAGCTG	6166
Oy	6080	CTGGCTTGCACCTTAACATCTCCAGGTCTCAGTATCACTTCTGCTACTTATGACACATTA	6139
Db	6167	ATGAGCTPAAAAAGTCCATGCATTAATCTCATACTGTTTAAAGAAAGTTTATGAAATTTCT	6226
Oy	6140	GGAGTTAGCAAAACCTTTTTC-----AAC	6166
Db	6227	GTTAGGCTCATTAAGAGCTGTCTTGAGGCAATGCGGCTGTGGGCTGCAGTTGAGCA	6286
Oy	6167	CCCCACTAAAATTTAATGACAAAAGCTGTATATTGTGGATACAGTGTGATTAATG	6226
Db	6287	AGCTCTTATATGATATCTGTCAATAGATGTTTGGAGCTGCAAAAAGGCCAAGGCATTA	6346
Oy	6227	A-----TCATATGTGCAATGTG	6244
Db	6347	ATGGGTGGCACTGGGATCCCCAGATCCAGCTCACTTCAATGTCCTTGCTTGTTTA	6406
Oy	6245	CAAGTTCATTAATATAGATTAATATAGGCCCATCAACAGCTTATGGGTGTAATGCAAG	6304
Db	6407	AGAAAGGGGTGTAACCTCTCTGCCAGCTTTTAAACAGCTTCAATTAAGTATAGGTGACCC	6466
Oy	6305	TAAATATAGTATAGATGCTGTGGTGTCTTAAAGTCAGAAAGGCATGATTTTAAGGCTTGG	6364

Db 7571 TTAATTGTATGATCACTTAATAAATAGTCCAAAAGGAAGAAAACAATATATAGATTA 7512
Qy 1368 AAAAAACAGCTAGTATAGTTAGATTCACATATACATAA-----AAATAGA 1417
Db 7511 GCCAAGCAGCTATATTTTGAACAATAAGTGGTTTGAATTCAGCATGTTTAAAAATGA 7452
Qy 1418 GATATATATTTTAAAAATGAATAATCTCCAGTTTTCATATATGCTTATTCGAAG 1477
Db 7451 GATATATATTTTAAAAATAGG--AATGATCTGTTAGCTGTCATTAACATTTACTTAAAG 7393
Qy 1478 CACAGATATAGGACACGGGCTTTTATTTCTGGTCACTTCTAAAGATATAGATCTAT 1537
Db 7392 CAGAGATATAGGACATGGGCTCTTTTCTGATTCACCTCCATATGATATAGATCTAT 7333
Qy 1538 GAAATGGTGGAAAATAGATCCGTGACCAAAACGCTGACTCAATAGCTTACGGAGATCA 1597
Db 7332 AAAGCTGGTAGAAAATGAGTCCGTGACCAAAATGCTTACTCACCCACTATAGAGATCA 7273
Qy 1598 AAGGCTGCTACTCAATCAAGAA--TCTACTACGGCAAAAGCCATGGCTTTCTTGAAA-- 1654
Db 7272 AAACATTTTAACTAAATCTGAATCTACTAAGCAAAACAAATGCTTTCTTGAAAAT 7213
Qy 1655 ---CCGTTTAAAGATTTCTGGGATTTGTGCAAAAGACCTTGTGGCCCTCACCG 1711
Db 7212 ATGTAGGTTTAAAAAATTTCTGGATTTGTCTGTAAA--TACCCTCCGGCTTAAATAG 7154
Qy 1712 TGAAGTTTAAAGGAAGACTTCCCATCTTCAAGGTGGAAAGCTTGGAGGTGTCTTG 1771
Db 7153 TGAAGTTTAAAGGAACACTTGACATCTC---MAGGTGAAAAGATAGAGGTGTCTTG 7097
Qy 1772 TGGCTCTCTATAGTGTGTAGTACTTCTCAGAAAGACGACTGGAATATGATATGTCT 1831
Db 7096 TGGGCTCTCTGTGTGTAGTGTGTCTCTCAGAAAGACGACTGGAATATGATATGTCT 7037
Qy 1832 GATGTCATATCATTCACAAATACCAAAAACCCCTGGTCCCGATGGCTTAAAGAGC 1891
Db 7036 GATGTCATATTTTTCACAAAT--TAAAAAAGATCAGATATCTGGGGCTTAAAGAGC 6979
Qy 1892 AACTTGTGCTCTCCATCAACAAGCAGACACCTAAACAGTAAAGACTCAGACTCTTA 1951
Db 6978 AGCTTGTACTTCCCGCTCAACAAGCAGAACTTCAAGAAAGGTAAAGGTTCGGCAACT 6919
Qy 1952 CAGACAA--TCACTGTGTGTGTACATGTAACCGACGAATGCTCCCTGATGTTTT 2009
Db 6918 TGTATCAATGTGTGTGTGTATGAATACTTGTGATTAATTTGTCTTCAAGTGTCT 6859
Qy 2010 GCCTTTTGTCTCTCACTAAGGCTCTCTCTCACTTATCACTGTGACACTGTGCG 2069
Db 6858 TTGACCAAGGTTCTCTCTCC-----CAGTCAACAGTTGCTCGAGTTAGAAAT 6811
Qy 2070 ATCTGTAGTGTCTCTCTGAGAAATCTATAGTTTTTCCCTTATGGGACTTTGGCCGC 2129
Db 6810 GTGTGCAATGGCCGCTGCAAGAAATGTGTAGGCTCTTCTTATGGGAAACCTGGGCAC 6751
Qy 2130 CAGCTGTCTGTCTCTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2189
Db 6750 CAGCTGTCTGTCTCTGT 6691
Qy 2190 CGGATGCAAGCTTGAAGTGTCAAACTCCAGAGCCGATACATGCTCAACGCACTTAT 2249
Db 6690 CCACTGAGGCTTGAAGTGTCAAACTCCAGAGCCGATACATGCTCAACGCACTTAT 6631
Qy 2250 GCTGAGCAAGAGGATCAGCTGCACTCTTCTCT-----C 2285
Db 6630 GCTGAGCAAGAGGATACATCTCAATCTGCTCTTCTGTTGATCTATGGAATCC 6571
Qy 2286 CATACCCCTTGTCCATTTTCTGTGAAGCACTTGAACCTTTTATGAGGCTTTATCTCC 2345
Db 6570 AAATAGTTTAAACCTTTCTTCAAGCATCTTAAAGCTTTTGAAGAACCACTGTTAT 6511
Qy 2346 GCAAGTCTACTACTATGTTTCTGTCTTGAAGACTCTTAAAGACTGGGCTTTT 2405
Db 6510 CCTGTAGG--GTATATAAATTTCTGTTTTCAGAGACTTGTGGAAATCTGGCTTTT 6453

Qy 2406 TCTATTTCTATTTCAAGGCTCTCAGACCATTTCTATCTTGGCCTTCAAGACATATAC 2465
Db 6452 TTTTCTTTTGTGAATCTTCTCC-----TTCCATTTTGGCTTTATGATATATAGA 6403
Qy 2466 TGAATTTTATCTCAGAGGCGCATTTAGAAGCCACCCAGACATGCAATCTTCC---A 2522
Db 6402 TGAATTTTCCCAAAGGCGCATTCAGTATCCATCTGATGATTTTTTTTCCCTTA 6343
Qy 2523 TTTCTGTGCTCTCTTCTGAACTCACTCTTGTGACTC----- 2565
Db 6342 TGCCTGTGTCATTTGTTCTTAACTCATGCAATCATGAAATCTGCTTTAGCTTATG 6283
Qy 2566 -----CTGAACCCACTGCGGACATATCATCTTCAAGGCTTTCTTCCATCTC 2617
Db 6282 ATGTCTCTGGGAGACGAGATGGGACATGCTATGATATATATTTTCTTATTTG 6223
Qy 2618 CTGTCAACCCAGGCACTTATGGGTTTC--TCTTTCAAGGCACTTGCAGATTAACACA 2676
Db 6222 CTCAATGTCCAGACCTTATGCTTCTTCTCTTCTTCCAGGCTTGGCTGATTAACACA 6163
Qy 2677 CAGAGTCCGGCTCATTCGGGAGAACTGTTCCAGAGATCACTGTATAGTCTCACTGTG 2736
Db 6162 CAGACGTTGCTCTCATTTGGGAGAACTGTTCCAGGAGTCACTGTATAGCTACAGTTGTG 6103
Qy 2737 ATAGCAAGGC-----TAGCTGGGAGCTGTGTGAACCTCTGGGATAG-- 2780
Db 6102 ACBAACAGGCGCTGTGCGCTCCATGGATCTTGGGAGTGTGTGTATGATGTTTGTGTC 6043
Qy 2781 -TCTGACATATGACCCCTGTGTCTTGTGTCTCTGATCACTGAGGCTTAAAGATAGTACCT 2839
Db 6042 TTAATCTTATGACCTTCTGTCTTCTTCTTCCCTTCCAGATATGAGAGCTGTACTCT 5983
Qy 2840 GATGAAGCAGGCTCTCAACTTCACTCCGGAAGAGCTTGTGCTCCCTCAGACAGTT 2899
Db 5982 GATGAAGCAGGCTCTCAACTTCACTCCGGAAGAGCTTGTGCTCCCTCAGATATAGTT 5923
Qy 2900 CAGCCCTATATGCAAGAGGTGTATCTTCTGACCAAACTCAGCAATCATGCTCACTC 2959
Db 5922 CAGCCCTATATGCAAGAGGTGTGCTTCTGCGCAGGCTCAGAAACAGGCTAAGAC 5863
Qy 2960 CTGTGTATGCTGTACTTGTGTACTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3019
Db 5862 ATGTGTATGCTGTACTTGTGTACTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5803
Qy 3020 AACCGAGGCTCGCCCTCTCTCTTCAAAAGTGAAGAGGCTCAGACACACACC 3079
Db 5802 ACCCTCTTACCCCACT 5743
Qy 3080 ATCATAGGCACTTGAATATAGTCACAAAAGCTTGTGCTTCAATTGATATATCTTTAG 3139
Db 5742 TTGGCAGCAGTGTATCAGAGTCA-----TTTGGATCATAGATATTTCTTTTTC 5690
Qy 3140 TTTGTATGATGAGCTTATATTTGTTTATCATGGAAGAAATCACTCAATTTCTGTA 3199
Db 5689 TTTGACTGTGTCACTTGTATGTTTATGTTGTGAATGGGCTGTGAACCTTATGATGTA 5630
Qy 3200 GATGAGAAAGATGTGTGGAGCAAGAAAAGGCTTATATAGAGAAACAGATCTGCTGATGA 3259
Db 5629 GAAGCCGATTTGTTGTCTCTGGAAAAAAGCACTCA----- 5591
Qy 3260 TAGTACTTATGGGAGGAGCAGGCGGATATCCATGAGTACAAAGTCTTG--TGGGAGAG 3318
Db 5590 -----GGTTGCTATAGATGAGAAAGGTTGGGAGAAACATCTAGATGTGGAAA 5542
Qy 3319 GAAATCCATGATATCAAGTACTTGTGTGATATGATATCACTGATATCAAGTACTTGTG 3378
Db 5541 TGGATCATTTGATCTTATGTTGTGAGGAGGAGATGATGAGAAATTTAGAGAG 5482
Qy 3379 GGGGAGGAGAAATGAGCAGAGCAAAAGTGAAGAGAAAGATGAGAGGCTCATGCT 3438
Db 5481 AAAGTGGAAATGAGAAAGCTTAAA-----GTCCGT 5451

QY 3439 TGGGGGTGTAAGGTCCTCTTTTCATGTGTGAGAGTTAAGAAAACA-GTGTG 3497
DB 5450 GGTGGGTGGGCAACCTGTTCCCTGTGTATGTATGGAGCCACAAAATCGGAGCGTG 5391
QY 3498 TGAAGTGTATGTCTTCAGACACCCCACTATGAAAATATCCACGAGGAGCGGAGAC 3557
DB 5390 TGAAGTGTATGTCCGCTGACATTTGAAACTATGAAAAAAGTTGAGTGAAGTGGCCCA 5331
QY 3558 TGTGGAGACCTGGCATTTAGGGA--AGGCGCGGCTTTTCACAGAGAACTTTATGCTC 3615
DB 5330 GTAAAGGCCCTGAGACTTACTGAGAGGGCTTAATTTTCAATGAGATGTTTATGTTAC 5271
QY 3616 ATCTCTTGCTGACCTCCCACTTGATGATGAGTTGAGTCAAGTCTTCTGTTCTA----- 3670
DB 5270 ATTTCTGTTCTAAGACATGCAATTTCTGAGATACCATTTAGAGTTTATTTCTTTACGA 5211
QY 3671 -----CCGTTCTTGCTAGTGTGGAACCTTCAGTGGAGTTCCCAAGA 3714
DB 5210 ATTTGCATTAACACTCTCCGCTCTTTTCCAAATGCAAACTCAGTGGAGTTTCCCAAGA 5151
QY 3715 CGAGACAGCTCTTCTGTAGAGGAGGACCTGATTTCACTGTCTAGAGACGAATAG 3774
DB 5150 TGAAGAGAGGTCTCTGTAGAGGAGGACCTGATTTCTGCGCTCAAGGGAATTTCAAGAG 5091
QY 3775 CTAGAGAACTTGTGTCACGTAATCTAGTCAACGCGGCAAAAATGACTGAAGCC 3834
DB 5090 CTAGAGAACTTGTGTCACGTAATCTAGTCAATTTGGGCAAAAATTTACTAGAGCT 5031
QY 3835 TCTATTCAGGTAAAGGTGACGCTGATATCTAGATGATGGGCTCCACCGGA 3894
DB 5030 TTAATTCAGGTAAATTTGTAATCTGATCTTCAAGGCTGAGGCTTCAATTAAGTTACGA 4971
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DB 4970 CAACATTAAGATGATATGCTGTATTTGTTATGATGATTTGAAGGTATGATACCTGCA 4911
QY 3954 CATCCAGAGAAATGTCAAGAGGCTGAAAGACAGATGAAAAAGTACTATTGGCAAGCA 4013
DB 4910 TATCCAGAGAAATGTCAAGAGGCTGAAAGACAGATGAAAAAGTACTATTGGCAAGCA 4851
QY 4014 CAATCTAAGCAATTCAGTGA--GAGCGTGGGATTTCTTCTGCTCCAGTCCCT 4971
DB 4850 CAATCTAAGCAATTCAGTGAAGAGACAAATTTGTTTCTTCTTCTTCTTCTTCTTCTTCT 4791
QY 4072 TCTACTTTGTATGATTTATTTGATCTGCTGATCTGATCTGATCTGATCTGATCTG 4131
DB 4790 ATCACTTTGTATTTTCACTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4735
QY 4132 ACCGTATCTAGCTGGGTCTATGATTTTCAATCTGTGTCTAATTT--GTATGTCAC 4188
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QY 4189 AATTTGAGAGCTGAGAAAGCTAGCTGACAGCTGATCCCTGATTTCCAGCTGACCTTG 4248
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QY 4249 GGTGTGTGACAGATCATGCTAGAGACAGATCCCTGATTTCCAGCTGACCTTG-C 4307
DB 4614 GGTGTGTGACAGATCATGCTAGAGATGAGGTCTCTGATTTCCAGCTGACCTTCTTCTTCTTCT 4555
QY 4308 CTGTGTGACATGTGTATTTCTTTGCTTATTTAGTATTTGGAAA--GCCAGTTCCCA 4365
DB 4554 CCGGTGTGTATGATGATTTGTTGTATGATTTATTTCTTGTAGGAAAATTTTCAATTTCTTA 4495
QY 4366 CGGAGCTACATATCTGAGAAACCATGATTTGAAAATAGAAA-----GCTGGGCAAAAC 4421
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DB 4434 TTAATTTGAGTCACTTTGTAAGTCAATTAATGATGCTTTGAACTTGAAGATTAATCT 4375
QY 4482 CAGATTAACAACAAAGAGCTGATTTGCCAATGAGCAAGTATTTGAAATCACTGTAT 4541

DB 4374 CAGAACATGAGAAAAGAGATGACTGTGATATAGGCTTAATTTCTGGA-----GTAA 4322
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QY 4662 GATTAATATATGATGATGAAATGATGAGTGAAGAACCTTCTTCTTCTTCTTCTTCTTCT 4721
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QY 4722 -----TTCTTATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4773
DB 4142 TCAAGACCTTCAATCTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4083
QY 4774 ATCTGTGTGACCTATTAATATGATCTTTACAGAAACATGCTGTGTGCTCTTTGG 4833
DB 4082 ATCCATGTGGGCTGTGTATCAATTTCTATAGTAAATGATACATCATGCTGCTATTTGG 4023
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QY 5463 -----GACCACCAAGGTTTAAATGAGAAACATCTCAGGCTGCTCAT 5506
DB 3389 GGTTTTGGAGGATTAATTTCTTCTTGTGGGGGTAAAGAGAAACGAGGTTGTGTAT 3330
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 Qy 6838 TTTTATGTCACTGATG--ATACACAGAAAAATATGACTTTAAAAATTTGTT-- 6891
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 Qy 7168 TATCAACAATCCATCATCATCATTAACCAATCATCTCATGATTTCAAGCTGACC 7227
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 Qy 7228 CATATTATA 7236
 Db 1508 CTAAAGAAA 1500
 RESULT 12
 HSA277248
 LOCUS HSA277248 5397 bp DNA linear PRI 30-MAY-2001
 DEFINITION Homo sapiens IL-22 gene for interleukin 22, exons 1a-5.
 ACCESSION AJ277248.1 GI:11967707
 VERSION AJ277248.1
 KEYWORDS IL-22 gene; interleukin 22.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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 AUTHORS Dunoulier, L., Van Roost, E., Ameye, G., Michaux, L. and Renaud, J.C.
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 MEDLINE 21069354
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QY 2471 TTATCTACAGAGGGGCAATT--AGAAAGCCACCAGACGTGCAATTACTTCCATTCTC 2528
 Db 1077 TTTTCCCAAAGAGCGGCATTCAGTAATTCATCTGATGATTTTTCCTTTATGCGCTC 1136
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VERSION     AX459972.1  GI:21725708
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            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
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  Dumoulier, L. and Renaud, J.C.
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  LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
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Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

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Qy      2094 ATCTATAGTTTTTCCCTTATGGGGACTTTGGCCGACGCTGCTGCTTCTCATTTGCCCT 2153
Db      89 ATCTGAGCTTCTTCTTATGGGGAACCTGGCAACAGCTGCTCTTCTTGGCCCT 148
Qy      2154 GTGGCCCAAGAGGCAATATCGCTGCCCTGCAACCCGGTGAAGCTTGAAGTGTCAA 2213
Db      149 CTGTGTACAGAGGAGACACCTGCCCATCACTCCACGTGACAGGCTTACAAAGTCCAA 208
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:06:30 ; Search time 6517.75 Seconds

(Without alignments)
18499.535 Million cell updates/sec

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Perfect score: 7445

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Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	149	2.0	149	17	AZ895851 RPT-24-2
5	113	1.5	534	17	AQ762065 HS_3136_B
6	110.4	1.5	377	17	AQ212781 HS_3118_B

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700 bp	mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500012D04;interleukin 10-related T cell-derived inducible factor, full insert sequence.	AK005228	AK005228.1 GI:12837639	HTC; CAP trapper.	Mus musculus (strain:C57BL/6J) adult male cerebellum cDNA to mRNA, clone:1500012D04.	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	ORGANISM	REFERENCE	1	Garnica, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning	10349636	REFERENCE	2	Garnica, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20499374	JOURNAL	GENOME RESEARCH	11042159	REFERENCE	1	Garnica, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20499374	JOURNAL	GENOME RESEARCH	11042159	REFERENCE	2	Garnica, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20499374	JOURNAL	GENOME RESEARCH	11042159	REFERENCE	3	Garnica, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20499374	JOURNAL	GENOME RESEARCH	11042159	REFERENCE	4	Garnica, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20499374	JOURNAL	GENOME RESEARCH	11042159	REFERENCE	5	Garnica, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20499374	JOURNAL	GENOME RESEARCH	11042159	REFERENCE	6	Garnica, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)	20499374	JOURNAL	GENOME RESEARCH	11042159	REFERENCE

ALIGNMENTS

accession AZ449260 clone UUCG1M0247J21 F, DNA sequence.
 version AZ449260.1 GI:10602872
 keywords GSS.
 source Mus musculus
 organism Mus musculus
 reference Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Euteheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 authors Dunam, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A., and Wright, D., Weiss, R.
 title Mouse whole genome scaffolding with paired end reads from 10kb
 journal Unpublished (2000)
 comment Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0247J21"
 /clone_lib="Mouse 10kb plasmid library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42mV; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 119 a 155 c 116 g 172 t
 ORIGIN
 Query Match 7.0%; Score 519.8; DB 17; Length 562;
 Best Local Similarity 97.5%; Pred. No. 3.6e-94;
 Matches 549; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 2350 GTCCACACTGCTGCTGCTCTTAAAGATC-TTAAAGACGCGGCTTTTCT 2408
 DB 1 GTCCACACTGCTGCTGCTCTTAAAGATC-TTAAAGACGCGGCTTTTCT 60
 QY 2409 ATTCTATTGAAGGCTCAGACCATTTCCATCTTGAGACACATATATCGA 2468
 DB 61 ATTCTATTGAAGGCTCAGACCATTTCCATTTTGGCCTTACGATACATATACGA 120
 QY 2469 ATTTATCTACAGAGGCGCATTTAGAAAGCACCAGACATGCAATCTTCATTTCTC 2528

Db 121 ATTTATCTACAGAGGCGCATTTAGAAAGCACCAGACATGCAATCTTCATCTC 180
 QY 2529 TGTGCTCTCTTGAAGTCACTCTCTTGGCTACTCTTGAAGCCACTGCGACATACA 2588
 Db 181 TGTGCTCTCTTGAAGTCACTCTTGGCTACTCTTGAAGCCACTGCGACATACA 240
 QY 2589 TCTTACTTACAGGCTTTTCTTCATCTCTTGGTCACTTGAAGGCTTTCTCTC 2648
 Db 241 TCTTACTTACAGGCTTTTCTTCATCTCTTGGTCACTTGAAGGCTTTCTCTC 300
 QY 2649 TTTGAGGCGGCTTGAAGTCACTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGG 2708
 Db 301 TTTGAGGCGGCTTGAAGTCACTTGAAGGCTTGAAGGCTTGAAGGCTTGAAGG 360
 QY 2709 CGAGAGTCACTGTAAGTCTCTCTCTGATGAGGAGGCTGAGGAGGCTGAGG 2768
 Db 361 CGAGAGTCACTGTAAGTCTCTCTGATGAGGAGGCTGAGGAGGCTGAGGAGG 420
 QY 2769 CCTCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2828
 Db 421 CCTCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 2829 CAGGCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2888
 Db 481 CAGGCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
 QY 2889 TCAGACAGGTTCCAGCCTTACAT 2911
 Db 540 TCAGACAGGTTCCAGCCTTACAT 562

RESULT 3
 AV030414 256 bp mRNA linear EST 31-Aug-1999
 LOCUS AV030414 Mus musculus adult C57BL/6J cerebellum Mus musculus cDNA
 DEFINITION AV030414.1 GI:4829962
 ACCESSION AV030414
 VERSION AV030414.1
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 reference 1 (bases 1 to 256)
 authors Carninci, P., Shibata, K., Ozawa, Y., Kono, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayashino, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Natsushima, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y., Tomioka, N., Watanabe, S., Yamane, M., Yamamura, T., Yokoyama, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 RIKEN Mouse ESTs
 Unpublished (1999)
 JOURNAL
 COMMENT Contact: Chie Owa
 Genome Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@rtc.riken.go.jp
 Email: genome-res@rtc.riken.go.jp
 Thermolabile and thermostable DNA polymerases for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (http://genome.etc.riken.go.jp) for further details.
 location/Qualifiers
 1..256
 /organism="Mus musculus"
 /strain="C57BL/6J"

	/db xref="taxon:10090"
	/clone_id="Mus musculus adult C57BL/6J cerebellum"
	/sex="male"
	/tissue_type="cerebellum"
	/dev stage="adult"
	/note="Organ: mammary gland; Vector: pT73D-Pac (pharmacia
	Ri / 1st strand cDNA was primed with a Not I - oligo (dT)
	priemer [5'
	TGTTACCATCTGAAGTGCGGCCGGCCGATGTGTTTTTTTTTTTTTTTTTT
	T 3']; double-stranded cDNA was ligated to Eco RI
	adaptors (Pharmacia), digested with Not I and cloned into
	the Not I and Eco RI sites of the modified pT73 vector.
	RNA provided by Dr. Minoru Ko, Wayne State Univ. library
	constructed and normalized by Bento Soares and M.Fatima
	Bonaldo."
BASE COUNT	88 a 29 c 41 g 98 t
ORIGIN	
Query Match	2.3%; Score 173; DB 9; Length 256;
Best Local Similarity	90.3%; Pred.No. 2.6e-24;
Matches 196; Conservative	0; Mismatches 20; Indels 1; Gaps 1;
Dy	6917 TAGAAAAAAGCTATGTAAGTCAATTTCCTCATAACCATATTATATAGTAGTTAT 6976
Dd	40 TGGGAGGATACCCATATGCATATTCCTTCCATAACCGATACCTATTATATGTAAGTTAT 99
Oy	6977 TTATTATAGATACATTTTATTTATATGTCAGTTATTAATNGATTTATTATTAGAACA 7036
Dd	100 TTATTATAGATACATTTTATTTATATGTCAGTTATTAATNGATTTATTATTAGAABA 159
Oy	7037 ATTATCTGCTATTTGATATTT-AGTAAAGGCAAATAATATTTATGACATTAAGTAAA 7095
Dd	160 ATTTATCGATGTTGATATTTAGATATAAGCAATAATATTATGATATATACATATGAA 219
Oy	7096 ACAAGATATCTTAGGCTTTAATTAACACATGATATC 7132
Dd	220 ACAAGATATCTTAGGCTTTAATTAACACATGATATATC 256
RESULT 4	AZ895851 149 bp DNA linear GSS 05-MAR-2001
ZLOCUS	RPci-24-21IK19.TV RPci-24 Mus musculus genomic clone RPci-24-21IK19
DEFINITION	, DNA sequence.
ACCESSION	AZ895851
VERSION	AZ895851
KEYWORDS	AZ895851.1 GI:13214796
SOURCE	GSS.
ORGANISM	Mus mouse. house mouse. Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus. 1 (bases 1 to 149) Zhao,S., Niemann,W., Malek,J., Shatsman,S., Akintec,B., Levine,M., Teegaye,G., Geer,K.K., Krol,M., Shareshbeyn,A., Gregoregis,E., Russell,D.P., de Jong,P. and Fraser,C.M. Mouse BAC end Sequences from Library Rpci-24 Unpublished (1998) Other_GSSs: Rpci-24-21IK19.TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: szhao@igf.org Clones are derived from the mouse BAC library Rpci-24. For BAC library availability, please contact Pieter de Jong (pjeong@mail.nih.gov). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.html). BAC end page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html Plate: 211 row: K column:19
JOURNAL	
TITLE	
COMMENT	

FEATURES	Source	Location/Qualifiers
	1. 149	/organism="Mus musculus"
		/strain="C57BL/6J"
		/db_xref="taxon:10090"
		/clone="RPCT-24-211K19"
		/clone_11b="RPCT-24"
		/sex="Male"
		/cell_type="Spleen/Brain"
		/note="Vector: pTRABAC1; Site 1: BamH1; Site 2: BamH1; RPCT-24 Mouse BAC library produced by Pieter de Jong. The library was cloned in the pTRABAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
BASE COUNT	49 a	24 c 18 g 58 t
ORIGIN		
Query Match	2.0%;	Score 149; DB 17; Length 149;
Best Local Similarity	100.0%;	Pred. No. 1.9e-19;
Matches 149;	Conservative 0;	Mismatches 0; Gaps 0;
Qy	1155	TGTCAGAGAAATTGCAAGTATGTATTTATTTATTTAAAAAATCTATGCTTAAAT 12144
Db	1	TGTGAGAGAAATTAGCAAGTATGTATTTATTTATTTAAAAAATCTATGCTTAAAT 60
Qy	1215	GTCATATAGATTGTTCACTACCAATATTTCCAACTTAACCTGACCTTGCTATGATTTT 12744
Db	61	GTCATATAGATTGTTCACTACCAATATTTCCAACTTAACCTGACCTTGCTATGATTTT 120
Qy	1275	AACCTTGATTTTGATCTATCACTATCAACATACAG 1303
Db	121	AACCTTGATTTTGATCTATCACTATCAACATACAG 149
RESULT 5		
AQ762065		534 bp DNA linear GSS 28-JUL-1999
LOCUS		HS 3136 B1 H07 T7C CIR Approved Human Genomic Sperm Library D Homo
DEFINITION		sapiens genomic clone Plate=3136 Col=13 Row=P, DNA sequence.
ACCESSION		AQ762065
VERSION		AQ762065.1 GI:5640181
KEYWORDS		GSS.
SOURCE		human.
ORGANISM		Homo sapiens
		Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE		1 (bases 1 to 534)
AUTHORS		Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
		Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
		Hood L.
TITLE		Sequence-tagged connectors: A sequence approach to mapping and
		scanning the human genome
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE		99380589
COMMENT		Contact: Mahairas GG, Wallace JC, Hood L
		High Throughput Sequencing Center
		University of Washington
		401 Queen Anne Avenue North, Seattle, WA 98109, USA
		Tel: (206) 616-3618
		Fax: (206) 616-3887
		Email: jwallace@u.washington.edu
		Clones may be purchased from Research Genetics (info@resgen.com).
		BAC end Web Server: http://www.htsc.washington.edu
		Plate: 3136 Row: P Column: 13
		Seq primer: T7
		Class: BAC ends
		High quality sequence stop: 534.
FEATURES		Location/Qualifiers
Source		1. 534
		/organism="Homo sapiens"
		/db_xref="taxon:9606"

RESULT 6
LOCUS AOQ212781
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

AOQ212781 377 bp DNA linear GSS 18-SEP-1996
HS_3118_B2_B08_MR_C1T Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3118 Col=16 Row=D, DNA sequence.
AOQ212781
AOQ212781.1 GI:3623982
GSS.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 377)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contract: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	COMMENT
<p>RESULT 7</p> <p>A0104025/c</p>	<p>389 bp DNA linear GSS 28-Aug-1998</p>	<p>A0104025</p>	<p>HS_3108_B1_C01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=1 Row=F, DNA sequence.</p>	<p>AQ104025</p>	<p>AQ104025.1 GI:3478961</p>	<p>GSS.</p> <p>human.</p>	<p>Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.</p> <p>1 (bases 1 to 389)</p> <p>Mahairas G.G., Wallace J.C., Smith R., Swartzell S., Holzman T., Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and Hood L.</p>	<p>Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome</p> <p>Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)</p>	<p>99380589</p>	<p>Contact: Mahairas GG, Wallace JC, Hood L</p> <p>High Throughput Sequencing Center</p> <p>University of Washington</p> <p>401 Queen Anne Avenue North, Seattle, WA 98109, USA</p> <p>Tel: (206) 616-3618</p> <p>Fax: (206) 616-3887</p> <p>Email: jwallace@u.washington.edu</p>	<p>Sequence Tagged Connector</p> <p>Plate: 3108 row: F column: 1</p>	

Class: BAC ends
High quality sequence stop: 389.

FEATURES
Location/Qualifiers

source

1. .389
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3108 Col=1 Row=F"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC clones in E-Coli DH10B"

BASE COUNT 119 a 86 c 65 g 118 t 1 others
ORIGIN

Query Match 1.2%; Score 87.6; DB 17; Length 389;
Best Local Similarity 64.0%; Pred. No. 3.7e-07;
Matches 165; Conservative 0; Mismatches 89; Indels 4; Gaps 2;

QY 3782 AATCTAGGTCAACGTGAATCTAGGTCAACGGGGCAAAATGACTGAACGCTCTATTTC 3841
|||||
DB 291 AATCTAGGTCACTGTTAAATCTAGGTCACTTGTG--CAAAATTACTAAGAGCTTTATTTC 235
|||||

QY 3842 CAGTGAACGGTCAAGTGGCTCAGATATATCTAGGATTTGGGCTCCACCGGATAAGATT 3901
|||||
DB 234 CAGGTGAATTGTACTGTACTTCCATGGGTGTGGAGGTTATATAAGTTTACGACACACATT 175
|||||

QY 3902 CTGTTAGTGA-CTCTGCTTTTATTTTTCAGACATCAAGCGGTGACGACCAAGACATCCAG 3960
|||||
DB 174 AAGATAGTATATCTGTTATTTTATAGCATATGAAGTGATGACCTGCATATCCAG 115
|||||

QY 3961 AAGATGTCAAGAGGTGAAGAGACAGTGAAGAAAGGTACTTGTGGCAAGCCACATACT 4020
|||||
DB 114 ACGAATGTGCAAAAGGTGAAGACACAGTGAAGAAAGGTAGACTGATTAAGTGTCAATGTT 55
|||||

QY 4021 AAGCATTCAGTAGAGA 4038
|||||
DB 54 AAGTCATGCATAGAGA 37
|||||

RESULT 8
BI301790 626 bp mRNA linear EST 20-JUL-2001
LOCUS
DEFINITION UI-R-DL0-cin-d-08-0-UI-s1 UI-R-DL0 Rattus norvegicus cDNA clone
BI301790
UI-R-DL0-cin-d-08-0-UI 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

EST.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 626)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized rat tongue library cDNA library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive

elements were found in this cDNA sequence: 12-236, >B3\$SINE/B2
311-349, >U2\$H1RNA
Seq primer: M13 Forward
POLYA=yes.

FEATURES
source
Location/Qualifiers

1. .626
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DL0-cin-d-08-0-UI"
/clone_lib="UI-R-DL0"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pRT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-DL0
library is a non-normalized Rat Tongue library constructed
in pRT73 PAC vector according to the procedure described
by Bonaldo, Lennon & Soares (Genome Research Genome 6:
791-806, 1996). The oligonucleotide used to prime first
strand synthesis contained the sequence tag GCCGA between
the Not I cloning site and dT18 stretch.
TAG LIB=UI-R-DL0
TAG TISSUE=rat tongue
TAG_SEQ=GCCGA"

BASE COUNT 142 a 149 c 135 g 200 t
ORIGIN

Query Match 1.2%; Score 86.6; DB 13; Length 626;
Best Local Similarity 65.3%; Pred. No. 5.4e-07;
Matches 143; Conservative 0; Mismatches 74; Indels 2; Gaps 1;

QY 370 TGTTTTATCTTTTATTAATAATTCACACATCAGTGTGTCAGACTGTTTCAAC 429
|||||
DB 4 TTTTATTTTATTTTGAATAATGAAAAAATTTATTTATGTATGCTGTTTCC 63
|||||

QY 430 CACATGTATGTCTGTGCACCAAGTCTGCTGTGGGGCAAGACAGACAGAG 489
|||||
DB 64 TGGATGTATGTCTGTGCACCAAGTATGTGCGGGTCTATGAGGCCGAAGAGGATT 123
|||||

QY 490 GGTGCGCTGCACCGAGTCAAGATGTTGTGACCCACATGAGATGCTGGAGTTAG 549
|||||
DB 124 GATCTACTGCACTCGAGTTTACAGCACTTGAACCACTGTGGTGTAGATTGA 183
|||||

QY 550 ACCGAGTCTTCAGAAAGTGCAGAAATGCTTTTAACCA 588
|||||
DB 184 GCCCAGGTCTCTACAAAGC--CAAGGCTCTTAACCA 220
|||||

RESULT 9
BF416659 448 bp mRNA linear EST 28-NOV-2000
LOCUS
DEFINITION UI-R-CA0-bku-d-01-0-UI-s1 UI-R-CA0 Rattus norvegicus cDNA clone
BF416659
UI-R-CA0-bku-d-01-0-UI 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

EST.
Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 448)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized rat tongue library cDNA library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive

Email: mscares@blue.ueg.uiowa.edu
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized cerebellum library cDNA library preparation. M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.reagen.com). The following repetitive elements were found in this cDNA sequence: 33-240, >B3#SINE/B2 284-313, >ID R#SINE/ID 349-391, >PB1D7#SINE/Alu
 Seq primer: M13 Forward
 POLYA=yes

FEATURES

source

Location/Qualifiers
 1. 448
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UT-R-CA0-bku-d-01-0-UT"
 /clone_lib="UT-R-CA0"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The UT-R-CA0 library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratseq.ueg.uiowa.edu. The subtraction has been previously described in (Bonaldi, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_LIB=UT-R-CA0
 TAG_TISSUE=cerebellum
 TAG_SEQ=CGAAGC"
 BASE COUNT 93 a 85 c 97 g 172 t 1 others
 ORIGIN

Query Match 1.1%; Score 84.2; DB 12; Length 448;
 Best Local Similarity 61.8%; Pred. No. 1.7e-06;
 Matches 134; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

370 TGTTTTAACTTTTATTAATTCACACATCATGTTGTGCAAGTCTGTTTCACC 429
 1 TTTTATTTTATTTTAAATTAAGACTTTATTTATTTGATTTGATTTTGGC 60
 430 CACATGATGTCGTGTCACCAAGTGTGCTGCTGTTGGGGGAGAGAGAGAG 489
 61 TGCATGTACGTACGTACGTACGTACGTACGTACGTACGTACGTACGTACGT 120
 490 GGTGCTGTGCAACCGAGTCAAGAGTGTGTGAGCACCATGAGATGCTGGAGT 549
 121 GATCACTGAGAGTGGAGTTACGACAGTGTGAGCGCCCATGTGTGTAAGATT 180
 550 ACCCAGGTCTCCAGAGTGCAGCAATGCTTTTAC 586
 181 ACCCAGATCTCTGAGAGAGCAGCAGTGTCTTAC 217

RESULT 10
 B0561085/c 262 bp mRNA linear EST 20-JUN-2002
 LOCUS B0561085 262 bp mRNA linear EST 20-JUN-2002
 DEFINITION H4068B12-5 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
 H4068B12 5', mRNA sequence.
 ACCESSION B0561085
 VERSION B0561085.1 GI:21461970
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 262)
 Vanburen,V., Piao,Y., Dudekula,D.B., Qian,Y., Carter,M.G., Martin
 P.R., Stagg,C.A., Bassey,U., Aliba,K., Hamatani,T., Kargul,G.J.,

REFERENCE
 AUTHORS

Luo, A.G. and Ko, M.S.H.
 Assembly, verification, and initial annotation of NIA 7.4K mouse
 cDNA clone set
 Unpublished (2002)
 Other ESTs: H4068B12-3
 Contact: Yong Qian
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
 Email: cdna@gsun.gsc.nia.nih.gov
 This clone set has been freely distributed to the community. Please
 visit http://lgsun.gsc.nia.nih.gov/cDNA/NIA_7.4k.html for details.
 Plate: H4068 row: B column: 12
 Seq primer: -21M13 Reverse
 High quality sequence stop: 262
 POLYA=no.

FEATURES

source

Location/Qualifiers
 1. 262
 /organism="Mus musculus"
 /strain="C57BL/6"
 /db_xref="taxon:H4068B12-5"
 /clone="H4068B12"
 /clone_lib="NIA Mouse 7.4K cDNA Clone Set"
 /sex="mixed"
 /dev_stage="mixed"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
 BASE COUNT 83 a 58 c 58 g 63 t
 ORIGIN

Query Match 1.1%; Score 84; DB 14; Length 262;
 Best Local Similarity 64.8%; Pred. No. 2.1e-06;
 Matches 158; Conservative 0; Mismatches 80; Indels 6; Gaps 2;

377 ATCTTTTATTAATTAATTCACACATCATGTTGTGCAAGTCTGTTTCACC 436
 250 ACCGGTTTAAATTTTGTAGATTATTTATTTAGTGCATGAATTTTACCTGCAT 191
 437 ATGCTGTGACCAAGTGTGCTGCTGCTGTTGTGGGGCAGAGAGAGAGAG 494
 190 ATGATGTGACCAAGTGTGATGCTTATGTTGTGAGTCAAGAGAGAGAGAG 131
 495 CCGGACCGAGAGTCAAGAGTGTGTTGTGAGCACCATGAGATGCTGGAGTTAG 554
 130 CTTAGACTGTGTTTACATGATGCTGTGATGCTGTGATGCTGTGATGCTGT 71
 555 GGTCTCTCAGAGTCAAGAGTGTGTTTACACACAGCAGCATTTCTCTCCAG 614
 70 GGTCTCTCAGAGTCAAGAGTGTGTTTACATGCTTATCTA---CAGAGTGTCTCTCTT 15
 615 CAAC 618
 14 CAAC 11

RESULT 11
 BB346070/c 645 bp mRNA linear EST 24-OCT-2001
 LOCUS BB346070 645 bp mRNA linear EST 24-OCT-2001
 DEFINITION BB346070 RIKEN full-length enriched, 10 days neonate cerebellum Mus
 musculus cDNA clone B930060A17.3', mRNA sequence.
 ACCESSION BB346070
 VERSION BB346070.2 GI:16405012
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 645)
 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagata,T., Hara,A.
 Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda

REFERENCE
 AUTHORS

, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanka, I., Atawa
, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

FEATURES

source

1. 626
/organism="Mus musculus"
/strain="C57BL/6J"
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/sex="mixed"
/tissue_type="head"
/dev_stage="6 days neonate"
/lab_host="DH10B"
/note="Site 1: SalI; Site 2: BamHI. cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTTTTCTTTTCTTTT 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCGAGTTAATTAATTAATCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified Bluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
BamHI"

BASE COUNT 224 a 123 c 102 g 177 t
ORIGIN

Query Match 1.1%; Score 83.2; DB 9; Length 626;
Best Local Similarity 67.3%; Pred. No. 2.6e-06;
Matches 132; Conservative 0; Mismatches 63; Indels 1; Gaps 1;

396 CACAAATCAGTGTGTCAGTCTGTTTACCAACATGATGTCGTGACCAAGTGC 455
265 CATTATTACTTATGATGATGGTGTGTTGCTGCTTGAAGCTTGACCACTGTG 206
456 TGCCTGTGCTTGGGGGCAAGAGAGAGAGG-TGCCCTGGACCGAGTACGGA 514
205 TGCCTGTGCTGAGAGACACGAGAGAGGTCGTGATCCCTGGAGTCGAGATACGA 146
515 TGGTTGTAGCCACCATGATGCTGGAGTTAGACCCAGGTCTCCAGAAATGACAGA 574
145 TGGTTGTAGCCACCATGATGCTGGAAATTAATCAAGCCCTCTGGAAGATCACA 86
575 AATGCTTTAACCACA 590
85 AGTGCTCTTAGGCCA 70

RESULT 15
AA833456/c 382 bp mRNA linear EST 23-FEB-1998
LOCUS A:833456

DEFINITION uc91a01.r1 Soares_NMPu Mus musculus cDNA clone IMAGE:1432968 5',
mRNA sequence.
AA833456
ACCESSION AA833456.1 GI:2907184
VERSION 1
KEYWORDS EST

ORGANISM

house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 382)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellendberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE

The Mashu-HMI Mouse EST Project

COMMENT

Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washu-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:917036

Predicted full length read
vector to vector length is 470
Seq primer: -28m3 rev2 ET from Amersham
High quality sequence stop: 366.
Location/Qualifiers

FEATURES

source

1. 382
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/clone_lib="Soares_NMPu"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pTZ19-Pac (Pharmacia) with
a modified polylinker; 1st strand cDNA was prepared from
pregnant mouse uterus, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pTZ19
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldi."

BASE COUNT 114 a 80 c 82 g 106 t
ORIGIN

Query Match 1.1%; Score 83; DB 9; Length 382;
Best Local Similarity 64.1%; Pred. No. 3.1e-06;
Matches 125; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

396 CACAAATCAGTGTGTCAGTCTGTTTACCAACATGATGTCGTGACCAAGTGC 455
296 CATTATTACTTATGATGATGGTGTGTTGCTGCACTAGACCTGTGACCACTGTG 237
456 TGCCTGTGCTTGGGGGCAAGAGAGAGAGGTCCTTGACCCGAGTACGAT 515
236 TGCCTGTGCTGAGAGACACGAGAGAGGTCCTTGAGACTGGAGATACAGAT 177
516 GATTGTAGCCACCATGATGCTGGAGTTAGACCCAGGTCTCCAGAAATGACAGA 575
176 GATTGTAGCCACCATGATGCTGGAAATTAATCAAGCCCTCTGGAAGATCACA 117
576 AATGCTTTAACCACA 590
116 GTGCTCTTAGGCCA 102

Search completed: July 19, 2003, 19:39:07

Mon Jul 21 05:36:40 2003

Job time : 6522 secs

us-09-751-797-8.rst

Page 11

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:02:25 ; Search time 1021.03 Seconds

(without alignments)
16420.772 Million cell updates/sec

Title: us-09-751-797-8

Perfect score: 1 gtcctaccctgcttaagat.....gatttaactatgctat 7445

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : N Geneseq, 101002:*

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7445	100.0	7445	22	AA514859
2	7445	100.0	7445	24	AAAD27134
3	7441.8	100.0	7445	24	AAAD30628
4	7433	99.6	7444	21	AAA28816
5	4245.2	57.0	5935	21	AAA28816
6	4245.2	57.0	5935	22	AA514878
7	4245.2	57.0	5935	24	AAAD30660
8	4245.2	57.0	5935	24	AAAD27153
9	686	9.2	4797	22	AA514876

10	686	9.2	4797	24	AAAD30646	Human TIF genomic
11	686	9.2	4797	24	AAAD27151	Human T cell deriv
12	682.4	9.2	4796	21	AAAD28840	Human T cell induc
13	601.4	8.1	1119	21	AAAD28815	Murine T cell indu
14	601.4	8.1	1119	22	AA514858	Mouse cDNA encodin
15	601.4	8.1	1119	24	AAAD30627	Mouse TIF alpha CD
16	601.4	8.1	1119	24	AAAD27133	Mouse T cell deriv
17	598.2	8.0	1166	21	AAAD28174	Murine T cell indu
18	555.2	7.5	1111	21	AAAD28817	Murine T cell indu
19	555.2	7.5	1111	22	AA514860	Mouse cDNA for T c
20	555.2	7.5	1111	24	AAAD30629	Mouse TIF beta CDN
21	555.2	7.5	1111	24	AAAD27135	Mouse T cell deriv
22	555.2	7.5	1111	24	AAAD27135	Mouse T cell deriv
23	221.4	3.0	504	21	AAAD3454	Mouse secreted exp
24	217.6	2.9	1177	21	AAAD81773	Human GIL-19/AB289
25	215.6	2.9	1116	22	AAAD09717	Human cytokine, 2C
26	215.6	2.9	1116	22	AAAD81741	Human IL-TIF polyP
27	215.6	2.9	1116	24	ABR10503	Human cDNA encodin
28	214.2	2.9	1152	22	AAAD28134	Human PRO10096 CDN
29	214.2	2.9	1152	22	AAAD87053	Nucleotide sequenc
30	214.2	2.9	1152	24	ABR15737	Human angiogenesis
31	214.2	2.9	1152	24	ABR11847	CDNA encoding huma
32	214.2	2.9	1152	24	ABR188248	Human PRO10096 CDN
33	214.2	2.9	1152	24	ABR33657	CDNA encoding huma
34	211.2	2.8	1132	22	AAAD84310	Human EXCS encodin
35	210.4	2.8	1139	22	AAAD28841	Human interleukin-
36	126	1.7	690	21	AAAD28839	Human T cell induc
37	126	1.7	690	22	AA514875	Human cDNA encodin
38	126	1.7	690	24	AAAD30645	Human TIF-cDNA, H
39	126	1.7	690	24	AAAD27150	Human TIF DNA frag
40	122	1.6	418	24	AAAD30638	Human TIF DNA frag
41	92	1.2	537	22	AAAD28842	Human interleukin-
42	87.2	1.2	501	22	AAAD09720	Degenerate sequenc
43	78	1.0	215980	24	AA538337	Complementary stra
44	75.8	1.0	48974	20	AA553300	Mouse Presentin-1
45	71	1.0	3119	24	AAAD39131	Rat Obesity-specif

ALIGNMENTS

RESULT 1	
AA514859	AA514859 standard; DNA; 7445 BP.
ID	AA514859
AC	AA514859;
XX	
DT	19-DEC-2001 (first entry)
XX	
DE	Mouse partial genomic DNA for T cell derived inducible factor, TIFalpha.
XX	
KW	Mouse; T cell derived inducible factor; TIFalpha; ds; anti-allergic;
KW	antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;
KW	cancer; lymphoma; immune system disorder; allergy; asthma;
KW	acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
KW	thyroiditis; melanoma; hepatoma.
XX	
OS	Mus musculus.
XX	
PN	US2001024652-A1.
XX	
PD	27-SEP-2001.
XX	
PF	29-DEC-2000; 2000US-0751797.
XX	
PR	18-OCT-1999; 99US-0419568.
PR	26-OCT-1998; 98US-0178973.
PR	16-JUL-1999; 99US-0354243.
XX	
PA	(DUMO/) DUMOUTIER L.
PA	(LOUAH/) LOUAHED J.
PA	(RENA/) RENAUD J.
XX	

PI Dumoutier L, Louahed J, Renaud J;
XX WPI; 2001-638496/73.
XX
XX
XX New isolated nucleic acid molecules encoding T cell inducible factors,
PT useful as markers for expression or effect of interleukin (IL)-9 in a
PT subject and diagnosing susceptibility to asthma or allergy -
XX
XX Claim 1; Page 11-14; 26pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule, which encodes
CC a T cell derived inducible factor (TIF) which are upregulated by the
CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor
CC activation. The TIF proteins (or their mutants) may be used to test IL-9
CC ant/agonists for their potency against lymphomas, immune system
CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
CC or inhibit differentiation of tissue types in which they are active and
CC therefore be used to develop treatments for melanomas and hepatomas.
CC The present sequence a partial genomic sequence for mouse Tifalpa.
XX
XX
SQ Sequence 7445 BP; 2058 A; 1570 C; 1597 G; 2220 T; 0 other;
Query Match 100.0%; Score 7445; DB 22; Length 7445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GCACACAGAGCAGTATTTATAGCATGTGTCTGACCATGACGATACAGAGTGAATG 120
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DB 121 TAAAGAGCGCTATTTATGACATTAACCAACATGTTATGTTTCTTCTGCAAGCAACT 180
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QY 361 TGAACCTCCCACTCTCACTTCGGCTCTGATGCGCACCTTTCAACTTTGCAATTTA 420
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QY 6001 GAGTCAAGGCTTTGAGTGAAGCACTCATATAGTATGATCATGTCAGGTGAGGAGCTA 6060
DB 6001 GAGTCAAGGCTTTGAGTGAAGCACTCATATAGTATGATCATGTCAGGTGAGGAGCTA 6060
QY 6061 CTTGTCAAGGCGGAGCTCTGCTGCTTGGCACTTAACATCTCAGGTCTCAGTATCACTTC 6120
DB 6061 CTTGTCAAGGCGGAGCTCTGCTGCTTGGCACTTAACATCTCAGGTCTCAGTATCACTTC 6120
QY 6121 CTGCTACTTGAACAGTGAAGATGAGATGAGCAAACTTTTTCACACCCCACTAAATTT 6180
DB 6121 CTGCTACTTGAACAGTGAAGATGAGATGAGCAAACTTTTTCACACCCCACTAAATTT 6180
QY 6181 AATTGACAAAAGACTGTGTAATTTGTGGAATACAGTGTGATTAATGATGTGTCAT 6240
DB 6181 AATTGACAAAAGACTGTGTAATTTGTGGAATACAGTGTGATTAATGATGTGTCAT 6240
QY 6241 TGTGCAAGGTTCAATAGATAGATTAATAGGCCATCAACAGCTTATGGGTGCAATG 6300
DB 6241 TGTGCAAGGTTCAATAGATAGATTAATAGGCCATCAACAGCTTATGGGTGCAATG 6300
QY 6301 CAAGTAATATAGGATAGCTGTGAGTCTTAAAGTCAAGAAAGGAGTGAATTTAAGTCT 6360
DB 6301 CAAGTAATATAGGATAGCTGTGAGTCTTAAAGTCAAGAAAGGAGTGAATTTAAGTCT 6360
QY 6361 TTTGGCAAAATCATATTAATCTCATGCTAAATAATACATTAATGATTAATCTTTAG 6420
DB 6361 TTTGGCAAAATCATATTAATCTCATGCTAAATAATACATTAATGATTAATCTTTAG 6420
QY 6421 AGAAGGCTGATCTTGTGTTTGTGCTCAGCAAGCAAAATGTCAACAGCTTTCTTACAG 6480
DB 6421 AGAAGGCTGATCTTGTGTTTGTGCTCAGCAAGCAAAATGTCAACAGCTTTCTTACAG 6480
QY 6481 GTACCACTTTAGAAAAATGTAACCTGTGCTCAAAATGTTGTTGTTTCTTATTTTCAATGCT 6540
DB 6481 GTACCACTTTAGAAAAATGTAACCTGTGCTCAAAATGTTGTTGTTTCTTATTTTCAATGCT 6540
QY 6541 TGAAGAGAGTGAAGATCAAGGAGATTTGGGAACTGAGACTGCTGTTTATGCTCTGAG 6600
DB 6541 TGAAGAGAGTGAAGATCAAGGAGATTTGGGAACTGAGACTGCTGTTTATGCTCTGAG 6600
QY 6601 AATGCTTGTGCTGTGAGCGAAGAAAGTGAAGAAACGAAACATGCTCTTCTGCTTC 6660

[illegible]

Query	Match	100.0%	Score 7441.8	DB 24	Length 7445
Best Local Similarity	100.0%	Pred. No. 0			
Matches 7443	Conservative 0	Mismatches 2	Indels 0	Gaps 0	
OS	Mus musculus.				
XX	WO200210393-A2.				
XX	07-FEB-2002.				
PD	27-JUN-2001, 2001WO-US20485.				
XX	27-JUL-2000, 2000US-0626617.				
PR	(LUDW-) LUDWIG INST CANCER RES.				
XX	Dumontier L, Renaud J;				
PI	WPI, 2002-195964/25.				
XX	Stimulating expression of STAT transcription factor and inducing				
XX	production of acute phase protein in a cell, involves contacting a cell				
PT	capable of expressing STAT with T cell derived inducible factors -				
PT	Example 7; Page 49-53; 64pp; English.				
XX	The invention relates to nucleic acid molecules encoding T cell				
CC	derived inducible factors (TIFs) also known as interleukin-21 (IL-21).				
CC	TIF polynucleotides are upregulated by the cytokine, IL-9, IL-TIF or				
CC	IL-21 molecules are implicated in activation of STAT transcription				
CC	factors, acute phase proteins and inflammation. The present sequence				
CC	is mouse TIF alpha genomic DNA.				
XX	Sequence 7445 BP, 2059 A, 1568 C, 1597 G, 2221 T; 0 other;				
QY	1 GTCTATCACCTGCTTAAGATTTTCTTAATTATTAATAAACTATTCTTAATAATGAAAA	60			
DB	1 GCTCTATCACTGGCTTAAGATTCCTTAATTATTAATAAACTATTCTTAATAATGAAAA	60			
QY	61 GCAACGAGGAGCGATTTATAGCANTGGTCTGACCATGCGAGTACAGAGTGAATGG	120			
DB	61 GCAACGAGGAGCGATTTATAGCANTGGTCTGACCATGCGAGTACAGAGTGAATGG	120			
QY	121 TAAGAGGCGCTTATTCAGCATTAACAACATGTTATTTCTTGGCAAGCAAACT	180			
DB	121 TAAGAGGCGCTTATTCAGCATTAACAACATGTTATTTCTTGGCAAGCAAACT	180			
QY	181 TGAATCTATGCTTTAAACAATCTTCAAGCCTTAATATATGCTTACGACTGGAGTCCG	240			
DB	181 TGAATCTATGCTTTAAACAATCTTCAAGCCTTAATATATGCTTACGACTGGAGTCCG	240			
QY	241 CCGCTGTCCAAAGAGCTCTTGAGACGCTCTCCTGTGGTCCATTTATATGCTCTTGA	300			
DB	241 CCGCTGTCCAAAGAGCTCTTGAGACGCTCTCCTGTGGTCCATTTATATGCTCTTGA	300			
QY	301 TCGATCTCCCAACCTCTCACTTCGGCTCTGATGAGCCACTTTCACCTTCTGCATTTA	360			
DB	301 TCGATCTCCCAACCTCTCACTTCGGCTCTGATGAGCCACTTTCACCTTCTGCATTTA	360			
QY	361 TGAATCCATGTTTTTAATCTTTTATTAATAATATTCACCAATCAGTGTGTCAGATC	420			
DB	361 TGAATCCATGTTTTTAATCTTTTATTAATAATATTCACCAATCAGTGTGTCAGATC	420			
QY	421 TGTTCACCCACATATATGCTGTGTGACCAACATGCTGCTGTGTGTGTGGGGGCAAGA	480			
DB	421 TGTTCACCCACATATATGCTGTGTGACCAACATGCTGCTGTGTGTGTGGGGGCAAGA	480			
QY	481 GCAGAGAGAGGTGCTCTGCGACCGAGTACAGATGTTGTAGCCACATGAGATGCT	540			
DB	481 GCAGAGAGAGGTGCTCTGCGACCGAGTACAGATGTTGTAGCCACATGAGATGCT	540			
QY	541 GGGAGTTAGACCCAGGCTCTCCAGAAATGTCAGCAAAATGCTTTAACACACGACGCAATT	600			
DB	541 GGGAGTTAGACCCAGGCTCTCCAGAAATGTCAGCAAAATGCTTTAACACACGACGCAATT	600			

Db 541 GGGAGTTAGACCCAGGTCCTCCAGAAAGTCAGCAAAATGCTTTAACACACCGAGGCATT 600
Qy 601 TCTCTCTCCAGCCCCCAACATGAGTGTCTTTAGATTCCACCTAGAAATAGATCTGATGCG 660
Db 601 TCTCTCTCCAGCCCCCAACATGAGTGTCTTTAGATTCCACCTAGAAATAGATCTGATGCG 660
Qy 661 TTCACCTACCTGCCACTCCCTCTTTGATCTTTCTGCGAAGAAACACCAAAAAGCAAGAT 720
Db 661 TTCACCTACCTGCCACTCCCTCTTTGATCTTTCTGCGAAGAAACACCAAAAAGCAAGAT 720
Qy 721 CCCACACTGCTTTGGCTCCTCAAGTCTGACCTCTCAACAGGTCAAGATCTCCAGTGT 780
Db 721 CCCACACTGCTTTGGCTCCTCAAGTCTGACCTCTCAACAGGTCAAGATCTCCAGTGT 780
Qy 781 CCCTCTAACACTTTCCCAAGTGTCCCTCTAACACTTTCTCAAGTGTCCCTCTAACACTTT 840
Db 781 CCCTCTAACACTTTCCCAAGTGTCCCTCTAACACTTTCTCAAGTGTCCCTCTAACACTTT 840
Qy 841 CTCACAGTGTCCCTCTAACACTTTGATCTCAATTAGCTGAGGGGAGAAAGATCTCACACA 900
Db 841 CTCACAGTGTCCCTCTAACACTTTGATCTCAATTAGCTGAGGGGAGAAAGATCTCACACA 900
Qy 901 GTGATTTTATGACTCTCGGCTCTAGTCTAGTGTAGGACATTTGGGTGAGTGTGAGGT 960
Db 901 GTGATTTTATGACTCTCGGCTCTAGTGTAGTGTAGGACATTTGGGTGAGTGTGAGGT 960
Qy 961 AGGCGTGTGCTCCCGCTGCTTAGAAGAAAGCTTCTAGTGTCTAGTGTCTAGTGTCTATCG 1020
Db 961 AGGCGTGTGCTCCCGCTGCTTAGAAGAAAGCTTCTAGTGTCTAGTGTCTAGTGTCTATCG 1020
Qy 1021 GGATTCAGTGTACATTCACATTCGAAATAATCCAGATTTTGTGAATTTCTCTCTCACT 1080
Db 1021 GGATTCAGTGTACATTCACATTCGAAATAATCCAGATTTTGTGAATTTCTCTCTCACT 1080
Qy 1081 ATCCATCTATATAGTATGTTATTTAGAGTCAATTTAAATAATATTTTGAAGACTATGCG 1140
Db 1081 ATCCATCTATATAGTATGTTATTTAGAGTCAATTTAAATAATATTTTGAAGACTATGCG 1140
Qy 1141 TTGCAACAAGTAAATGTCAAGAAATAGCAAAATGTATAGTATTTTAAATAATAA 1200
Db 1141 TTGCAACAAGTAAATGTCAAGAAATAGCAAAATGTATAGTATTTTAAATAATAA 1200
Qy 1201 TCTATGCTTAAATATGTCTATATAGATTTTCACTACCGATATTTCCAACTTAACCTGACC 1260
Db 1201 TCTATGCTTAAATATGTCTATATAGATTTTCACTACCGATATTTCCAACTTAACCTGACC 1260
Qy 1261 TTGGCTATGATTTCAACCTTTGTATTTGATCTACCATTAACAGTCTGTGAACCAAGACAT 1320
Db 1261 TTGGCTATGATTTCAACCTTTGTATTTGATCTACCATTAACAGTCTGTGAACCAAGACAT 1320
Qy 1321 TCTGTGGCAATGGGAGCTGTGAAGAAAGCAACATCTTATTTAAATAATAA 1380
Db 1321 TCTGTGGCAATGGGAGCTGTGAAGAAAGCAACATCTTATTTAAATAATAA 1380
Qy 1381 GTTATATGTTAGGATTCATATATCTAAATAATAATAATAATAATAATAATAATAATA 1440
Db 1381 GTTATATGTTAGGATTCATATATCTAAATAATAATAATAATAATAATAATAATAATA 1440
Qy 1441 AATATATCTCCAGTTTTCATATATGCTTATTTCAAAAGCACAGAAATATAGACAACGGGCT 1500
Db 1441 AATATATCTCCAGTTTTCATATATGCTTATTTCAAAAGCACAGAAATATAGACAACGGGCT 1500
Qy 1501 TTTATTTCTGATCACTTCTAAAGAGATAGAAATCTATGAAGTTGGTGGGAAATGATGCTC 1560
Db 1501 TTTATTTCTGATCACTTCTAAAGAGATAGAAATCTATGAAGTTGGTGGGAAATGATGCTC 1560
Qy 1561 GTGACCAAAACCGCTGATCTCAATAGCTACGGAGATCAAAAGGCTGCTTATCTCAATTCAGA 1620
Db 1561 GTGACCAAAACCGCTGATCTCAATAGCTACGGAGATCAAAAGGCTGCTTATCTCAATTCAGA 1620
Qy 1621 TCTACTAGGCAAAAGCATGCTTCTTTGAAACCGTGTATTAAGAAATTTCTGGGATTT 1680
Db 1621 TCTACTAGGCAAAAGCATGCTTCTTTGAAACCGTGTATTAAGAAATTTCTGGGATTT 1680

Qy 1681 GTGTGCAAAAGCACTTGTGTGGCCCTCAACGGTACGTTTATAGGGAAGACTTCCATCTCT 1740
Db 1681 GTGTGCAAAAGCACTTGTGTGGCCCTCAACGGTACGTTTATAGGGAAGACTTCCATCTCT 1740
Qy 1741 CAAGGTGGGAAGGCTTGAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1800
Db 1741 CAAGGTGGGAAGGCTTGAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1800
Qy 1801 AGAAGACAGACTGGAATATGATATATGTGATGTCTATATCATATTCACAAATAA 1860
Db 1801 AGAAGACAGACTGGAATATGATATATGTGATGTCTATATCATATTCACAAATAA 1860
Qy 1861 ACCGTGTGTCCCGATGCTTAAAGCAGCACTTCTGCTCTCCATCAACAGCAGAG 1920
Db 1861 ACCGTGTGTCCCGATGCTTAAAGCAGCACTTCTGCTCTCCATCAACAGCAGAG 1920
Qy 1921 ACACCTAAACAGTAAAGACCTCAAGCCTCAACAGCAATCAATCTGTGTGTGTGTGTGT 1980
Db 1921 ACACCTAAACAGTAAAGACCTCAAGCCTCAACAGCAATCAATCTGTGTGTGTGTGTGT 1980
Qy 1981 CCCGACGAACATGCTCCCTGATGTTTGTGCTTTTGTCTCTCACTAACAGGCTCTCT 2040
Db 1981 CCCGACGAACATGCTCCCTGATGTTTGTGCTTTTGTCTCTCACTAACAGGCTCTCT 2040
Qy 2041 CTCACCTTATCAACTGTGTGACACTTGTGTGATCTGTGATGCTGTCTGAGAAATCTATG 2100
Db 2041 CTCACCTTATCAACTGTGTGACACTTGTGTGATCTGTGATGCTGTCTGAGAAATCTATG 2100
Qy 2101 AGTTTTCCTTTATAGGGAATTTTGGCCGCAAGCTGCTTCTTCAATTTGCTGTGGGC 2160
Db 2101 AGTTTTCCTTTATAGGGAATTTTGGCCGCAAGCTGCTTCTTCAATTTGCTGTGGGC 2160
Qy 2161 CAGAGAGCAAAATGCGCTCCCGTCAACACCCGGTCAAGCTTGAAGGTGTCCAACTTCAG 2220
Db 2161 CAGAGAGCAAAATGCGCTCCCGTCAACACCCGGTCAAGCTTGAAGGTGTCCAACTTCAG 2220
Qy 2221 CAGCGGTATCATGTCACACCGCACTTTATGCTGCGCAAGAGATACAGCTGATCTCTT 2280
Db 2221 CAGCGGTATCATGTCACACCGCACTTTATGCTGCGCAAGAGATACAGCTGATCTCTT 2280
Qy 2281 CTCTCCATACCGGCTGTGCAATTTTCTGAAAGCACTTGCAAACTTTTATAGGGGCGCTTTA 2340
Db 2281 CTCTCCATACCGGCTGTGCAATTTTCTGAAAGCACTTGCAAACTTTTATAGGGGCGCTTTA 2340
Qy 2341 TCTCGCAGGTCTACATGATGTTTCTGCTCTTATAGAGACTCTTTAAGAGACTGGGT 2400
Db 2341 TCTCGCAGGTCTACATGATGTTTCTGCTCTTATAGAGACTCTTTAAGAGACTGGGT 2400
Qy 2401 CTTTTCATTTCTATTTCAAGGCTCTCAGACCAATTTCTATCTTTGGCTTCAGAGACA 2460
Db 2401 CTTTTCATTTCTATTTCAAGGCTCTCAGACCAATTTCTATCTTTGGCTTCAGAGACA 2460
Qy 2461 TATACGAAATTTTATCTACAGAGGCGATTTAGAAAGCCACCCAGACTGCAATCTTTC 2520
Db 2461 TATACGAAATTTTATCTACAGAGGCGATTTAGAAAGCCACCCAGACTGCAATCTTTC 2520
Qy 2521 CATTTCTGTGCTCTCTCTGAACTCATCTCTTGGCTACTGCTGAGACCCGCTGG 2580
Db 2521 CATTTCTGTGCTCTCTCTGAACTCATCTCTTGGCTACTGCTGAGACCCGCTGG 2580
Qy 2581 GACATATCATCTCTACAGGCTTTCTTCATCTCTCTGATCTCCAGGCACTTAAGGT 2640
Db 2581 GACATATCATCTCTACAGGCTTTCTTCATCTCTCTGATCTCCAGGCACTTAAGGT 2640
Qy 2641 TTTCTCTTTTCAAGGCGCTTGGCAATTAACAAACAGAGCTGCTGCTCATCGGGAGA 2700
Db 2641 TTTCTCTTTTCAAGGCGCTTGGCAATTAACAAACAGAGCTGCTGCTCATCGGGAGA 2700
Qy 2701 AACTGTCGAGAGAGTCAAGTATGCTCTCACTGATAGAGACAGAGGCTAGCTGCGGAGC 2760
Db 2701 AACTGTCGAGAGAGTCAAGTATGCTCTCACTGATAGAGACAGAGGCTAGCTGCGGAGC 2760

QY 2761 TGGTGGACCTCTGGGATAGTCTGACGTATGACCCCTGCTGCTTCTTGTCTTACCTGACAG 2820
DB 2761 TGGTGGACCTCTGGGATAGTCTGACGTATGACCCCTGCTGCTTCTTGTCTTACCTGACAG 2820
QY 2821 CTTAAAGATCAGTGTCACTGATGATGAGAGAGTGTCTCACTTCAACCTGAGAGAGCTTGTGC 2880
DB 2821 CTTAAAGATCAGTGTCACTGATGATGAGAGAGTGTCTCACTTCAACCTGAGAGAGCTTGTGC 2880
QY 2881 TCCCCAGTCAAGACAGTGTCCAGCCCTACATGACAGAGAGTGTGACTTCTTCTGACCAAC 2940
DB 2881 TCCCCAGTCAAGACAGTGTCCAGCCCTACATGACAGAGAGTGTGACTTCTTCTGACCAAC 2940
QY 2941 TCAGCAATCAGTCACTGCTCTGTGTATGATCTGACTCTGTGCTACCTATGCTCTCTCTT 3000
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QY 3001 CCTCTTCTTCCATTAAGAACCCGAGGCTCGGCCCTCTCTCTTCTCAACAGAGAGAG 3060
DB 3001 CCTCTTCTTCCATTAAGAACCCGAGGCTCGGCCCTCTCTCTTCTCAACAGAGAGAG 3060
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DB 3061 GGGCTCTGACACCAACCATCATATAGGCCACTTGAATAGTCAACAAAGCTTGTGCTTC 3120
QY 3121 AATTGATTAATCTTTGAGTTGTATGATGAAAGCTTTATTTTATCCATGAAAGA 3180
DB 3121 AATTGATTAATCTTTGAGTTGTATGATGAAAGCTTTATTTTATCCATGAAAGA 3180
QY 3181 AATCAATCAAAATTTGTAGATGATGAAAGATGTTGGAAACGAAAGAGGCTTAATAGA 3240
DB 3181 AATCAATCAAAATTTGTAGATGATGAAAGATGTTGGAAACGAAAGAGGCTTAATAGA 3240
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DB 3241 GAAACAGATCTGCTGATATAGTACTTATGAGGGAGACAGGGGGGATATCCACTGAGTA 3300
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DB 3301 CAAGTACTTGTGGGAGAGAAATCCATGATGAAAGTCTTGTGGCATGAGATCCAC 3360
QY 3361 TGAGTCAAGATCTTGTGGGGAGAGAAATGAGCAACAGCAAAATTTGAAGGAGAGAG 3420
DB 3361 TGAGTCAAGATCTTGTGGGGAGAGAAATGAGCAACAGCAAAATTTGAAGGAGAGAG 3420
QY 3421 ATGAGAGAGGCTCATGTTGGGGAGTGTGAAAGTCACTCCCTTTCATGTATGAGAGT 3480
DB 3421 ATGAGAGAGGCTCATGTTGGGGAGTGTGAAAGTCACTCCCTTTCATGTATGAGAGT 3480
QY 3481 TAAAGAAAAACAGTGTGATGATTTGATGTTTCAAGACACCCCACTATGAAACATATCC 3540
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DB 3541 ACGAGAGAGGAGACAGTGTGAGAGACCTGGCATTTAGGAGAGGCGGCTTTTACACG 3600
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DB 3601 AGAAATCTTATGCTCATCTTGTGCTACATCCACCTTGTATGAGGTTCAAGTCAAGT 3660
QY 3661 TTCTGTTTACCGTCTTGTCTACTGCTGAGAACTTCAGTATGATTTCCCAAGAGAGAG 3720
DB 3661 TTCTGTTTACCGTCTTGTCTACTGCTGAGAACTTCAGTATGATTTCCCAAGAGAGAG 3720
QY 3721 CAGCTCTTCTGTAGAGAGAGGACTGATTTCACTGTCTTAGAGAAAGCAATAGCTCAGA 3780
DB 3721 CAGCTCTTCTGTAGAGAGAGGACTGATTTCACTGTCTTAGAGAAAGCAATAGCTCAGA 3780
QY 3781 GAAATCTAGGTCAAGTGAATAGTATGATGACAGGGGCAAAATGATGAGAGGCTCTAT 3840
DB 3781 GAAATCTAGGTCAAGTGAATAGTATGATGACAGGGGCAAAATGATGAGAGGCTCTAT 3840
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DB 3841 CCAGGTGAACGCTCACTGCTCAGATATATGAGGATTTGGGCTCCACCGGATAGAT 3900
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DB 3901 TCTGTATGATGATCTGCTTTTATTTTGGACACATACAGCGGTGACGACCAAGATCCAG 3960
QY 3961 AAGAAATGACAGAGGCTGAGAGACAGTGAAGAAAGTACTTATTTGGCAAGCCACATATCT 4020
DB 3961 AAGAAATGACAGAGGCTGAGAGACAGTGAAGAAAGTACTTATTTGGCAAGCCACATATCT 4020
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DB 4021 AAGCAATCAGTATGAGAGAGGAGATTTCTTCTGCTCCAGTCCCTTCTTACTTTG 4080
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DB 4081 TAACTTTTATTTGACTTGTCTATCTGTGCTTCCATTAAGTCTGCTAGTCACTGTATC 4140
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DB 4141 TAGCTGGTCTATAGATCTTTCAATCTGTGTCTAAATTTGTAGTCAATTTGAGCT 4200
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DB 4201 AGCAAGAAAGCTTATGATCTGACGCACTCATGAGCACTTGTCTGAGAGATGCTGTAGAG 4260
QY 4261 AGTCAATCTGAAGACAGCATCCCTGATTTCCAGCTCTGACCTTGTGAGGAGATG 4320
DB 4261 AGTCAATCTGAAGACAGCATCCCTGATTTCCAGCTCTGACCTTGTGAGGAGATG 4320
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DB 4621 TTAATGCTGCTGTTTCAAGAGTAAAGTAAATATAGTATGATTAATAGTCTAG 4680
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DB 4681 AAAGTATGAGTGAAGAACCTTTCTTACTTTTACCTTCACTTCTTATTTTCTTTC 4740
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DB 4741 TTCAACCCCTGATCAAGCACTATGATTAAGCACTTCTGCTGAGCTTATATGACTTT 4800
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DB 4801 ACAGCAAAACAATTTGCTGTGTGCTTGTGGGAGAGGAAACGAGATAGAGAGGCTC 4860
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DB 4861 AGGCTAGCAATGATCTTGGCTTAAAGCCAGAGGCAATGTTGATAGCAGAGAAAGTAG 4920
QY 4921 GCTCTTGCAGAGTGTGTGCTTAAGTATGAGAAACGAGAGGCTCCGTTGATGAT 4980

Db 4921 GCTCTGCAAGTGGGTGCTTAAATATCAGAAACAGGAAGCTCCGGTTGATGGAAT 4980
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Db 5281 ACTTTTTCCTTAAATGCTTAATGCTTAATCACTTCACTCACTTTGACTTTTATACC 5340
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Db 5581 TAGCTGCTTGGGCTTCAATACAAAGAACTGTGGAGGACAAAGTGAAGAGGAAATG 5640
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Db 5641 AAAAGGAAAAACAGATGTAGAGACTTGAACAGCTACAAATCCTCTACAGACGATTT 5700
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Db 5701 TTTCTTGAACAATCTAGAAAGTATGAGATTTGAGGATTTGACAGGAGGAACTGTGTCAT 5760
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Db 5761 TTGAATCTGGGTTTGTCTCTCATGAGGTTGAAAGGCTACCCCTTTTAACTCCGAA 5820
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Db 5821 TGGAGAGGAAAGAAAGGGGTGTATGACTCTACCTGAGGTTTACTAGTTTAAACCAATG 5880
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Db 5881 GAAAGACACTGGGACCTCTCTTGAACAAAAAATGAAACCTGTGTTTGTCTGTT 5940
Qy 5941 TGTCTTTTGTAAAGAACACAGGCAAGCCGACCAATGAGGTTGAATGTGGGCTTT 6000
Db 5941 TGTCTTTTGTAAAGAACACAGGCAAGCCGACCAATGAGGTTGAATGTGGGCTTT 6000
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Db 6001 GAGTCAAGGCTTTGAGTGAACACTCATATGTTGATCATGTGTAGAGTGAAGGCTA 6060

Qy 6061 CCTGTACGCGGAGCCCTGTGCTTGGCATTAATCATCTCCAGGTCTCAGTATCACTTC 6120
Db 6061 CCTGTACGCGGAGCCCTGTGCTTGGCATTAATCATCTCCAGGTCTCAGTATCACTTC 6120
Qy 6121 CTGTACTTGAACAGTTAGAGATTTAGGAAACCTTTTTCGACCCGACCAATTTT 6180
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6961 ATATATGTAAGTATTTATTTATTAAGTATACATTTTATTAATGCTTATTAATG 7020
6960 ATATATGTAAGTATTTATTTATTAAGTATACATTTTATTAATGCTTATTAATG 7019
7021 ATTTATTTATGAACATTAATCTGCTATGATTTATGATTAAGGCAAAATATTTATG 7080

Db 712 AGACATGATCTTTTCTATTTCTATTTCAAGGCTCAGAGCACTTCCATCTTGGCC 771
Qy 2451 TCAGACACATATAGTATTTATCTACAGAGCCGATTTAGAAAGCCAGAGCTG 2510
Db 772 TCAGACACATATAGTATTTATCTACAGAGCCGATTTAGAAAGCCAGAGCTG 831
Qy 2511 CAATATTTTCATTTCTCTGCTCTCTTCTGAACTCATCTCTTGGCTACTCTGAG 2570
Db 832 CAATATTTTCATCTGCTGCTCTCTTCTGAACTCATCTCTTGGCTACTCTGAG 891
Qy 2571 ACCCACTGGGGAATATATCTCTACTTACAGGCTTTTCTCATCTCTTGTACCCAG 2630
Db 892 ACCCACTGGGGAATATATCTCTACTTACAGGCTTTTCTCATCTCTTGTACCCAG 951
Qy 2631 CACTTGGGTTTCTCTCTTCTGAGGCGCTTGCAGATATACAAACAGAGCTCGGCTC 2690
Db 952 CACTTGGGTTTCTCTCTTCTGAGGCGCTTGCAGATATACAAACAGAGCTCGGCTC 1011
Qy 2691 ATCGGGGAGAACTGTTCCGAGAGTCACTGTAAGTCTCTCATCTGTAAGAGAGGCTAG 2750
Db 1012 ATCGGGGAGAACTGTTCCGAGAGTCACTGTAAGTCTCTCATCTGTAAGAGAGGCTAG 1071
Qy 2751 CTGCGGAGGCTGATGAGCCCTCTGGGATAGTCTGAGCTATGACCCCTGCTCTTCTG 2810
Db 1072 CTGCGGAGGCTGATGAGCCCTCTGGGATAGTCTGAGCTATGACCCCTGCTCTTCTG 1131
Qy 2811 TACTCGAGGCTTAAAGATCAGTCTACTGATGAGAGGCTGCTCACTTCACTCGGAA 2870
Db 1132 TACTCGAGGCTTAAAGATCAGTCTACTGATGAGAGGCTGCTCACTTCACTCGGAA 1191
Qy 2871 GACGTTCTGCTCCCGAGTGAAGAGGTTCCAGCCCTCACTGAGAGAGGCTGCTTCT 2930
Db 1192 GACATCTGCTCCCGAGTGAAGAGGTTCCAGCCCTCACTGAGAGAGGCTGCTTCT 1251
Qy 2931 CTGACCAAACTCAGCATCAGCTCAGTCTCTGTAAGTGTGACTGCTGCTACTTACTG 2990
Db 1252 CTGACCAAACTCAGCATCAGCTCAGTCTCTGTAAGTGTGACTGCTGCTACTTACTG 1311
Qy 2991 CCTCTCTCTCTCTCTCTATTTCCAGTATGAGAAACCGAGGCTCTGCTCTCTCTCA 3050
Db 1312 CCTCTCTCTCTCTCTCTATTTCCAGTATGAGAAACCGAGGCTCTGCTCTCTCTCA 1371
Qy 3051 AGAGTGAAGAGGCTCTCAGCACCACCATCATAGGCCACTTGAATAGTCAAAAG 3110
Db 1372 AGAGTGAAGAGGCTCTCAGCACCACCATCATAGGCCACTTGAATAGTCAAAAG 1431
Qy 3111 CTTTGGCTTCAATTTAGTATTAATCTTTGAGTTTGTATGAGTGAAGCTTTATTC 3170
Db 1432 CTTTGGCTTCAATTTAGTATTAATCTTTGAGTTTGTATGAGTGAAGCTTTATTC 1491
Qy 3171 CATGGAAGAAATCAACTCAATTTCTGTAGATGAGAAAGATGTGGGAACGAAAG 3230
Db 1492 CATGGAAGAAATCAACTCAATTTCTGTAGATGAGAAAGATGTGGGAACGAAAG 1551
Qy 3231 CCTAGATAGAGAAACAGATCTGCTAGTATAGTACTTAT-----GGGGGAGCAGGGGGCG 3286
Db 1552 CCTAGATAGAGAAACAGATCTGCTAGTATAGTACTTAT-----GGGGGAGCAGGGGGCG 1611
Qy 3287 ATATCCACTGATGATCAAGTACTTTGGGGAGAGAAATCCATGATGATCAAGTACTTGT 3346
Db 1612 ATATCCACTGATGATCAAGTACTTTGGGGAGAGAAATCCATGATGATCAAGTACTTGT 1669
Qy 3347 GCATGAGATCACTGATCAAGTACTTTGGGGGAGAGAAATGAGACAGCAAAAGT 3406
Db 1670 -----GGGGGAGAGAAATGAGACAGCAAAAGT 1697
Qy 3407 TGAAGGGA---AGGAAGTGAAGAGGCTCATGTTGGGGGTGGAAGGCTCACTCC-TT 3462
Db 1698 TGAAGGGAAGAGAGATGAGAGGCTCATGTTGGGGGTGGAAGGCTCACTCC-TT 1757
Qy 3463 TTCCATGTATGAGAGTATGAAGAAACAGTGTGATGTTGATGTTCTTCAGACACCC 3522

Db 1758 TTCCATGTATGAGAGTATGAAGAAATCAGTGTGTGATGATGTTCTTCAGACACCC 1817
Qy 3523 CAATATGAAACATATCCAGAGAGCGGAGACTGTGGAGACCTGGCACTTTAGGAA 3582
Db 1818 AA-----CTATGGCAGACTGTGGAGACTGGCACTTTAGGAA 1855
Qy 3583 GGGCGGCTTTTCAACAGAAACTTATATGCTCATCTCTTGTCTACACTCCACCTTGT 3642
Db 1856 GGGCGGCTTTTCAACAGAAACTTATATGCTCATCTCTTGTCTACACTCCACCTTGT 1915
Qy 3643 ATGAGTTTACGTCAGGTTTCTTCTTACCTTTCTGCTACTGTGGGAACTTCACTAG 3702
Db 1916 ATGAGTTTACGTCAGGTTTCTTCTTACCTTTCTGCTACTGTGGGAACTTCACTAG 1975
Qy 3703 ATTCGCCAAAGACGAGACAGCTCTCTGTAAGGAGGAGCTGGATTTCACTGTCTAG 3762
Db 1976 ATTCGCCAAAGACGAGACAGCTCTCTGTAAGGAGGAGCTGGATTTCACTGTCTAG 2035
Qy 3763 AGAAGAAATAGCTCAGAGAAATCTAGTCAACGTGAATCTAGTCAACGCGGCAAAA 3822
Db 2036 AGAAGAAATAGCTCAGAGAAATCTAGTCAACGTGAATCTAGTCAACGCGGCAAAA 2095
Qy 3823 TGACTGAAGCTCTTATTTCCAGTGAACGCTCAGCTGCTCAGTATATCTGATTTGG 3882
Db 2096 TGACTGAAGCTCTTATTTCCAGTGAACGCTCAGCTGCTCAGTATATCTGATTTGG 2155
Qy 3883 GCTCCACCGAGTAAGATCTGTTAGTGTGCTGTTTATTTTGCAGACATCAGCGGT 3942
Db 2156 GCTCCACCGAGTAAGATCTGTTAGTGTGCTGTTTATTTTGCAGACATCAGTGT 2215
Qy 3943 GACGACCAAGATCAGAGAAATGTCAGAGGCTGTAAGAGACACTGAAAGAGTACTA 4002
Db 2216 GACGACCAAGATCAGAGAAATGTCAGAGGCTGTAAGAGACACTGAAAGAGTACTA 2275
Qy 4003 TTGGCAAGCAAAATCTAAGCATTCAGTATGAGAGACGTTGGGATTTCTTCTCTCT 4062
Db 2276 TTGGCAAGCAAAATCTAAGCATTCAGTATGAGAGACGTTGGGATTTCTTCTCTCT 2335
Qy 4063 CCAAGTCCCTTCTACTTTGTAACATTTATTTAGCTGTCTACTATCTGCTCACTACTG 4122
Db 2336 CCAAGTCTCTTCTTCTTGTATTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTCT 2395
Qy 4123 CTTAGTGCACCTGATCTAGTGGGTCTAAGATCTTCAATCTGTGTCTAATTTGTA 4182
Db 2396 CTTAGTGCACCTGATCTAGTGGGTCTAAGATCTTCAATCTGTGTCTAATTTGTA 2455
Qy 4183 AGTCACATTTCTGAGCTTACGAGAAAGCTTACTCAGCCAGTCTATGAGCACTTGTCTG 4242
Db 2456 AGTCACATTTCTGAGCTTACGAGAAAGCTTACTCAGCCAGTCTATGAGCACTTGTCTG 2515
Qy 4243 GAGATGAGCTTGTGACAGAGTCAATGCTGAGAGACAGCATCCCTGATTTCCAGCTTGA 4302
Db 2516 GAGATGAGCTTGTGACAGAGTCAATGCTGAGAGACAGCATCCCTGATTTCCAGCTTGA 2575
Qy 4303 CTTCGCTTACGCTGCAATGCTGTAATTAATTTGCTGTAATTAATTTGGGAAAGCCAGTTC 4362
Db 2576 CTTCGCTTACGCTGCAATGCTGTAATTAATTTGCTGTAATTAATTTGGGAAAGCCAGTTC 2635
Qy 4363 CCAAGGACTTATATATCTGAGAAACATGCTTGAATTTGAAAGCTGGGCAAACT 4422
Db 2636 CCAAGGACTTATATATCTGAGAAAGCAATGCTTGAATTTGAAAGCTGGGCAAACT 2695
Qy 4423 TACTGAGATGATTTTGTAGCTCATTTAAACGATGCTGGAATGTGGCAAAATCAACC 4482
Db 2696 TACTGAGATGATTTTGTAGCTCATTTAACTGATGCTGGAATGTGATCAATCAACC 2755
Qy 4483 AGAATPACAAACAAAGAGCTGATTTGCAATATAGCAAGTATTTAGATCACTGATAT 4542
Db 2756 AGAATPACAAACAAAGAGCTGATTTGCAATATAGCAAGTATTTAGATCACTGATAT 2815
Qy 4543 AATAGCTATCATTTTATTTAAATATAGGCTTATATA---TATATTTAAGATTAAACA 4598
Db 2816 AACAGCTCATCTTATTTAAATATAGTCTATTTAGTCTCCTATTTAAGATTAAACA 2875

QY	4595	CAAGAAGTGAATAGCCTCCCAATTTACTTGCGCTGGTTCCAAAGAATATAATATACATC	4658
Db	2876	CAAGAAGTGAATAGCCTCCCAATTTACTTGCGCTGGTTCCAAAGAATATAATATACATC	2935
QY	4659	ATGATTAATAATATAGTGTCAATGAAGATATAGATAGAAACCCCTTCCCTTACTTTTAACCT	4718
Db	2936	ATGATTAATAATATAGTGTCAATGAAGATATAGATAGAAACCCCTTCCCTTACTTTTAACCT	2995
QY	4719	TCATTTCTTAGT-----TTTTTTTTTCTTCAACCCCTGATCAAGCACTAGTAAGACCT	4773
Db	2996	TCATTTCTTAGTATAATATTTTTTTTTTCTTCAACCCCTGATCAAGCACTAGTAAGACCT	3055
QY	4774	ATCTGCTGTAGCTATTATATATAGCTTTACAGAAACAACATTGCTGTGTGCTCTTTTGG	4833
Db	3056	ATCTGCTGTAGCTATTATATATAGCTTTACAGAAACAACATTGCTGTGTGCTCTTTTGG	3115
QY	4834	GGAAGGGGAACAGATAGCAGAGAGGCTCAGGCTAGCAAGTCT-GACTTGCCCTTAAGCCAG	4892
Db	3116	GGAAGGGGAACAGATAGCAGAGAGGCTCAGGCTAGCAAGTCTGAGACTCAACTTAAGCCAG	3175
QY	4893	AGGCATGCTGTATAGCAGAGAAAGTGAGGCTCTTTCGCAAGTGGGTGTGCTTTAAGTAATCA	4952
Db	3176	AGGCATGCTGTATAGCAGAGAAAGTGAGGCTCTTTCGCAAGTGGGTGTGCTTTAAGTAATCA	3235
QY	4953	GAAAACAGAAAGCTCCGGTGTATGGAATTAATCATAGTAATATCACTTATCTTC--CT	5009
Db	3236	GAAAACAGAAAGCTCCGGTGTATGGAATTAATCATAGTAATATCACTTATCTTCCTTCT	3295
QY	5010	TCATATCAACCTTAATCGTCTCTTTTCTTGTTGTAGCTGATTAACAACCTGTTTTC	5068
Db	3296	TCATATCAACCTTAATCGTCTCTCTTTTCTTGTTGTAGCTGATTAACAACCTGTTTTC	3355
QY	5070	TTTTGAGGTCTCATAGCTCTTTGTAGATTTTATAGTGTCTGCAAGTCTCTGTAGAGGTTT	5129
Db	3356	TTTTGAGGTCTCATAGCTCTTTGTAGATTTTATAGTGTCTGCAAGTCTCTGTAGAGGTTT	3415
QY	5130	GTTACCTTTGACACCTGGCGCTTGATGTTAGATGCAAGGCAACACTTGTGAATGCTT	5189
Db	3416	GTTACCTTTGACACCTGGCGCTTGATGTTAGATGCAAGGCAACAACACTTGTGAATGCTT	3475
QY	5190	GTTAAAAAGTTATTTATCTTATCTTTGCTCTTTGAAAAGGTGAAGGTGTGTGAGAAAG	5249
Db	3476	GTTAAAAAGTTATTTATCTTATCTTTGCTCTTTGAAAAGGTGAAGGTGTGTGAGAAAG	3535
QY	5250	AACATCAAGAGATGTGTCTCTGAGAGAAAACCTTTTTTCCCTTAATATGCTATATA	5309
Db	3536	AACATCAAGAGATGTATTTCTGTAGAGAAAC-TTTTTTTTCCCTTAATATGCTATATA	3594
QY	5310	TCCACTTTCACTCAACTTTGACTTTTATATACCATGCTGTCACATGAAAGAGTTTAAAGCC	5369
Db	3595	TCCACTTTCACTCAACTTTGACTTTTATATACCATGCTGTCACATGAAAGAGTTTAAAGCC	3654
QY	5370	CGCTCTCATGCTCTGGGAAAAGCAACAATAGGGAGGAAGATGTTATGCTAGAAATCTG	5429
Db	3655	CGCTCTCGTGGCTCTGGGAAAAGCAACAATAGGGAGGAAGATGTTATGCTAGAAATCTG	3714
QY	5430	ACCGGCAAGGGAACCTGATCAAGCTCCCCGGAAGCAACAAGGTGTAATAGTGGGAACA	5489
Db	3715	ACTGGCAGGGAACCTGGGTCAAGCTCCCCAAGCAACAAGGTGTAATAGTGGGAACA	3774
QY	5490	GTCACAGGTGAGGCTCATGTATATAGATGGAACAAGACAGAGGAAGATATAGCTACAAAGTT	5549
Db	3775	GTCACAGGTGAGGCTCATGTATATAGATGGAACAAGAGGAAGGAATATAGCTACAAAGTT	3834
QY	5550	TCATATGAGTCCGGAATCTTTAAAGATACAAAATAGCTGCTTGAGCTTCATTAACAAGAG	5609
Db	3835	TCATATGAGTCTTAATAGTCTTTAAAGATACAAAATAGCTGCTTGAGCTTCATTAACAAGAG	3894
QY	5610	TCTGGGAAGGACAGAG--TGAGAGGGAATATGGAAGGGAAGAAACAAGATGTATAGAGA	5666
Db	3895	TCTGGGAAGGACAGAGCATTTGAGAGGGAATGGAAGGGAAGAAACAAGATGTATAGAGA	3952

QY	5667	CTTGAACGCTACAAATCCCTTACCACAGATTTTCTTGGACAATCTAGAA-----GCT	5722
Db	3953	TTTGGAAAAGCTACAAATCTCTCCAGAGAGATTTTTCTTGGAGGAATCTAGAACAGAGGT	4012
QY	5723	AGTGAATTAAGT-CATTGACAGGGGAGCTGCTTGTGCCATTTGAATCTGGGTTTTGTCTC	5781
Db	4013	GGTGAATTAAGTGAATGCGAGAGAGACTTGTGTTGCCATTTGAATCTGGGTTTTGTCTC	4072
QY	5782	TCCATTGAGGTTGAAAGGCTCACC-TTTTTACCTCGAATGAGAGAGAAAGAGGGGT	5840
Db	4073	TCCATTGAGGTTGAGAGGCTCACCTTTTTTACCCTGGATAGAGAGAGAAAGAGGGGT	4132
QY	5841	GTTATGATCTCTACCTGAGATTTTAATAAGTTATAGCAATGGAATAAGACACTCGGGACCTC	5900
Db	4133	GTTTATGATCTCTACCTGAGATTTTAATAAGTTATAGCAATGGAATAAGACACTCGGGACCTC	4192
QY	5901	CTCTTTGAC-----AAAAAATAGGAACCTGTTGTTGCTTGTGTTGTTGCTTTTG	5950
Db	4193	CTCTTGACATAAAAAAATAGGAACCTGTTGTTGCTTGTGTTGTTGCTTTTG	4252
QY	5951	TTAAGAAAGACA-----	5963
Db	4253	TTAAGAAAGACAAGGCAAGCTGGGAGTGGGCCATGCTTTAATCCAGCAATTGGGAG	4312
QY	5964	-----	5963
Db	4313	GCAGAGCAGGTGACTTTCTTAATTTCAAGCCAGACCTGTGCTACAAAGTAGTTCCAGGA	4372
QY	5964	-----	5963
Db	4373	CAGCCAGGGCTATACAGAGAAACCTCTGCTCTCGGAAAAAATAGAAAGAAAGAAAG	4432
QY	5964	-----	5963
Db	4433	AAAAAAG	4492
QY	5964	-----	5963
Db	4493	GAA	4552
QY	5964	-----	5963
Db	4553	GAA	4612
QY	5964	-----GGCAAGCCCGACCATGAGGT	5985
Db	4613	AAGAGAAAAAGAAAAAGAAAAAGCAAGCAAGACACTGGCAAGACATGCCCAATGGGA	4672
QY	5986	TGAATGTGGGCTTTTGAAGTCAAGGCTTTTGAAGTTAGACACTCATCAATAGTTGATCAGG	6045
Db	4673	CGTATGTGGGCTTTTGAAGCAAGGCTTTTGAATTTGAGGGCTCATCAATAGTTGATCAGG	4732
QY	6046	TCAGGTGAGGGCTPACTGTCAAGCCGAGCCCTGTGCTTCCGACTTAACATCTCCAGG	6105
Db	4733	TCAGGTGAGGGCTPACTGTCAAGCCGAGCCCTGTGCTTCCGACTTAACATCTCCAGG	4792
QY	6106	TCTCAGTATCACTCCGCTCACTTAGACAGATTAGAGGTTGAGCAAACTTTTTCGAA	6165
Db	4793	TCTCAGTATCACTCCGCTCTTCAAGCAGATAGAGATTGAGCAAACTTTTTCGAA	4852
QY	6166	CCCCCACTAAATTTAATTGACAAAGACTGTGTAAATTTGTGGGATACAGTGTATAT	6225
Db	4853	CCCCCACTAAATTTAATTGACAAAGCAGTGTAAATTTGTGGGATACAGTGTATAT	4912
QY	6226	GATCTATGTGTGCAATGTGCAAGGTTCAATTAAGTATATATATATATATATATATAT	6285
Db	4913	GATCTATGTGTGCAATGTGCAAGGTTCAATTAAGTATATATATATATATATATATAT	4972
QY	6286	TATGGGTTGAAAGAGCAAGTAATTAAGTATATATATATATATATATATATATATAT	6345
Db	4973	TATGGGTTGAAAGAGCAAGTAATTAAGTATATATATATATATATATATATATATAT	5011
QY	6346	CATGATTTTAAAGTCTTGGGCAAAATCATATATATCATGCTAAATAATATATATAT	6405

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Db 5032 CATGATTTAAAGGCTTGAGCAATCATATTAATCTCATGTAATAAAGCATTAATGTA 5091
Qy 6406 TTATTAATCTTTTAAAGAGAGCTGATCTGTTGGTTGGCTCAGCAAGCAATGTCACC 6465
Db 5092 TTATCAATCTTTTAAAGAGAGCTGATCTGTTGGTTGGCTCAGCAAGCAATGTCACC 5151
Qy 6466 AGCTCTTCTTAACTGCTGACCATTTAGAAATGCTAAGTCTGCTCAAAATGGTTGTAAT 6525
Db 5152 AGCTCTTCTTAACTGCTGACCATTTAGAAATGCTAAGTCTGCTCAAAATGGTTGTAAT 5211
Qy 6526 CTATATTTTCATAGCTTGAAGAGAGTGAAGTCAAGCGATTTGGGGAACTGGACCTGCT 6585
Db 5212 CTATATTTTCATAGCTTGAAGAGAGTGAAGTCAAGCGATTTGGGGAACTGGACCTGCT 5271
Qy 6586 GTTATGCTCTGAGAAATGCTTGGCTGAGCGAGAAAGAGCTGAGAAACGAGAACTG 6645
Db 5272 GTTATGCTCTGAGAAATGCTTGGCTGAGCGAGAAAGAGCTGAGAAACGAGAACTG 5331
Qy 6646 CTCCTTCTGCTCTTCTTAAAGAGCAATTAAGTCCCTGAATGCACTTTTAACTAAAGGA 6705
Db 5332 CTCCTTCTGCTCTTCTTAAAGAGCAATTAAGTCCCTGAATGCACTTTTAACTAAAGGA 5391
Qy 6706 AAGTGAAGAGCTAAGCTCATCATCATTAAGAAATTTTCACTGAAGAACTGGCTCAGTTGA 6765
Db 5392 AAGTGAAGAGCTAAGCTCATCATCATTAAGAAATTTTCACTGAAGAACTGGCTCAGTTGA 5451
Qy 6766 AAAAGAAATAGTGTCAAGTGTCCATGAGAGACAGAGGAGTGAAGTGAATACCAAGAGT 6825
Db 5452 AAGAGAAATAGTGTCAAGTGTCCATGAGAGAGAGTGAAGTGAATACCAAGAGT 5511
Qy 6826 TCATGACAAATATTTTATGTCATGATGATCAACAGAAATTAATGACTTTTAAAAA 6885
Db 5512 TCATGACAAATATTTTATGTCATGATGATCAACAGAAATTAATGACTTTTAAAAA 5571
Qy 6886 TTGTTGAAAGAGAGTACCTCTCATCTCTTTAGAAAAAGAGCTTATGTAATCTTATTC 6945
Db 5572 TTGTTGAAAGAGAGTACCTCTCATCTCTCTAGAAAGAAAGCCATGTAATCTTATTC 5631
Qy 6946 CATATCCAAATATTTATATATGATGATTTATTTATATGATATCACTTTATATATGTC 7005
Db 5632 CATATCCAAATATTTATATATGATGATTTATTTATATGATATCACTTTATATATGTC 5691
Qy 7006 AGTTATTAATATGATGATTTATTTATAGAAACATTTCTGTAATGATATTT-AGTATAG 7064
Db 5692 AGTTATTAATATGATGATTTATTTATAGAAACATTTCTGATGATGATTTAGATATAA 5751
Qy 7065 GCAAAATTAATATTTATGACATTAATGAGAAACAGATATCTTAGAGCTTTAATAACCA 7124
Db 5752 GCAAAATTAATATTTATGATATTAATGATAGAAACAGATATCTTAGAGCTTTAATAACCA 5811
Qy 7125 TGGATATGATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7184
Db 5812 TGGATATGATTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5871
Qy 7185 TCATCATATTAACCAATCATTTCTCATGATTTTCTGCTGAGCCATATTAATCTGTTAA 7244
Db 5872 TCATCATATTAACCAATCATTTCTCATGATTTTCTGCTGAGCCATATTAATCTGTTAA 5931
Qy 7245 GTTG 7248
Db 5932 TTG 5935

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RESULT 6

AA514878 standard; DNA; 5935 BP.

AA514878;

19-DEC-2001 (first entry)

Mouse partial genomic DNA for T cell derived inducible factor, TIFbeta.

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XX Mouse; T cell derived inducible factor; TIFbeta; ds; anti-allergic;
KW anti-leukemic; cytokine; interleukin-9; IL-9; STAT transcription factor;
KW cancer; lymphoma; immune system disorder; allergy; asthma;
KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
XX thyroiditis; melanoma; hepatoma.
OS Mus musculus.
XX
XX US2001024652-A1.
XX
XX 27-SEP-2001.
XX
XX 29-DEC-2000; 2000US-0751797.
XX
XX 18-OCT-1999; 99US-0419568.
XX 26-OCT-1998; 98US-0178973.
XX 16-JUL-1999; 99US-0354243.
XX
XX (DUMO/) DUMOUTIER L.
XX (LOUA/) LOUAHED J.
XX (RENA/) RENAULD J.
XX
XX Dumoutier L, Louahed J, Renauld J;
XX
XX WPI; 2001-638496/73.
XX
XX New isolated nucleic acid molecules encoding T cell inducible factors,
XX useful as markers for expression or effect of interleukin (IL)-9 in a
XX subject and diagnosing susceptibility to asthma or allergy
XX
XX Claim 1; Page 21-23; 26p; English.
XX
XX The invention relates to an isolated nucleic acid molecule, which encodes
XX a T cell derived inducible factor (TIF) which are upregulated by the
XX cytokine interleukin-9 (IL-9) and induce STAT transcription factor
XX activation. The TIF proteins (or their mutants) may be used to test IL-9
XX ant/agonists for their potency against lymphomas, immune system
XX disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
XX autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
XX or inhibit differentiation of tissue types in which they are active and
XX therefore be used to develop treatments for melanomas and hepatomas.
XX The present sequence a partial genomic sequence for mouse TIFbeta.
XX
XX Sequence 5935 BP; 1732 A; 1174 C; 1346 G; 1683 T; 0 other;
XX
XX Query Match 57.0%; Score 4245.2; DB 22; Length 5935;
XX Best Local Similarity 88.3%; Pred. No. 0;
XX Matches 5039; Conservative 0; Mismatches 178; Indels 487; Gaps 20;
XX
XX 1971 TACCATGCTACCGCAGCAATGCTCCCGATGTTTGGCTTTGCTCTCACTAAC 2030
XX 293 TACCATGCTACCGCAGCAATGCTCCCGATGTTTGGCTTTGCTCTCTCACTAAC 352
XX
XX 2031 AGGCTCTCTCTCACTTATCAATGTTGACATTTGTCGATCTGATGCTGCTGCA 2090
XX 353 AGGCTCTCTCTCACTTATCAATGTTGACATTTGTCGATCTGATGCTGCTGCA 412
XX
XX 2091 GAAATCTATGAGTTTTCCTTATGAGGACCTTGGCCGACGCTGCTTCTCATTCG 2150
XX 413 GAAATCTATGAGTTTTCCTTATGAGGACCTTGGCCGACGCTGCTTCTCATTCG 472
XX
XX CCTGAGGAGCCAGAGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2210
XX 473 CCTGAGGAGCCAGAGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 532
XX
XX CAACTTCAGCAGCGGATACATGTCATCAACCGCACTTTATGCTGAGCAAGAGGATACACT 2270
XX 533 CAACTTCAGCAGCGGATACATGTCATCAACCGCACTTTATGCTGAGCAAGAGGATACACT 592
XX
XX GCATCTCTTTCTCTCCATACCGCTTGGCATTTTCTCTGAAAGCATTTGCAAACTCTTAG 2330
XX 593 GCATCTCTTTCTCTCCATACCGCTTGGCA-TTCTCTGAAAGCATTTGCAAACTCTTAG 651

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QY 2331 GGGCGTTTATCTCCGAGGCTCACTACCTATGTTTCTGTCTTTAGAGACTTTA 2390
 Db 652 GGGCCCTTATCTCCGAGGCTCACTACCTATGTTTCTGTCTTTAGAGACTTTA 711
 QY 2391 AGGACTGGGCTTTTCTATTTCTATTTGAAGGCTCAGAGACCATTTCTGATTTGGCCT 2450
 Db 712 AGGACTGGGCTTTTCTATTTCTATTTGAAGGCTCAGAGACCATTTCTGATTTGGCCT 771
 QY 2451 TCAGGACATATATCTAAATTTTATCTAAGAGCGCATTTAGAAACCAACCCACGACTG 2510
 Db 772 TCAGGACATATATCTAAATTTTATCTAAGAGCGCGTTTAGAAACCAACCCACGACTG 831
 QY 2511 CAATATCTTCAATTTCTGTGTCTCTTTCTGAATCTAATCTCTTGGCTACTCTGTAG 2570
 Db 832 CAATATCTTCAATCTGTGTGTCTCTTTCTGAATCTAATCTCTTGGCTACTCTGTAG 891
 QY 2571 ACCCACTGGGACATACCTCTACTTACAGAGGCTTTCTTCCATCTCTGTGACCGAG 2630
 Db 892 ACCCACTGGGACATACCTCTACTTACAGAGGCTTTCTTCCATCTCTGTGACCGAG 951
 QY 2631 CAATAGGTTTCTCTCTTTTCAAGCGCAGCTTGAGATTAACAACAAGAGCTCCGAGCTC 2690
 Db 952 CAATAGGTTTCTCTCTTTTCAAGCGCAGCTTGAGATTAACAACAAGAGCTCCGAGCTC 1011
 QY 2691 ATCCGGGAGAAACTGTTCGAGAGAGTCAAGTAAAGTCTCACTGTATGAGAGGAGCTAG 2750
 Db 1012 ATCCGGGAGAAACTGTTCGAGAGAGTCAAGTAAAGTCTCACTGTATGAGAGGAGCTAG 1071
 QY 2751 CTGCGGAGCTGTGAGACCTCTGGGATAGTCTGAGATAGACCCCTGTCTTCTTGTG 2810
 Db 1072 CTGCGGAGCTGTGAGACCTCTGGGATAGTCTGAGATAGACCCCTGTCTTCTTGTG 1131
 QY 2811 TACCTGAGAGCTAAAGATGATGCTACCTGATAGAGAGGCTGCACTTCAACCTGAA 2870
 Db 1132 TACCTGAGAGCTAAAGATGATGCTACCTGATAGAGAGGCTGCACTTCAACCTGAA 1191
 QY 2871 GACGTTCTGCTCCCGAGTCAGACAGGTTCCAGCCCTCAATGAGAGAGTGTACCTTTC 2930
 Db 1192 GACGTTCTGCTCCCGAGTCAGACAGGTTCCAGCCCTCAATGAGAGAGTGTACCTTTC 1251
 QY 2931 CTGACCAAACTCAGCAATCAGCTCAGCTCTGTGTAGTGTGCTCTGAGTACTTATGCT 2990
 Db 1252 CTGACCAAACTCAGCAATCAGCTCAGCTCTGTGTAGTGTGCTCTGAGTACTTATGCT 1311
 QY 2991 CCTCTCTCTCTCTCTCTATTTCAATGAGAAACCGAGGCTGCTGCTCTCTCTCA 3050
 Db 1312 CCTCTCTCTCTCTCTCTATTTCAATGAGAAACCGAGGCTGCTGCTCTCTCTCA 1371
 QY 3051 AGAGTGAAGAGGCTCAGACCAACCATCATAGGCCATTGAATAGATCAAAAG 3110
 Db 1372 AGAGTGAAGAGGCTCAGACCAACCATCATAGGCCATTGAATAGATCAAAAG 1431
 QY 3111 CTTTGGCTTCAATTTGATTAATCTTGAAGTTTGTATGAGGAGCTTATTTGTTATC 3170
 Db 1432 CTTTGGCTTCAATTTGATTAATCTTGAAGTTTGTATGAGGAGCTTATTTGTTATC 1491
 QY 3171 CATGAAAGAAATCAATCAATTTCTGTAGATGAGAAAGATGTTGGGAAAGGAAAG 3230
 Db 1492 CATGAAAGAAATCAATCAATTTCTGTAGATGAGAAAGATGTTGGGAAAGGAAAG 1551
 QY 3231 CCTAGATAGAGAAAGATCTGTGATATAGTATTTAT --- GGGGAGAGAGAGGAGG 3286
 Db 1552 CCTAGATAGAGAAAGATCTGTGATATAGTATTTATTTAGGGGGGGGGGAGGGGCG 1611
 QY 3287 ATATCCATGAGTAAAGTACTTGTGGGAGAGAAATCCACTGATCAAGTACTTGTG 3346
 Db 1612 ATATCCATGAGTAAAGTACTTGTGGGAGAGAAATCCACTGATCAAGTACTTGTG 1669
 QY 3347 GCATGAGATCCACTGATCAAGTACTTGTGGGAGAGGAAATGGACAGAGCAAAAGT 3406
 Db 1670 -----GGGGAGAGAAATGGACAGAGCAAAAGT 1697

QY 3407 TGAAGGA---AGAAATGAGAGGAGGCTCATGTTGGGGGNGTGAAGGTCATCC--TT 3462
 Db 1698 TGAAGGAAAGAGAAATGAGAGGCTCATGTTGGGGGNGTGAAGGTCATCC--TT 1757
 QY 3463 TTCATGATGAGAGTTAAGAAACAGTGTGTGATTTGATGTCTTCAGACACCC 3522
 Db 1758 TTCATGATGAGAGTTAAGAAACAGTGTGTGATTTGATGTCTTCAGACACCC 1817
 QY 3523 CAATATGAAATATTCACAGAGAGCGGAGACTGTGGAGACCTGGCATTTAGGAA 3582
 Db 1818 AA-----CTATGGCAGACTGTGGGAGACTGGCATTTAGGAA 1855
 QY 3583 GGGCGGCTTTTCAACGAGAACTTTATGCTCATCTGTGTACACTCCACCTTG 3642
 Db 1856 GGGCGGCTTTTCAACGAGAACTTTATGCTCATCTGTGTACACTCCACCTTG 1915
 QY 3643 ATGAGTTCAAGTCAAGTTTCTTCTACCGTTCTGCACTGTGAAACTTCAGTAG 3702
 Db 1916 ATGAGTTCAAGTCAAGTTTCTTCTACCGTTCTGCACTGTGAAACTTCAGTAG 1975
 QY 3703 ATTCGCCAAAGACGAGACAGCTCTTGTGAAGAGAGGACCTGATTTCACTGTCTAG 3762
 Db 1976 ATTCGCCAAAGACGAGACAGCTCTTGTGAAGAGAGGACCTGATTTCACTGTCTAG 2035
 QY 3763 AGAAGAAATAGCTCAGAGAACTTGTGTCAAGTAAATTTAGTTCACAGCGGCAAAA 3822
 Db 2036 AGAAGAAATAGCTCAGAGAACTTGTGTCAAGTAAATTTAGTTCACAGCGGCAAAA 2095
 QY 3823 TGACTGAAGGCTATTTCAGAGTGAAGGTCACGCTCAGATATCTAGATTTAG 3882
 Db 2096 TGACTGAAGGCTATTTCAGAGTGAAGGTCACGCTCAGATATCTAGATTTAG 2155
 QY 3883 GCTCCACCGGATTAAGATTCTGTATGAGTGTCTTATTTTGAAGACATCAGCGGT 3942
 Db 2156 GCTCCACCGGATTAAGATTCTGTATGAGTGTCTTATTTTGAAGACATCAGCGGT 2215
 QY 3943 GACGACCAAACTCAGAAAGATGTCAAGAGCTGAAAGAGACAGTGAAGAGTAACTA 4002
 Db 2216 GACGACCAAACTCAGAAAGATGTCAAGAGCTGAAAGAGACAGTGAAGAGTAACTA 2275
 QY 4003 TTGGCAAGCACAATCTAAGCAATCAGTAGAGAGCGGGGATTTCTTCTGTCTTC 4062
 Db 2276 TTGGCAAGCACAATCTAAGCAATCAGTAGAGAGCGGGGATTTCTTCTGTCTTC 2335
 QY 4063 CCAAGTCCCTTACTTGTATGATATTTATTTGATGATCTTATCTATCTGATTA 4122
 Db 2336 CCAAGTCCCTTACTTGTATGATATTTATTTGATGATCTTATCTATCTGATTA 2395
 QY 4123 CTTAGCTGACCTGTATCTAGCTGGGTCTATGATTTTCAATCTGTCTTAAATTTGTA 4182
 Db 2396 CTTAGCTGACCTGTATCTAGCTGGGTCTATGATTTTCAATCTGTCTTAAATTTGTA 2455
 QY 4183 AGTCAAAATTCGAGAGCTGAGAAAGCTTAGCTGAGCAGCTCATGAGACTTCTG 4242
 Db 2456 AGTCAAAATTCGAGAGCTGAGAAAGCTTAGCTGAGCAGCTCATGAGACTTCTG 2515
 QY 4243 GAGATGAGCTGTGACAGAGTCAATGCTAAGAAAGACATCCCTGATCCAGCTGTGA 4302
 Db 2516 GAGATGAGCTGTGACAGAGTCAATGCTAAGAAAGACATCCCTGATCCAGCTGTGA 2575
 QY 4303 CTTGCTAGTGGCCTGTATTTACTTTGGCTTATTAAGTATTTGGGAAAGCCAGTTG 4362
 Db 2576 CTTGCTAGTGGCCTGTATTTACTTTAGCTGTATTAAGTATTTGGGAAAGCCAGTTG 2635
 QY 4363 CCAAGGACCTTACATCTGAGAAACATGACATGAAACCTAAGAAAGCTGGGCAAACT 4422
 Db 2636 CCAAGGACCTTACATCTGAGAAACATGACATGAAACCTAAGAAAGCTGGGCAAACT 2695
 QY 4423 TACTAGATGATTTTGTAGCTCATTTAAAGAGTGTCTGAAATGTGAGAAATCAACC 4482
 Db 2696 TACTAGATGATTTTGTAGCTCATTTAAAGAGTGTCTGAAATGTGAGAAATCAACC 2755
 QY 4483 AGAATTAACAAAGAGAGCTGATTTGCAATATGACAAAGTATTTAGAAATCACTGATTT 4542

Db 2756 AAAAAAAAAAAAAAAAAAGAGCTGATTTGCAAAATAGGCAAGATTAAGATCACTGATTT 2815
 Qy 4543 AATAGCTATCATCTTAATTAATAATATAGGGCTATATA----TATATTAAGATTAAACA 4598
 Db 2816 AACAGGTGCATCTTAATTAATAATATAGTGTCTATTTAGCTGCTATTTAAATTAACA 2875
 Qy 4599 CAAGAGTGATAGCCTCCCAATTTAATTGGCTGTGTTTCAAAAAGTAAAAATATCAGTC 4658
 Db 2876 CAAGAGTGATTAATCTCCCAATTTAATTGGCTGTGTTTCAATAGATTAATAATATCAGTC 2935
 Qy 4659 ATGATTAATTAATAGTGCATAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 4718
 Db 2936 ATAGATTAATTAATAGTGCATAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2995
 Qy 4719 TCATTTCTTAACT-----TTTTTTTTCTTCAACCTGATCAAGCAGTAAAGTAAAGTAAAGT 4773
 Db 2996 TCATTTCTTAACTTTATTTTCTTCAACCTGATCAAGCAGTAAAGTAAAGTAAAGTAAAGT 3055
 Qy 4774 ATCTGCTGAGCTATTAATTAATAGCTTTACAGCAAAACATTTGCTGTGTGCTCTTTGG 4833
 Db 3056 ATCTGCTGAGCTATTAATTAATAGCTTTACAGCAAAACATTTGCTGTGTGCTCTTTGG 3115
 Qy 4834 GGAAGGAAACAGATTAAGCAGAGGCTCAGGCTAGCAAGTCT--GACTTGCTCTAAAGCCAG 4892
 Db 3116 GGAAGGAAACAGATTAAGCAGAGGCTCAGGCTAGCAAGTCTGACTCAACCTAAAGCCAG 3175
 Qy 4893 AGGATGTTAGTAGAGAGAAAGTGAAGGCTCTGCAAGTGGGTGTGTTAAGTAAATCA 4952
 Db 3176 AGGATGTTAGTAGAGAGAAAGTGAAGGCTCTGCAAGTGGGTGTGTTAAGTAAATCA 3235
 Qy 4953 GAAACAGAAAGCTCGGTTGATGGAATTAATGATTAATTAATTAATTAATTAATTAATTA 5009
 Db 3236 GAAACAGAAAGCTCGGTTGATGGAATTAATGATTAATTAATTAATTAATTAATTAATTA 3295
 Qy 5010 TCTATCGAACTTAATTCGCTCTTTTCTGTGTGTGAGCTGATTAACACACTTGTTTTC 5069
 Db 3296 TCTATCGAACTTAATTCGCTCTTTTCTGTGTGTGAGCTGATTAACACACTTGTTTTC 3355
 Qy 5070 TTTTGAAGTTCATGCTTGTGATTTTGAATTTTGAAGTCTGCAAGTCTTGTGAAGGTTT 5129
 Db 3356 TTTTGAAGTTCATGCTTGTGATTTTGAAGTCTGCAAGTCTTGTGAAGGTTT 3415
 Qy 5130 GTTACCTTGACACCTGGGCTTGATGATGATGATGATGATGATGATGATGATGATGATG 5189
 Db 3416 GTTACCTTGACACCTGGGCTTGATGATGATGATGATGATGATGATGATGATGATGATG 3475
 Qy 5190 GTTAAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5249
 Db 3476 GTTAAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3535
 Qy 5250 AACTCAGAGAGATGCTCTGTPAGAAAACCTTTTTCCTTCCCTTAATGCTATTA 5309
 Db 3536 AACTCAGAGAGATGCTCTGTPAGAAAACCTTTTTCCTTCCCTTAATGCTATTA 3594
 Qy 5310 TCCACTTTGATCACTTTGACTTTTATACATGCTGATCAATGAAAGTGTAAAGGCT 5369
 Db 3595 TCCACTTTGATCACTTTGACTTTTATACATGCTGATCAATGAAAGTGTAAAGGCT 3654
 Qy 5370 CGCTCTCATGCTTGGGAAAGACCAATAGGGAAAGATTTATGCTGAAATCTG 5429
 Db 3655 CGCTCTCATGCTTGGGAAAGACCAATAGGGAAAGATTTATGCTGAAATCTG 3714
 Qy 5430 ACCGCGAGGGAATCTGTCAGAGCTCCCGGAAGACCAACAGAGTGTAAAGTAAAG 5489
 Db 3715 ACTGCGAGGGAATCTGTCAGAGCTCCCGGAAGACCAACAGAGTGTAAAGTAAAG 3774
 Qy 5490 GTCCAGGTTGGGCTCATGTAATGAATGAACAGAGGAGGAAATGAAGTAAAGT 5549
 Db 3775 GTCCAGGTTGGGCTCATGTAATGAATGAACAGAGGAGGAAATGAAGTAAAGT 3834
 Qy 5550 TCATAGGTCGCGAGTCTTAAGATCAAAATAGCTTGGGCTTCAATACAAAGGAG 5609

Db 3835 TCATAGGTCGCTAAGTCTTTAAGATCAAAATAGCTGTGGCTTCAATAAAGAGAG 3894
 Qy 5610 TCTGGAAAGGAGAGAG---TGAGAGGAAATGAAAGGAAAAAAGAAATGTAAGAGA 5666
 Db 3895 TCTGGAAAGGAGAGAGATTAAGAGGAGATGAAAGGAAAAAAG---AATGTAGAGA 3952
 Qy 5667 CTGAAACAGCTAAATCTCTTACCAAGCATTTTCTTGAACAATCTAAG---GGT 5722
 Db 3953 TTTGAAAGCTTAACAATCTCTTACCAAGCATTTTCTTGAAGAAATCTAAGCAAGGCT 4012
 Qy 5723 AGTGATTAAGT--GATTCAGAGGAGACTGCTTGGCCATTTGAATCTGGTATTGTCTC 5781
 Db 4013 GGTGATTAAGTGTGATTCAGAAAGACTGCTTGGCCATTTGAATCTGGTATTGTCTC 4072
 Qy 5782 TCATAGGTCGCTAAGTCTTTAAGATCAAAATAGCTGTGGCTTCAATAAAGAGAG 5840
 Db 4073 TCATAGGTCGCTAAGTCTTTAAGATCAAAATAGCTGTGGCTTCAATAAAGAGAG 4132
 Qy 5841 GTTATGACTCTTACCTGAGTTTATCTAGTTTGAAGTAAAGTAAAGTAAAGTAAAGT 5900
 Db 4133 GTTATGACTCTTACCTGAGTTTATCTAGTTTGAAGTAAAGTAAAGTAAAGTAAAGT 4192
 Qy 5901 CTCTTGAAC-----AAAAAATGAAACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5950
 Db 4193 CTCTTGAACAAAAAATGAAACCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 4252
 Qy 5951 TTAAGAAAGCACA----- 5963
 Db 4253 TTAAGAAAGCACAAGGAGCTGGGATGATGATGATGATGATGATGATGATGATGATGATG 4312
 Qy 5964 ----- 5963
 Db 4313 GCAAGAGAGTGAATTTCTAATTAAGAGCAGCTGCTGCTAACAAGTGAATTCAGAGA 4372
 Qy 5964 ----- 5963
 Db 4373 CAGCCAGGCTATACAGAGAAACCTGTCTGGGAAAAAAGAAAAAAGAAAGAAAG 4432
 Qy 5964 ----- 5963
 Db 4433 AAAAGAAAGAAAG 4492
 Qy 5964 ----- 5963
 Db 4493 GAG 4552
 Qy 5964 ----- 5963
 Db 4553 GAG 4612
 Qy 5964 ----- 5963
 Db 4613 AAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 4672
 Qy 5966 TGAATGCTGCTTTGAGTCAAGGCTTTGAGTTGAGCACTCATTAATGATGATGAG 6045
 Db 4673 GATATGCTGCTTTGAGTCAAGGCTTTGAGTTGAGCACTCATTAATGATGATGAG 4732
 Qy 6046 TCAAGTGAAGGCTAAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6105
 Db 4733 TCAAGTGAAGGCTAAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4792
 Qy 6106 TCTAGATCACTTCTGCTAATTAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 6165
 Db 4793 TCTAGATCACTTCTGCTAATTAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4852
 Qy 6166 CCCCCACTTAATTAATTAAGCAAAAGCTGTAAATTTGGGATTAAGTGAATTAAT 6225
 Db 4853 CCCCCACTTAATTAATTAATTAAGCAAAAGCTGTAAATTTGGGATTAAGTGAATTAAT 4912
 Qy 6226 GATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6285
 Db 4913 GATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4972

QY	6286	TATGGGCTGTAAGCAAGTAATATAGTAATATCCCTGTGTCCTTAAGGTCAAGAAAG	6345
Db	4273	TATGGGTGTGAAAGCAAGTAATATAGTAATCCCTGT	5031
QY	6346	CATATATTTTAAAGTCTTGGGCAATCATATTTATACTCATGCTATAAATAATCATTATGTTGA	6405
Db	5032	CATGATTTTAAAGCTTGGGCAATCATATTAATTAATCTCATGTTAAATAATGCATTAATGTTGA	5091
QY	6406	TTATTAATCTTTTGAAGAAGGCTGATCTTGGTTTGGTGTCTGACGAAGCAAAATGTCAAC	6455
Db	5092	TTATCAATCTTTTGAAGAAGGCTGATCTTGGTTTGGTGTCTGACGAAGCAAAATGTCAAC	5151
QY	6466	AGCTCTTCTCTAACTGTAACCACTTGAAGAAATGCTACCTGTGCTCAAAATGGTTGTAAT	6525
Db	5152	AGCTCTTCTCTAACTGTAACCACTTGAAGAAATGCTACCTGTGCTCAAAATGGTTGTAAT	5211
QY	6526	CTTATATTTTCAATAGCTTGGAGAGAGTGAAGATCAAGCGATTTGGGGAACTGACCTGCT	6585
Db	5212	CTTATATTTTCAATAGCTTGGAGAGAGTGAAGATCAAGCGATTTGGGGAACTGACCTGCT	5271
QY	6586	GTTTATATCTCTGAGAAATGGTCTGCTGACGAGAAAGCTTAAAGAAAGAAAGAACTG	6645
Db	5272	GTTTATATCTCTGAGAAATGGTCTGCTGACGAGAAAGCTTAAAGAAAGAAAGAAAGAACTG	5331
QY	6646	CTCCCTCCGCTCTCTAAAAAGAACATTAATGATCCCTGAATGGAATTTTCTACTAAAGGA	6705
Db	5332	CTCCCTCCGCTCTCTAAAAAGAACATTAATGATCCCTGAATGGAATTTTCTACTAAAGGA	5391
QY	6706	AAGTGAAGAGCTAAAGTGCATCATCTATTGAAGAATTCACATGAAACCTGGCTCAGTTGA	6765
Db	5392	AAGTGAAGAGCTAAAGTGCATCATCTATTGAAGAATTCACATGAAACCTGGCTCAGTTGA	5451
QY	6766	AAAAAGAAATAGTGTCAAGTGTCTCATGAGACCAAGGTAACTTTGATTAACCAAAAGAT	6825
Db	5452	AAAAAGAAATAGTGTCAAGTGTCTCATGAGACCAAGGTAACTTTGATTAACCAAAAGAT	5511
QY	6826	TCATTTGACAAATATTTTATTTGTCACTGATGATACAAAGAAAAATATGTACTTTAAAAAA	6885
Db	5512	TCATTTGACAAATATTTTATTTGTCACTGATGATACAAAGAAAAATATGTACTTTAAAAAA	5571
QY	6886	TTGTTTGAAGAGAGTTACCTCTCATTCCTTTAGAAAAAAGCTTATGTAACCTTCATTTTC	6945
Db	5572	TTGTTTGAAGAGAGTTACCTCTCATTCCTTTAGAAAAAAGCTTATGTAACCTTCATTTTC	5631
QY	6946	CATATCCAAATTTTATATATGTAAGTTATTTATTAATAAGTATATACATTTATTAATGTC	7005
Db	5632	CATATCCAAATTTTATATATGTAAGTTATTTATTAATAAGTATATACATTTATTAATGTC	5691
QY	7006	AGTTTATTTAATGATGATTTATTTTATGAAACATATCTGCTATTGATTTT -AGTATPAG	7064
Db	5692	AGTTTATTTAATGATGATTTATTTTATGAAACATATCTGCTATTGATTTT -AGTATPAG	5751
QY	7065	GCAAAATAATATTTATGACAAATACATGAGAAACAAAGATATCTTAGGCTTTAATAAACACA	7124
Db	5752	GCAAAATAATATTTATGACAAATACATGAGAAACAAAGATATCTTAGGCTTTAATAAACACA	5811
QY	7125	TGGAATATATTAATCTCTGCTGTAATTTTCTCCCTTTAATAATGCAACATACCATCA	7184
Db	5812	TGGAATATATTAATCTCTGCTGTAATTTTCTCCCTTTAATAATGCAACATACCATCA	5871
QY	7185	TCATCATCATTAACCAATCATCTCATGATTTTCACTGTCGACCAATATTAATACGTTTAAA	7244
Db	5872	TCATCATCATTAACCAATCATCTCATGATTTTCACTGTCGACCAATATTAATACGTTTAAA	5931
QY	7245	GTTTG 7248	
Db	5932	TTTGG 5935	

AC	AAD30660;
XX	
DT	21-MAY-2002 (first entry)
XX	
DE	Mouse TIF beta genomic DNA.
XX	
KM	T cell derived inducible factor; TIF; interleukin-21; IL-21; mouse;
XX	STAT transcription factor; acute phase protein; inflammation; ds.
OS	Mus musculus.
FN	MO200210393-A2.
XX	
PD	07-FEB-2002.
XX	
PF	27-JUN-2001; 2001WO-US20485.
XX	
PR	27-JUL-2000; 2000US-0626617.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
XX	
P1	Dumoutier L, Renaud J;
DR	WPI; 2002-195964/25.
XX	
PT	Stimulating expression of STAT transcription factor and inducing
XX	production of acute phase protein in a cell, involves contacting a cell
PT	capable of expressing STAT with T cell derived inducible factors -
XX	
PS	Example 9; Page 61-64; 64pp; English.
XX	
CC	The invention relates to nucleic acid molecules encoding T cell
CC	derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
CC	TIF polynucleotides are upregulated by the cytokine, IL-9. IL-TIF or
CC	IL-21 molecules are implicated in activation of STAT transcription
CC	factors, acute phase proteins and inflammation. The present sequence
CC	is mouse TIF beta genomic DNA.
XX	
SQ	Sequence 5935 BP; 1732 A; 1174 C; 1346 G; 1683 T; 0 other;
	Query March 57.0%; Score 4245.2; DB 24; Length 5935;
	Best Local Similarity 88.3%; Pred. NO. 0; Mismatches 178; Indels 487; Gaps 20;
	Matches 5039; Conservative 0;
OY	1971 TACCATCTACCCGAGCAAGATGCTCCCTGATGTTTTGCTTTTCCTCTGCATTAC 2030
DB	293 TACCATCTATCGACAGCATGTGCCCTGAATGTTTTGGCTTTTCTCTCGCTAAC 352
OY	2031 AGGCTCTCTCTCACTTATCAACTGTGACATTTGCGATCTCTGATGCGTGTCTGCA 2090
DB	353 AGGCTCTCTCTCACTTATCAACTGTGACATTTGCGATCTCTGATGCGTGTCTGCA 412
OY	2091 GAATCTATGAGTTTTTCCCTTATGAGGAACTTTGGCCGACGCTGCTTTCATTGC 2150
DB	413 GAATCTATGAGTTTTTCCCTTATGAGGAACTTTGGCCGACGCTGCTTTCATTGC 472
OY	2151 CCTGTGGGCCGAGGACAATGCGCTGCGCTCAACACCCGCGCAAGCTTGAGGTGC 2210
DB	473 CCTGTGGGCCGAGGACAATGCGCTGCGCTCAACACCCGCGCAAGCTTGAGGTGC 532
OY	2211 CAACCTTCAGAGCGGTACATCGTCAACCGCACCTTTATGCTGCGCAAGAAGGTACACT 2270
DB	533 CAACCTTCAGAGCGGTACATCGTCAACCGCACCTTTATGCTGCGCAAGAAGGTACACT 592
OY	2271 GCATCTCTTTCTCTCCATACCGCCTTGCCATTTTCTGTGAAGCATTTGCAAACTCTTAG 2330
DB	593 GCATCTCTTTCTCTCCATACCGCCTTGCCCA- TTCTGTGAAGCATTTGCAAACTCTTAG 651
OY	2331 GGAGGCTTTATCTCCGAGGCTCTCACTACCTATGTTTCTGTCTTTAGAGACTCTTA 2390
DB	652 GGAGGCTTTATCTCCGAGGCTCTCACTACCTATGTTTCTGTCTTTAGAGACTCTTA 711

QY	6346	CATATATTTAAGCTTGGGCAAAATCATATATATCTCATGTCTAAAAAATATACATTTTNGTGA	6405
Db	5032	CATGATTTTAAAGCTTGGGCAAAATCATATTTATCTCATGTCTAAAAAATGCAATTTATGTTGA	5091
QY	6406	TTATTTAATCTTTTAAAGAAAGGCTGATACCTTGTTTTGGTGTCTAGCAAGCAAAATGTCACC	6465
Db	5092	TTATCAATCTTTTAAAGAAAGGCTGATACCTTGTTTTGGTGTCTAGCAAGCAAAATGTCACC	5151
QY	6466	AGCTCTTTCTAATCTGTATCCACTTTAGAAAATGCTACCTGTGTCAAAATTTGGTTGATTT	6525
Db	5152	AGCTCTTTCTAATCTGTATCCACTTTAGAAAATGCTACCCGTGTCAAAATTTGGTTGATTT	5211
QY	6526	CTTATTTTTCATAGCTTGAGAGAGATGTGAGAGATCAAGGCGATTTGGGGAACTGCACCTGCT	6585
Db	5212	CTTATTTTTCATAGCTTGAGAGAGAGATGTGAGAGATCAAGGCGATTCGGGGAACCTGCACCTGCT	5271
QY	6586	GTTTATGTCTCTGAGAAAATGCTTGGGTCTGACGCGAAGAAAGCTTATGAAAACGAAGAACTG	6645
Db	5272	GTTTATGTCTCTGAGAAAATGCTTGGGTCTGACGCGAAGAAAGCTTATGAAAACGAAGAACTG	5311
QY	6646	CTCCTTCCTGCTCTTAAAGAAACAATPAATCCCTGAATGGACTTTTCTACTAAAGGA	6705
Db	5332	CTCCTTCCTGCTCTTAAAGAAACAATPAATCCCTGAATGGACTTTTCTACTAAAGGA	5391
QY	6706	AAGTGAAGAGCTAAAGTTCATCATTTAGAAAGATTTTCAATGAAACCTGGCTCAGTTGA	6765
Db	5392	AAGTGAAGAGCTAAAGTTCATCATTTAGAAAGATTTTCAATGAAACCTGGCTCAGTTGA	5451
QY	6766	AAAAGAAAATAGTGTCAAGTGTGCTCATGATAGACACAGAGTATACCTTGATTAACCAAAAGAT	6825
Db	5452	AAGAGAAAATAGTGTCAAGTGTGCTCATGATAGACACAGAGTATACCTTGATTAACCAAAAGAT	5511
QY	6826	TCATTTGACAAATTTTATTTATGTCTACGTATGATACAAACAGAAAATPATGTACTTTAAAAAA	6885
Db	5512	TCATTTGACAAATTTTATTTATGTCTACGTATGATTAAGCAACAGAAAAGATPATGTACTTTAAAAAA	5571
QY	6886	TTGTTTGAAGAGAGTTACCTCTCATTTCTTTAGAAAAAAAGCTTATGTAACCTTCATTTTC	6945
Db	5572	TTGTTTGAAGAGAGTTACCTCTCATTTCTCTAGAAAGAAAAGCTTATGTAACCTTCATTTTC	5631
QY	6946	CATATCCAAATTTTATATATATGTAAGTTATTTATTAAGATATACATTTATTTATTTATGTC	7005
Db	5632	CATATCCAAATCTTTATATATATGTAAGTTATTTATTTATTAAGATATACATTTATTTATTTATGTC	5691
QY	7006	AGTTTATTTAATATGGAATTTATTTATAGAAACATTAATCTGATTTGATATTT-AGATTAAG	7064
Db	5692	AGTTTATTTAATATGGAATTTATTTATAGAAAAAATTAATCTGATTTGATATTTGAAGATTA	5751
QY	7065	GCAAAATATATTTTATGACATATACATATGGAACCAAGATATCTTAGGCTTTAATTAACACA	7124
Db	5752	GCAAAATATATTTTATGATATATACATATGGAACCAAGATATCTTAGGCTTTAATTAACACA	5811
QY	7125	TGGATATCATATAAATCTTGTCTGTGTAATTTTTCTCCCTTAAATATCAACATATCCATCA	7184
Db	5812	TGGATATCATATAAATCTTGTCTGTGTAATTTTTCTCCCTTAAATATCAACATATCCATCA	5871
QY	7185	TCATCATCATTAACCAATCATTTCTCATGATTTCAATGCTTGAACCAATTAATACCTGTAA	7244
Db	5872	TCGTCATCATTAACCAATCATTTCTCATGATTTCAATGCTTGAACCAATTAATACCTGTAA	5931
QY	7245	GTTG 7248	
Db	5932	TTTG 5935	
RESULT 8			
ID	AA027153	standard; DNA; 5935 BP.	
AC	AA027153;		
XX	09-APR-2002	(first entry)	
XX			

XX	Mouse T cell derived inducible factor (TIF) beta genomic DNA.
DE	
XX	T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;
KM	protein therapy; STAT activation; differentiation; mouse; ds.
XX	
XX	Mus musculus.
OS	
XX	US6331613-B1.
PN	
XX	18-DEC-2001.
PD	
XX	18-OCT-1999; 99US-0419568.
PF	
XX	26-OCT-1998; 98US-0178973.
PR	
XX	16-JUL-1999; 99US-0354243.
PA	
XX	(LUDW-) LUDWIG INST CANCER RES.
PI	
XX	Dumoutier L, Louhed J, Renaud J,
DR	WPI; 2002-105277/14.
XX	
PT	Nucleic acids encoding T cell derived inducible factors useful for
PT	inducing STAT activation in cells -
XX	
PS	Claim 1; Column 37-44; 24pp; English.
XX	
CC	The present invention relates to an isolated nucleic acid molecule, which
CC	encodes a T cell derived inducible factor comprising an amino acid
CC	sequence encoded by 6 defined nucleotide sequences. The nucleic acid
CC	molecules are shown to be up regulated by the cytokine interleukin-9
CC	(IL-9) and are described as T Cell Derived Inducible Factors (TIFs). The
CC	invention is used in protein therapy. The nucleic acid molecules encode
CC	proteins which induce STAT activation in cells. They can be used, for
CC	example, in the stimulation of regeneration of targeted tissues.
CC	Further, their inhibitors or antagonists can be used to retard, prevent
CC	or inhibit differentiation of other tissues. The present sequence is
XX	mouse TIF beta genomic DNA.
SQ	
	Sequence 5935 BP; 1732 A; 1174 C; 1346 G; 1683 T; 0 other;
	Query Match 57.0%; Score 4245.2; DB 24; Length 5935;
	Best Local Similarity 88.3%; Pred. No. 0;
	Matches 5039; Conservative 0; Mismatches 178; Indels 487; Gaps 20;
QY	1971 TACCATGCTACCGACGACATGCTCCCTGATGTTTGGCTTTTGGCTCTCTCACTTAC 2038
DB	293 TACCATGCTATCCAGCAGCATGTTCCCTGATGTTTGGCTTTTGGCTCTCTCGCTAAC 352
QY	2031 AGGCTCCCTCTCACTTATCAACAGTTGACACTGTGGATCTGTGATGGCTGCTGCA 2098
DB	353 AGGCTCTCTCTCACTTATCAACAGTTTGAACCTGTGGATCGGTGATGGCTGCTGCA 412
QY	2091 GAAATCTATGAGTTTTCCTTATGGGAGACTTTGGCCGACGTCCTGCTTCTCATTTGC 2156
DB	413 GAAATCTATGAGTTTTCCTTATGGGAGACTTTGGCCGACGTCCTGCTTCTCATTTGC 472
QY	2151 CTTGTGGCCCGACGAGGCAATGCGCTGCGCTCAACACCCGGTGCAGAGCTTGAAGTTC 2210
DB	473 CTTGTGGCCCGACGAGGCAATGCGCTGCGCTCAACACCCGGTGCAGAGCTTGAAGTTC 532
QY	2211 CAACCTTCAGAGCGGATACATCGTCAACCCGACCTTATGCTGGCCAAAGAGGTACAGCT 2270
DB	533 CAACCTTCAGAGCGGATACATCGTCAACCCGACCTTATGCTGGCCAAAGAGGTACAGCT 592
QY	2271 GCATCTCTTCTCTCAATACCGCCTTGCAATTTCTCTGAAGCACTTGAAGCAACTCTTTAG 2330
DB	593 GCATCTCTTCTCTCAATACCGCCTTGCA- TTCTCTGAAGCACTTGAAGCAACTCTTTAG 651
QY	2331 GGGGGCTTATCTCCGACAGGTCTCACTACCTATGTTTCTGTCTCTTTAAGACTCTTTA 2390
DB	652 GGGGGCTTATCTCCGACAGGTCTCACTACCTATGTTTCTGTCTCTTTAAGACTCTTTA 711

[illegible]

Db	1758	TTCCATGTGTATGGAGAGTTTAAAGAAAATCAGTGTGTGAGTTTGAATGTCTTTCAGACACCCC	1817
QY	3523	CAACTATGAAACATATTCACAGAGAGCCGGCAGACTGTGGAGACCTGGCATTTTAGAGAA	3582
Db	1818	AA-----CTATGGCACACTGTGGGAACCCGGCATTTTAGGAA	1855
QY	3583	GGGGCGGCTTTTTCACACAGAGAACTTTATGTCTCATCTCTGTGTCTACATCCCAACCTTTG	3642
Db	1856	GGGGCGGCTTTTTCACACAGAGAACTTTATGTCTCATCTCTGTGTCTACATCCCAACCTTTG	1915
QY	3643	ATGAGGTTTCACTCAGGTTTCGTTTCTACCGTCTTGCTACTGTGGAAACTTCAGTAGG	3702
Db	1916	ATGAGGTTTAACTCAGGTTTCGTTTCTACCGTCTTGCTACTGTGGAAACTTCAGTAGG	1975
QY	3703	ATTCCCCAAAGACAGAGACAGCTCTTCTGTAAAGAGAGGACCTGGAATTTCAGTCTCTAG	3762
Db	1976	ATTCCCCAAAGACAGAGACAGCTCTTCTGTAAAGAGAGGACCTGGAATTTCAGTCTCTAG	2035
QY	3763	AGAAAGAAATAGCTCAGAGAACTTAGTCAACGTGAATTTAGTCTCACAGCGGCAAAAA	3822
Db	2036	AGAAAGAAATAGCTCAGAGAACTTAGTCTCAACGTGAATTTAGTCTCACAGCGGCAAAAA	2095
QY	3823	TGACTGAACCCCTCTATTTCCAGGTGAACGGTCAACGGCTCAGATATACAGGATATTGG	3882
Db	2096	TGACTGAACCCCTCTATTTCCAGGTGAACGGTCAACGGCTCAGATATACAGGATATTGG	2155
QY	3883	GCTCCCAACGGATTAAGATTCTGTAGTAGTCTGCTTTATTTTGACGACATCAGCGT	3942
Db	2156	GCTCCCAACGGATTAAGATTCTGTAGTAGTCTGCTTTATTTTGACGACATCAGTGT	2215
QY	3943	GACGACCAAGAACATCCAGAAAGATGTGAGAGGCTGAAGAGACAGTGAAGAAAGTACTA	4002
Db	2216	GACGACCAAGAACATCCAGAAAGATGTGAGAGGCTGAAGAGACAGTGAAGAAAGTACTA	2275
QY	4003	TTGGCAAGCCAACTACTAAGCCATTAGTAGAGAGAGCTGGGATTTCTTCTCTGCTTC	4062
Db	2276	TTGGCAAGCCAACTACTAAGCCATTAGTAGAGAGAGCTGGGATTTCTTCTCTGCTTC	2335
QY	4063	CCACTCCCTCTACTTTTGTAACTATTATTTGACTTGTCTACTATCTGCTCATTACTGC	4122
Db	2336	CCACTCTCTTCTACTTTTGTAACTATTATTTGACTTGTCTACTATCTGCTCATTACTGC	2395
QY	4123	CTTAGCTGCACTGTATCTAGCTGGGTCTATAGATCTTTCAATCTGTCTAAATTTGTA	4182
Db	2396	CTTAGCTGCACTGTATCTAGCTGGGTCTATAGATCTTTCAATCTGTCTAAATTTGTA	2455
QY	4183	AGTCACAATTTGTGAGCTAGCAGAGAAAGCTTAGTACTGACAGTCTCATGAGCACTTGTCTG	4242
Db	2456	AGTCACAATTTGTGAGCTAGCAGAGAAAGCTTAGTACTGACAGTCTCATGAGCACTTGTCTG	2515
QY	4243	GAGGATGGCTTGTATCAGAGTCAATGTCTAGAGAGACACATCCCGATTCCAGCTCTGCA	4302
Db	2516	GAGGATGGCTTGTATCAGAGTCAATGTCTAGAGAGACACATCCCGATTCCAGCTCTGCA	2575
QY	4303	CTTGCTCTAGTGGCATGTATGTAACTTCTTGCTTGATTAAGTATTTGGAAAGCCAGTTC	4362
Db	2576	CTTGCTCTAGTGGCATGTATGTAACTTCTTGCTTGATTAAGTATTTGGAAAGCCAGTTC	2635
QY	4363	CCACGGACCTTACATATCTGAGAAACCATGTGATTTGAAAACCTGGGCACTAACT	4422
Db	2636	CCACGGACCTTACATATCTGAGAAACCATGTGATTTGAAAACCTGGGCACTAACT	2699
QY	4423	TACATAGAGATATTTTGGAGCTCAATTAACGGATGCTGTAATTTGTGCAAAATCAACCC	4482
Db	2696	TACATAGAGATATTTTGGAGCTCAATTAACGGATGCTGTAATTTGTGCAAAATCAACCC	2755
QY	4483	AGAAATTAACAACAAGAGCTGATTTGCCAAATAGAGACAATTTAGAAATCAGTGTATT	4542
Db	2756	AGAAATTAACAACAAGAGCTGATTTGCCAAATAGAGACAAGTATTTAGAAATCAGTGTATT	2815
QY	4543	AATAGCTATCATCTTAATTAATAATATAGGCGCTATTA-----TATATTTAGATTTAACA	4598


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Db 2816 AACGCTCATCTTAATTAATAATAGTGTCTATTAGTCCCTATTTAAGATTAAACA 2875
Qy 4599 CAAGAGTGAATAGCCTCCCAATTTACTTGGCTGTGTTCAAAAGAGTAAATAATCAGTC 4658
Db 2876 CAAGAGTGAATAGTCCCAATTTACTTGGCTGTGTTCAATAGAGTAAATAATCAGTC 2935
Qy 4659 ATGAGTTAATTAATAGTGTCAATGAAGATAGAGTAAACCTTTCTTACTTTTAACT 4718
Db 2936 ATAGATTAAATTAATAGTGTCAATGAAGATAGAGTAAACCTTTCTTACTTTTAACT 2995
Qy 4719 TCATTTCTTAGT-----TTTTTTTCTTCAACCCCTGATCAAGCCACTAGTAGACCT 4773
Db 2996 TCATTTCTTAGTATTATTTTCTTCAACCCCTGATCAAGCCACTAGTAGACCT 3055
Qy 4774 ATCTGTGTGATTAATTAATAGTGTCAATGAAGATAGAGTAAACCTTTCTTACTTTTAACT 4833
Db 3056 ATCTGTGTGATTAATTAATAGTGTCAATGAAGATAGAGTAAACCTTTCTTACTTTTAACT 3115
Qy 4834 GGAAGGAAACAGATAGCAGAGAGCTCAGGCTAGCAAGTCT-GACTTCCCTTAAAGCAG 4892
Db 3116 GGAAGGAAACAGATAGCAGAGAGCTCAGGCTAGCAAGTCTGAGCTCAACCTTAAAGCAG 3175
Qy 4893 AGGATGTTGATAGCAGAGAGAGTGAAGTGAAGTCTTGAAGTGGTGTGCTTAGTATCA 4952
Db 3176 AGGATGTTGATAGCAGAGAGAGTGAAGTGAAGTCTTGAAGTGGTGTGCTTAGTATCA 3235
Qy 4953 GAAACAGAAAGGCTCCGCTGATGAATTAATCAAGTAAATTAATCACTTATCTC---CT 5009
Db 3236 GAAACAGAAAGGCTCCGCTGATGAATTAATCAAGTAAATTAATCACTTATCTCCTCTCT 3295
Qy 5010 TCTATGAACCTTAATGCTCTCTTTTCTGTGTGTAGAGTGTATTAACACACTTGTTC 5069
Db 3296 TCTATGAACCTTAATGCTCTCTTTTCTGTGTGTAGAGTGTATTAACACACTTGTTC 3355
Qy 5070 TTTTGAAGTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5129
Db 3356 TTTTGAAGTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3415
Qy 5130 GTTACCTTGAACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5189
Db 3416 GTTACCTTGAACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3475
Qy 5190 GTGTAAAGGTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 5249
Db 3476 GTGTAAAGGTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 3535
Qy 5250 AACTCAGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5309
Db 3536 AACTCAGAGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3594
Qy 5310 TCCACTTTCAGTCACTTTTATACCTTTTATACCTTCTGACATGAAGAGTGTGTAGGCC 5369
Db 3595 TCCACTTTCAGTCACTTTTATACCTTTTATACCTTCTGACATGAAGAGTGTGTAGGCC 3654
Qy 5370 CGCTCTCATGCTCTGTGGAAGAACCAATAGGGGAGAAAGTATTAGTGTGAAGATCTG 5429
Db 3655 CGCTCTCATGCTCTGTGGAAGAACCAATAGGGGAGAAAGTATTAGTGTGAAGATCTG 3714
Qy 5430 ACCGCGAGGAAATGTGTCAAGAGTCCCCCGAAGAACCAACACAGAGTGTATTAGTAGACA 5489
Db 3715 ACTGCGAGGAAATGTGTCAAGAGTCCCCCGAAGAACCAACACAGAGTGTATTAGTAGACA 3774
Qy 5490 GTCCAGAGTGGGCTCATGTATAGATGAACAGAGGAGGAGATTAAGTCAAAAGTT 5549
Db 3775 GTCCAGAGTGGGCTCATGTATAGATGAACAGAGGAGGAGATTAAGTCAAAAGTT 3834
Qy 5550 TCATAGAGTCCGAGTCTTAAAGATCAAAATAGCTCTTGGGCTTCAATAACAAAGAG 5609
Db 3835 TCATAGAGTCCGAGTCTTAAAGATCAAAATAGCTCTTGGGCTTCAATAACAAAGAG 3894
Qy 5610 TCTGGGAAGGAGAGAG---TGAGAGGAAATGGAAGGAGGAGGAGGAGGAGGAGGAGGAG 5666
Db 3895 TCTGGGAAGGAGAGAGAG---TGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3952
Qy 5667 CTTGAACAGCTCAAAATCCTCTACAGAGATTTTCTTGGAAACATTCAGAA---GCT 5722
Db 3953 TTTGAAATCTCAAAATCCTCTACAGAGATTTTCTTGGAAATCTAGAAACAGAGGT 4012
Qy 5723 AGTGAATTAGGT-GATTGAGAGGAGCTTGGCTTTGGCAATTTGAATCTGGGTTTGTCTC 5781
Db 4013 GGTGATTTAGGTGAGATGAGAGAGCTTGGCTTTGGCAATTTGAATCTGGGTTTGTCTC 4072
Qy 5782 TCCATGAGTGTGAAGAGCTCAACC-TTTTACCCCTGAAATGAGAGGAGGAGGAGGAGT 5840
Db 4073 TCCATGAGTGTGAAGAGCTCAACC-TTTTACCCCTGAAATGAGAGGAGGAGGAGGAGT 4132
Qy 5841 GTTATAGCTCTAAGCTGAGATTCTTACTTAAATTAACGAATGAACAGACACTGGGACCTC 5900
Db 4133 GTTATAGCTCTAAGCTGAGATTCTTACTTAAATTAACGAATGAACAGACACTGGGACCTC 4192
Qy 5901 CTCTTGAC-----AAAAAAATGGAACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5950
Db 4193 CTCTTGACAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4252
Qy 5951 TTAAGAAAGCACA----- 5963
Db 4253 TTAAGAAAGCACAAGCAGCTGGGCAATGTGGCCATGCTTTATCCCAAGATTGGAG 4312
Qy 5964 ----- 5963
Db 4313 GCAGAGGAGAGTACTTTTAATTAATCAAGCCAGCTGTCTTCAAAATGATTCAGAGA 4372
Qy 5964 ----- 5963
Db 4373 CAGCCAGGCTATACAGAGAAACCTGTCTCGGAGAAAAAAGAGAGAGAGAGAGAGAG 4432
Qy 5964 ----- 5963
Db 4433 AAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4492
Qy 5964 ----- 5963
Db 4493 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4552
Qy 5964 ----- 5963
Db 4553 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4612
Qy 5964 ----- 5963
Db 4613 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4672
Qy 5986 TGAATGTGGTCTTTGAGTCAAGGCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 6045
Db 4673 CGTATGTGGTCTTTGAGTCAAGGCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4732
Qy 6046 TCAAGTGAAGGCTACCTGTCAAGGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 6105
Db 4733 TCAAGTGAAGGCTACCTGTCAAGGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 4792
Qy 6106 TCTCAGTATCACTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 6165
Db 4793 TCTCAGTATCACTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 4852
Qy 6166 CCCCACATAAATTTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6225
Db 4853 CCCCACATAAATTTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4912
Qy 6226 GATCTATGTGTGCTTTGCTGCAAGCTTCAATTAAGATTAATTAATTAATTAATTAATTA 6285
Db 4913 GATCTATGTGTGCTTTGCTGCAAGCTTCAATTAAGATTAATTAATTAATTAATTAATTA 4972
Qy 6286 TATGGGTGAATATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 6345
Db 4973 TATGGGTGAATATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5031
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QY 6346 CATGATTTTAAAGCTCTTGGGCAAAATATTAATCTAGCTTAAATAATCATATTGTGA 6405
DB 5032 CATGATTTTAAAGCTCTTGGGCAAAATATTAATCTAGCTTAAATAATCATATTGTGA 5091
QY 6406 TTAATTAATCTTTAGAGAGAGCTGATCTGTTGGTGTCTGAGAGCAAAATGTCCAC 6465
DB 5092 TTAATTAATCTTTAGAGAGAGCTGATCTGTTGGTGTCTGAGAGCAAAATGTCCAC 5151
QY 6466 AGCTCTTTTAACTGTGTACCTTTAGAAAATGTCTACTGTGTCTAAATTTGTTGTATT 6525
DB 5152 AGCTCTTTTAACTGTGTACCTTTAGAAAATGTCTACTGTGTCTAAATTTGTTGTATT 5211
QY 6526 CTATTTTATATAGCTTGGAGAGAGTGGAGAGATCAAGCGCATTTGGGAACTGCACTGCT 6585
DB 5212 CTATTTTATATAGCTTGGAGAGAGTGGAGAGATCAAGCGCATTTGGGAACTGCACTGCT 5271
QY 6586 GTTATATGCTCTGAGAGAAATGCTGTGCTGAGAGAGAGAGCTTAAAGAAAGAACTG 6645
DB 5272 GTTATATGCTCTGAGAGAAATGCTGTGCTGAGAGAGAGAGCTTAAAGAAAGAACTG 5331
QY 6646 CTCTCTTCTGCTCTTCTTAAAAAGAACATAAGATCCCTGAATGACCTTTTACTTAAAG 6705
DB 5332 CTCTCTTCTGCTCTTCTTAAAAAGAACATAAGATCCCTGAATGACCTTTTACTTAAAG 5391
QY 6706 AAGTGGAAGCTTACCTCATCTATCTATAGAAATTTTCAATGAACTTGGCTCACTTGA 6765
DB 5392 AAGTGGAAGCTTACCTCATCTATCTATAGAAATTTTCAATGAACTTGGCTCACTTGA 5451
QY 6766 AAAAGAAATAGTGTCAAGTGTGCTGAGAGAGAGAGAGCTTGTATGATCAAGAAAGAT 6825
DB 5452 AAAAGAAATAGTGTCAAGTGTGCTGAGAGAGAGAGAGCTTGTATGATCAAGAAAGAT 5511
QY 6826 TCATTTGACATATTTTATTTATGTCATGATGATGATGATGATGATGATGATGATGATG 6885
DB 5512 TCATTTGACATATTTTATTTATGTCATGATGATGATGATGATGATGATGATGATGATG 5571
QY 6886 TTGTTTGAAGAAGAGTTTACCTCTCATCTCTTCTTGAAGAAAAAGCTTATGATCTTCT 6945
DB 5572 TTGTTTGAAGAAGAGTTTACCTCTCATCTCTCTTGAAGAAAAAGCTTATGATCTTCT 5631
QY 6946 CATATCCAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 7005
DB 5632 CATATCCAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 5691
QY 7006 AGTTTATTAATGATGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 7064
DB 5692 AGTTTATTAATGATGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 5751
QY 7065 GCAAAATTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 7124
DB 5752 GCAAAATTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 5811
QY 7125 TGAATATTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 7184
DB 5812 TGAATATTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 5871
QY 7185 TCATCATCATTTTACCATCATCTCATGATTTTCAATGATTTTCAATGATTTTCAATGAT 7244
DB 5872 TCATCATCATTTTACCATCATCTCATGATTTTCAATGATTTTCAATGATTTTCAATGAT 5931
QY 7245 GTTG 7248
DB 5932 TTGG 5935

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RESULT 9
AAS14876
ID AAS14876 standard; DNA; 4797 BP.
XX
AC AAS14876;
XX
DT 19-DEC-2001 (first entry)
XX

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DE Human partial genomic DNA for T cell derived inducible factor, TIF.
XX
KW Human; T cell derived inducible factor; TIF; ds; anti-lymphocyte;
KW antileukemic; cytokine; interleukin-9; IL-9; STAT transcription factor;
KW cancer; lymphoma; immune system disorder; allergy; asthma;
KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
KW chryoiditis; melanoma; hepatoma.
XX
OS Homo sapiens.
XX
PN US2001024652-A1.
XX
PD 27-SEP-2001.
XX
PF 29-DEC-2000; 2000US-0751797.
XX
PR 18-OCT-1999; 99US-0419568.
PR 26-OCT-1998; 98US-0178973.
PR 16-JUL-1999; 99US-0354243.
XX
PA (DUNC/) DUMOUTIER L.
PA (LOUAH/) LOUAHED J.
PA (RENA/) RENAUD J.
XX
PI Dumoutier L, Louahed J, Renaud J;
XX
XX
XX WPI; 2001-638496/73.
XX
PT New isolated nucleic acid molecules encoding T cell inducible factors,
PT useful as markers for expression or effect of interleukin (IL)-9 in a
PT subject and diagnosing susceptibility to asthma or allergy
XX
XX
XX Claim 1; Page 17-19; 26pp; English.
XX
XX
XX The invention relates to an isolated nucleic acid molecule, which encodes
XX a T cell derived inducible factor (TIF) which are upregulated by the
XX cytokine interleukin-9 (IL-9) and induce STAT transcription factor
XX activation. The TIF proteins (or their mutants) may be used to test IL-9
XX ant/agonists for their potency against lymphomas, immune system
XX disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
XX autoimmune diabetes and chryoiditis. TIF molecules promote regeneration
XX or inhibit differentiation of tissue types in which they are active and
XX therefore be used to develop treatments for melanomas and hepatomas.
XX
XX The present sequence a partial genomic sequence for Human TIF.
XX
XX
XX Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;
XX
XX
XX Query Match 9 2%; Score 686; DB 22; Length 4797;
XX Best Local Similarity 53.8%; Pred. No. 2,7e-145; Indels 393; Gaps 44;
XX Matches 2644; Conservative 0; Mismatches 1875;
XX
XX
XX 2034 CTCTCTCTCACTTATCACTGTTGACCTGTGAGCTCTGATGCTGTGCTGAGAA 2093
DB 29 CTCTCTCTCACTTATCACTGTTGACCTGTGAGCTCTGATGCTGTGAGAA 88
QY 2094 ATCTATGAGTTTTCCTTATGAGGACCTTGTGAGGAGCTGCTGCTTCTATTTGCTT 2153
DB 89 ATCTGAGACTCTTCTTATGAGGAGCTGAGGAGCACTGCTCTCTCTGAGGCTT 148
QY 2154 GTGGGCGGAGAGGCAAAATGCGCTGCGCTCAACACCGGTGCAAGCTTGAAGTGTCCA 2213
DB 149 GTGGGCGGAGAGGAGGAGAGCTGCGCGCTCAACACCGGTGCAAGCTTGAAGTGTCCA 208
QY 2214 CTTCAGAGAGCGGTATCATGTCGAACCGGACCTTTATGCTGCGCAAGAGAGTACAGCTGCA 2273
DB 209 CTTCAGAGAGCGGTATCATGTCGAACCGGACCTTTATGCTGCGCAAGAGAGTATCATCTC 268
QY 2274 TCTCTTTCTCTCATACCGCTTGCATTTTCTGAGACACTTGAACCTTTTGAAGG 2333
DB 269 AATCGTCTCTTCTGTTGATCTTCTGATCTGATCAATTAATGATCTTAACTTTCTTCA 328
QY 2334 CGCTTATCTCCGAGAGTCTCACTACTTATTTT-----TCTCTCTTTAAG 2382

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4461 TGAATGTGGCAAAATCAACCCAGATATACAAACAAAGAGCTGGATTGGCAATATAGACA 4520
2477 TGAACCTTGGAAAGAAATCACTAGAACATGAGAAAAAGCTGAGACTTCATATAGAGCT 2536
4521 AGTATTGAAATCACTGATTTAAATAGTATCATCTTAATTAATAATATAGGGCTATATA 4580
2537 AATTCTGGA-----GTAAATTAACACTTATTTGAAATTATCATATAATATCATCGAAT 2589
4581 TATATTTAAGATTTAAACACAAAGATGAGATAGCCTCCCAATTATCTGGCTGTTCAAA 4640
2590 TTGATTATATGTTTAAAGAGAGAGAGAGACCAACC-CCGATCTCTTTATACAGGTTCAAT 2648
4641 AGAGTAAATATATCATGCTATGATTTATATATGTCATGAAAGATATGAGATGAAACC 4700
2649 AGAGTAAATATATGATTAAGATTTATATATGAAAGTCTGATTTGTTAGCT 2708
4701 TTTCCTACTTTTAACTTCA-----TTTCCTAGTTTCTTTTCTTCAACCTCGA 4752
2709 TTTTCTTCTCTCTCTCTCCCACTCAAGACCTTCATTTCTAGTTTCTTCTTCACTCCCTCA 2768
4753 TCAAGCACTAGTAAAGCACTATCTGCTGAGCTATATATGACTTTACAGCAACAAAC 4812
2769 ACAAATCCCTAGGAGCAATTTATCCATGAGGCTGTGTAATTTCTATAGTAATGAT 2828
4813 ATTGCTGTGCTCTCTTTGGGAGAGAGAAACAGATAGCAGAGGCTCAGGCTAGCAAGT 4872
2839 ACCATCATGTGCTCTATTTGGTGAAGAAAGACA--ACAAATGGAAGGCTTACACTAACAAAT 2886
4873 CTGACTGGCCCTAAAGCCAGAGGCACTGTTAGAGAGAGAAAGTGAAGCTCTGGCAG 4932
2887 GTGACTCACCCCAAAACCGAGAGATGATTTAGAGAGTGAAGTGAACGCTCTT--GCAAG 2945
4933 TGGGTGTGCTTAAATACAGAAACAGAAAGCTCCGTTGATGAAATATACAGTAAGA- 4991
2946 CAGGTAACTAAATATCTAGAAACAGAAAGCTCCAGTTGATGAAATTTTCACTAACAA 3005
4992 -----TATCTACCTTATCTCTTCTTATCGAACTTAATGCTCTCTTTCTTGTG 5042
3006 GCTTAACCTTAATTCCTCTTTTCTCTCTGACTTTTAAAAAAGCTTCTCTCTGAG 3065
5043 TGTAGGCTGATTAACACACTTGT--TCTTTTGAAGTTCATAGGCTTGTGATTTTA 5100
3066 CATCATTTATATAGTGTGACTGTTCTCTTGTATATGAAAGGCTTGTGATTTTAA 3125
5101 GTGCTCTGCACTTCTGT--TAGAGGTTTGTATACCTTGACACTCGGCTTGATGTA 5158
3126 TTGTAGAGCCAGTTCTCTTGTATATGAACTATATCTAGACATGAGAGGCTGAACTTA 3185
5159 GCATGCCAAAGCACACTTCTGAATGCTGCTGTGTAAGAGTTATTTCACTTACT-- 5215
3186 GCATGCCAAGACAGAGCATGCTTTACATCTTGTAAAAAATTAAGATTTCACTCT 3245
5216 -----TGTCTTGAAGAGTGAAGGCTGTGAGAAAGACATCAAGAGATGCTTCT 5270
3246 GCTTGTGCTTTTGAAGAGTGAAGTGAAGAGATATCTCAAGTGA----- 3296
5271 CTGTAGAAACCTTTTCTTCTCTTAAATGCTTAAATCACTTCACTCA---ACTT 5327
3297 -----TCTGTGATTTTCAAGACCTTTATCTCACTTTTGAAGAAATCAAT 3342
5328 TGACTTTTATACATGCTGTCTACATGAAAGAGTGTTAAGCCGCTCTCATGCTGTGAG 5387
3343 TCATTTTGTGCAATGAGTGTCCATGAGAGAGATGATTTTGTCTGAGAGCTTCA 3402
5388 AAAAGACCAATAGGAGAGAGATGATGCTGAGAAATCTGACCGGCGAGGAAATGCT 5447
3403 GAAAGCA--CAGAGAGAGAGCAATGTTTTCAGAGAAATCAACGAGAGAGAACTGT 3461
5448 CAGAGCTCCCGAAGAGACA-----CCACAGGTGTTAATAGTAG 5485
3462 CAGAGCTGTCTGAATAGGAGGTTTGGAGAGCATTATTCCTCTGCTGGGGGTAA 3521
5486 AACAGTCCAGGCTGCTATGTAATGATGAGACAGAGCGAGGAGAAATTAAGTCAAA 5545

3522 ACCAAGAGCAGGTTGTGTAATAT--GCATACAGACATGAGGAGATTAACCTTTAA 3580
5546 ACTTTCATAGGGTTC--CGAGTCTTAAAGATACAAATATAGCTGC--TTGGCTTCATACA 5602
3581 AATTCTTATATAGTCTTGGAGCTTTGAGTATACAAAGAAATATCTTTTGGCTTATGTCA 3640
5603 AAGAAAGTCTGGAAAGGCAAGATGAGAGGAAATGAAAGGAAACAAATGTG 5662
3641 AAAGAGATATGAAAG-----TGAAAGGGGAGAAAGCAAGGAAAGGAAAG 3688
5663 AGGACTGACAGCTACAAATCTTACAGACATTTTCTTGGAAATCTAGAGGT 5722
3689 AACCATGTTTATATAGAGACAAATGAGACAGGTTTCTTGAATATCAATATAG 3748
5723 AGTGATTAAGTATGTCAGAGGAGACTTCTTGCATTTGAATCTGGGTTTGTCTCT 5782
3749 ATAGATTAAGAGATTTTCAATGAGGAAATGCTTTTCACTGAATTTGGGTTCTCT--T 3805
5783 CCATTGAGTTGAAAGCGTACCTTTTAACTTGAATGAGAGAGAAAGAGGAGT 5842
3806 CGATTAGTTGGATCTCTCATCTGACTTTGACT---TGAGAGAGAAAGATGAAATGT 3861
5843 TATGACTCTTACCTGAGATTTTACTAGTTTACGCAATGGAACAGACACTCGGACCTCT 5902
3862 TAGACCTATATCTGTTTCTTATTAACCTAAAGCAGTGAAGAAAGCTTATTTGATTT 3921
5903 CTGCAAAAAAATGAAACCTGTTGTTGCTTGTGTTCTTTTGTAAAGAACAC 5962
3922 TTCCCAACAAAGATGAAACTTTTCTTTACTGTTGTCAAAGAGTGAAATGAAAG 3981
5963 AGGCAAGCCGACCAATGAGTGAATGTGGGCTTTTGAAGCAAGCTTTTGAAGTGA 6022
3982 CCTATGATATGTAATATCATGTTCAAGCTATTGAGAGATGTTTAAATCAG 4041
6023 CACTCATATAGT-----GATCATGCTCAGTGAAGGCG 6058
4042 GAGTGTCAATATTTGGCTTCTCTGACACACTTGAAGAAATGTCTTGTGACACAT 4101
6059 TACCTGTGAGCCGAGCCCTGTGCTTGCATTAACATCTCCAGGCTCAGTATCAT 6118
4102 AAATATCAAGAAATAGCTATAGCTATGCTAABAAAGCTATGATTAATCTACTGTT 4161
6119 TCTCTCTACTTACACAGTTAGAGCTTGAACAACTTTTTC----- 6163
4162 TAAAGAGTTATGATTTCTGTAGGGGCACTTCAAGCTGCTCGGCGCATGTGCGC 4221
6164 -----AACCCCACTAAATTTAATTTGACAAAGACTGTGTAATTG 6205
4222 CTGTGGGCTGAGGTTGACAACTCTTATAGTAATCTGTATAGATGATTTTGGAGC 4281
6206 TGGATATACAGTGTGTAATGA----- 6227
4282 TGCAAAACAGGCCAAGCATATGAGGTGCACTCGGATCCCGAGATCCAGCTCACT 4341
6228 -----TCTATGTGCTATGTGCAAGTTCAATATAGATTAATAGGCCATCAACAGC 6283
4342 TCAGTCTCTCTCTCTGTTAAGAGGGGTGTCAACTCTCTGCGCAGCTTTTAAACAGC 4401
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4402 TTCATTAAGTGTAGGAGTGAACCTGAATTTGATGCCCTGCTGGGCT--CTCACTCAGAGA 4460
6344 GGCATGATTTTAAAGCTTGGCAATCATATTAATTAATCACTTAAATAATCATATGTT 6403
4461 GCCGCTATTTTATAGCTCTTTTGGCAATCATATTAATTAATTAATTAATGTT 4508
6404 GATTATTAATCTTTTGAAGAGCTGATATCTGTTTGGTCTCAGACAGCAATGTCA 6463
4509 TACTATGATGTTTACAAATCTTAAACCTGAGTTTCTGTCTCATCAACTTAATCTTG 4568
6464 CCAAGCTCTTCTTAACTGCTACACTTTGAAAAATCTTACCTGTCTCAATTTGTTGTA 6523

Db 4569 CAATTCT--AATTGTCACCTTAGAAGAAACATGCAATTAATGCTCAAAATCTTTGCA 4625
OY 6524 TTTTATTTTTCATAGCTTGAGAGAGATGAGATCAAGCGATTTGGGAACTGGACCTG 6583
Db 4626 TTTTATTTTTCACAGCTTGGAGAGATGAGATCAAAAGCAATTTGGAAGACTGGATTGG 4685
OY 6584 CTGTTTATGCTCTGAGAAATGCTGGCTGCTGAGCGAGAAAGCTTAGAAAAAGAGAAC 6643
Db 4686 CTGTTTATGCTCTGAGAAATGCTGGCAATTTGACCGAGCAAGCTGAAATAATGATTAAC 4745
OY 6644 TGTCTCTGCTGCTCTTCAAAAAGCAATTAAGATCCCTGAATGACTTTT 6695
Db 4746 TAACCCCTTCTCTGCTAGAAATACATTAATGATGCCCAAGGCAATTTT 4797

RESULT 10

AAD30646
ID AAD30646 standard; DNA; 4797 BP.

XX AAD30646;

XX 21-MAY-2002 (first entry)

XX Human TIF genomic DNA.

XX T cell derived inducible factor; TIF; interleukin-21; IL-21; human;
KW STAT transcription factor; acute phase protein; inflammation;
KW chromosome 12; ds.

XX Homo sapiens.

XX WO200210393-A2.

XX 07-FEB-2002.

XX 27-JUN-2001; 2001WO-US20485.

XX 27-JUL-2000; 2000US-062617.

XX (LUDM-) LUDMIG INST CANCER RES.

XX Dumoutier L, Renaud J;

XX WPI; 2002-195964/25.

XX Stimulating expression of STAT transcription factor and inducing
PT production of acute phase protein in a cell, involves contacting a cell
PT capable of expressing STAT with T cell derived inducible factors -

XX Claim 6; Page 56-58; 64pp; English.

XX The invention relates to nucleic acid molecules encoding T cell
CC derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
CC TIF polynucleotides are upregulated by the cytokine, IL-9, IL-TIF or
CC IL-21 molecules are implicated in activation of STAT transcription
CC factors, acute phase proteins and inflammation. The present sequence
CC is human TIF genomic DNA located on chromosome 12.

XX Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;

XX Query Match 9.2%; Score 686; DB 24; Length 4797;

XX Best Local Similarity 53.8%; Pred. No. 2,7e-145;

XX Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

OY 2034 CTCTCTCTCACTTATTCACATGTTGACATTTGTGCGATCTTGATGGCTGTCTTGACAAA 2093
Db 29 CTCTCTCTCCACATCCACAGTTGCTCGAGTTAGATTGCTGCAATGGCCGCCCTCACAAA 88
OY 2094 ATCTATGAGTTTTCCTTATGAGGACCTTTGGCCGACAGCTGCTGCTTCTCATTTGCCCT 2153
Db 89 ATCTGAGCTCTTTCCTTATGAGGACCTTGCCACACAGCTGCTCTTCTTGGCCCT 148
OY 2154 GTGGGCCACGAGGACAAATGCGCTGCCGTCAACACCCGCGTCAAGCTTAGGTTCAA 2213

Db 149 CTGGTACAGGAGAGAGAGCTGCGCCCATCAGCTCCACATGACAGCTTGACAAATGCCAA 208
OY 2214 CTTCAGAGAGCCGATCATGCTCAACCGAACCTTTATGCTGGCAGAGAGTACACTGCA 2273
Db 209 CTTCAGAGAGCCGATCATGCTCAACCGAACCTTTATGCTGGCAGAGAGTACACTGCTC 268
OY 2274 TCTCTTCTCTCCATACCGCCCTTGCCATTTTCTGGAAGCACTTGCAAACTTTAGGGG 2333
Db 269 AATCTGCTCTTTCGCTGGATCTACCTTGGAATCCAAATAGTCTTAACTTTCTTCA 328
OY 2334 GCTTTATCTCCGAGGCTCTCACTACATGTTT-----TCTGCTCTTAAAG 2382
Db 329 GAGCATCTCTAAGACCTTTAGAACCCACTGTTTATCCCTGAGGGTAAATAATTTCTG 388
OY 2383 ACTCTTTAAGAGCTGGGCTTTTATTTATTTCAATTTCAAGGCTCAGAGCACTTCTCAT 2442
Db 389 TTTTTCAGAGCTCTTGGGAATCGGCTTTTCTTGAACCTTCTTCCAT 448
OY 2443 CTGGCCTTCAGAGACATATACATATTTTATCTACAGAGCGCATTT--AGAAAGCA 2500
Db 449 TTTGGCTTTATGATACATATGATATATTTTCCAAAGAGCGGCATTCAGTATTCAT 508
OY 2501 CCCAGACTGCATATCTTCCATTTCTGTGCTCTCTGTAACATACCTCTGTGGC 2560
Db 509 CTGATGATTTTTCCTTATGCTGCTGTCATGTTCTTAACTCATGACACATCTG 568
OY 2561 TACTC-----CTGAGACCCATCGCGGACATACATCTCTAC 2595
Db 569 AATCTGCTTTAGTCTTATGATGTTGCTCTGGGAGACGGAGTGGGACATGCTAT 628
OY 2596 TTACAGGCTTTCTCCATCTCTGTCACCCAGAGCATTAAGGTTTTC--TCTCTTTCAG 2654
Db 629 GTATTAATTTTTCCTTATGCTCAATGCTCAGACCTTATGCTTCTTCTTCTTCAG 688
OY 2655 GCCAGCTTGCAGATTAACAACAAGACAGCTCGGCTCATCGGGAGAAAATGTTCCAGGA 2714
Db 689 GCTAGCTTGGCTGATTAACAACAAGACAGCTCGGCTCATCGGGAGAAAATGTTCCAGGA 748
OY 2715 GTCACTGTAAGTCCCATGATGAGAGAGG-----TAGCTGGGAGCT 2761
Db 749 GTCACTGTAAGTCCCATGATGAGAGAGG-----TAGCTGGGAGCT 808
OY 2762 GATGACCTCTGGGATAG-----TCTAGATATGACCCCTGCTGCTCTGCTCACTG 2817
Db 809 GGTGATGATGATGTTTATGCTTATCCCTTATGACCTTTCTGTTCCCTTCCACTG 868
OY 2818 AGGCTAAAGATCAAGTCTTACCTGATGAAGCAGGTGCTCACTTCACTTGAAGAGCTTC 2877
Db 869 AGATGATGAGCGCTGCTATCTGATGAAGCAGGTGCTCACTTCACTTGAAGAGTGC 928
OY 2878 TGTCTCCCACTGACAGAGGTTTCCAGCCCTTACATGACAGAGTGTACTTTCTGACCA 2937
Db 929 TGTCTCCCACTGATGATGTTTCCAGCCCTTATGACAGAGTGTGTGCTTCCGACCA 988
OY 2938 AACTGACAAATCAGCTCAGCTCTGTTGAAGTCACTCTGCTCACTTATGCTCTCT 2997
Db 989 GGTCTAGCAACAGCTTAAGCACAATGTGAAGTTAGCTCTCAGCTTATGCCACTTACC 1048
OY 2998 CTTCCTCTTATTCAGTAAGAACCCGAGGCTCTGCTCTCTCTTCAAGAGTGA 3057
Db 1049 CTCTCTCTCTCTTCAAGAGACCCCTTACCCCACTCTCTCTCTCCCTTACCC 1108
OY 3058 GAGAGGCTCAGCACACACATCATATGCGCATCTGAATAAGTCAAGAGCTTGGC 3117
Db 1109 TAACTTACAGAGAAATGTTCTGGCAGAGTGTATCAGAGAGCA-----TTTGG 1161
OY 3118 TTCAATGATTAATCTTTGATTTGATGATGAGGCTTATTTATTTATCAATGAA 3177
Db 1162 ATCATAGATATTTGCTTTGCTTGAATGATGATCACTTGAAGTTATGATGGAATG 1221
OY 3178 AGAATCACTCAATTTCTGATGATGAGAAAGATGTTGGAAAGAAAAGGCTTAGAT 3237

Db 1222 GGGTCTGGAAGTGTACAGAACCCGCAATGGTTTGTCTCGGAAAAAAGCACTC 1281
Qy 3238 AGAAAAACAGATCTGCTGATATAGTACTTATGGGGGAGACAGGGGCGATATCCATCGA 3297
Db 1282 A-----GGTGGCTGAAGATGAGAAAGGTGTGG 1309
Qy 3298 GTACAGACTTGTGGGGAGAGAAAATCCAGTCAGTACAAAGTACTTGTGGCATGTAGATC 3357
Db 1310 GAAAAACATCTAGCTGTGAAAATGATCCATGATGCTAAGTTGTTGAGGGGAGGGGATGG 1369
Qy 3358 CACTGATGACAAAGTACTTGTGGGGGAGAGAAATGGCAACAGCAAAAGTTGAAGGAAAG 3417
Db 1370 CATGAGAGAAATTTGAAAGAGAAAGTGGAAATGGAAAGCTTAA----- 1415
Qy 3418 AAGATGAGAGCCCTCATGGTTGGGGGTGTGAAAGTCACTCTTTTCATGTGATGAG 3477
Db 1416 -----GTGGGTGGTGGGTGGGAGACTGTTGCTGCTGTGATGTCTAGTGGG 1460
Qy 3478 AGTTAAGAAAAACA-GTGTGAGTTTGTATGTCTTCAGACACCCCACTATGAAACAT 3536
Db 1461 AGCCCAAAATCGAGGGCGGTGAACTTGATGCCCTGAACTTTGAACTATGAAAAA 1520
Qy 3537 ATCCACGAGAGCGGGGACAGCTGTGAGAGACTGGCATTTAGGAAAGGCGC--GGCTTT 3594
Db 1521 AGTTGAGTGAAGTGGGCCCACTAAAGCCCTTAGGACTTACTGAAAGGGCTTAAATTT 1580
Qy 3595 CACACGAGAACTTTATGTCTCATCTTGTGTACACTCCACCTTTGATGAGTTCAAC 3654
Db 1581 CACATGAGATGTTTATGTACATTTCTTGTCTAAGCATGCAATTTTCGAGATATCAT 1640
Qy 3655 TCAAGTTTCTTTCT-----ACCTTCTTCTACTGTGTGAAAC 3693
Db 1641 TGAGTTTATTTCTTACAGAAATTTGCAATTAATCTACTCCGCTTTTCCCAATGCAAC 1700
Qy 3694 TTGAGTAGATTTCCCAAGAGAGAGACAGCTTCTGTAGAGAGAGAGAGCTGATTTCA 3753
Db 1701 CTCATGAGATTTCCCAAGAGAGAGAGAGAGAGTCTTGTAGAGAGAGAGAGAGTCTG 1760
Qy 3754 GTGTCTGAGAGACAAATAGCTCAAGAAATCTAGATCAACGTGAATCTAGATCAAC 3813
Db 1761 GGTTCAGAGGAAATCAAGAGCTCAAGAAATCTAGATCACTGTGAATCTAGATCAAT 1820
Qy 3814 GGGCAAAATGACTGAACCCCTTATTTCCAGGTGAACGGTCAAGTCTCAATATATC 3873
Db 1821 TGGGCAAAATCTAGAGCTTAAATCCAGGTGAATGTACTGTATCTCCATGAGTGG 1880
Qy 3874 AGATTTGGGCTCCACCGGATAGATCTGTAGGA-GTCCGCTTATTTTGGAGA 3932
Db 1881 GAGTTCAATAAGTTTCAAGCAACATTAAGATGATGCTTGTATTTATATAGCA 1940
Qy 3933 CATCAGCGGTGACGACAGAAATCAGAAAGATGTCAAGAGGCTGAAGAGACAGTGA 3992
Db 1941 TATTAAGGTGATGACGTGATATCCAGAGAAATGTCAAAAGCTGAAGACAGCTGA 2000
Qy 3993 AAAGTACTATTGGCAAGCACAATCTAAGCCATTCAGTAC-GAGAGTGGGATTC 4050
Db 2001 AAAGTAGACTGATATCTGATGCTAAGTCAATGCAATGAGAGAGCAAAATGTTGTT 2060
Qy 4051 TTTCTGTGCTCCAGTCCCTCTAATTTGTAACTTTATTTGATTTGTCTACTATCTG 4110
Db 2061 TTTCTTCTTTTCTTCTTCCATCACTTGTGTGATTTTCACTGTATCTCTACACAG 2120
Qy 4111 GTCCATTAAGCTTATGCTGACCTGTATCTAGCTGGTCTATAGATCTTTCAATGTG 4170
Db 2121 GGGCATTA-----CTTGTGTGTGTGTATGTAGATATATCTAATATCTAGATGAGTT 2176
Qy 4171 TCTTAATTT--GTAACTCAATTTGAGCTAGCAAGAAAGTTAGCTCAGCAGTCTC 4227
Db 2177 TCCAAATCTTGCAAAATTTGATGATTTCAAGAACTGTTGGGATCTTGTCTAGTCTAC 2236
Qy 4228 ATGAGACTTGTCTGGAGAGAGTGTGTGACAGAGTCAATGCTAGAGAGACAGATCCCG 4287
Db 2237 ATTAACCTCAGATTTCTGGGGTGTCTCAGTGGCAAGATAGGGCTAGAAATGCAAGTCTCTG 2296

Qy 4288 ATTCACAGCTGTGAC--TTGCTTAGTGCCATGTGTAAATTAATCTTGTGCTTATAGAT 4346
Db 2297 AATCCAGCCAGACATTTTCCGTTGTGTATACAGATATGTTTGTGATCAATTAATCT 2356
Qy 4347 TTGGAAAA--GCCAGTTCCACGAGCTTACATTAATCTGAGAACCATGATTTGAAAACTA 4404
Db 2357 TAGGAAATTTCAATTTCTTGTGATCATGTAAATCTGAGAAATCTTGTTTAAAAACA 2416
Qy 4405 GAAAGCTGGGCA---CAACTTAATAGATGATTTTGTAGCTCAATTAACGATGCTC 4460
Db 2417 GAAAAATCCATAGGGCAAAATTTATTTGAAGTCAATTTTGAAGTCAATTAATGATGCTT 2476
Qy 4461 TGAATGTGGCAAAATCAACCAGATTAACAACAAGAGTGTGATTTGGCAATAGGACA 4520
Db 2477 TGAACCTTGGAAATTAATCAACAACAATAGAAAGAGCTGACCTGATATAGGGCT 2536
Qy 4521 AGTATTTGAATCACTGATTAATAGCTATCATCTTAATTAATATAGGGCTATATA 4580
Db 2537 AATTTCTGA-----GTAAATAACTTTATTTGAATTTATCAATATATCATAGATA 2589
Qy 4591 TAAATTAAGATTAACAACAAGATGATAGCTCCCAATTTACTTGGCTGTTCAAA 4640
Db 2590 TTGATTAATGTTAAAGCAAGAGAGACAAAC--CCGATCTTTATACAGGTTCAAT 2648
Qy 4641 AGATTAATAATATCATGATGATTAATTAATGTCTATGAAGATATGAGATGAGAAACC 4700
Db 2649 AGAGTAAATAATTAATGATGATTAATTAATGATTAATGAGAAAGCTGAATGTGAGCT 2708
Qy 4701 TTTCTTACTTTTAACCTCA-----TTTCTTGTGTTTTTTTCTTCAACCTGA 4752
Db 2709 TTTTCTTCTCTCTCCCAATCAAGACTTTCATTTAGTTTCTTCTTCACTCTCA 2768
Qy 4753 TCAAGCCATGTAAGCACTATCTGTGAGCTATTAATGACTTTACAGCAAAAC 4812
Db 2769 ACAAATCCCTAGGAGAGATTAATTCATGATGGGTGGTGTATTTATATGATATGAT 2828
Qy 4813 ATGTGTGTGGCTCTTTGGGAGAGGAGACAGATAGCAGAGAGCTCAGGCTAGCACT 4872
Db 2829 ACCATCATGTGGCTTATTTGTGAAAGAAACA--ACAATGAGAGCTTGAATCAATA 2886
Qy 4873 CTGACTTGGCTTAAAGCCAGAGGCAATGTTATGACAGAAAGTGAAGCTCTTGGCAAG 4932
Db 2887 GTGACTCACCCAAAACCGAGAGATGATTAAGAGAGTGAAGTGAAGCTCTT--GCAAG 2945
Qy 4933 TGGGTGTCTTAAGTATCAAGAAACAGAGAGCTCCGTTGATGAGAAATTAATCAGTAA 4991
Db 2946 CAGGTACAACATTAATCAAGAAACATGAGAGCTCAGTTGATGGAATTTCAATACAA 3005
Qy 4992 -----TATCACTTATCTCTCTATTCGAACCTAAATGCTCTTTTCTTGTG 5042
Db 3006 GCTTAACCTTAATCCCTTTTCTTCTTGAATTTTAAAGAGCTTCTTCTAG 3065
Qy 5043 TGTAGCTGATTAACACACTGTT--TTCCTTGAAGTCAATGAGCTTGTAGATTTTA 5100
Db 3066 CATCAATTAATGATGATCACTGTCTTCTTGTAAATGAGAGCTTGTAGTTTAA 5125
Qy 5101 GTGCTGTCCAGATCTTGT--TAGAGGTTTGTAACTTGAACCTGGGCTTGAATGTA 5158
Db 3126 TGTGAAGCCAGTCTCTTGTATAGAACTATTAATGACATGAGAGGCTGAAATGTA 3185
Qy 5159 GCATCCCAAGGACACACTTGAATGATGCTGTGTAAGAAAGTTATTAATTAATCT 5215
Db 3186 GCATCCCAAGGACATGCTTGAACATCTTGAATTAATTAATTAATTAATTAATCT 3245
Qy 5216 -----TTGCTTGAAGAGTGAAGGCTGTGAGAAAGAACTCAGAGATGTCTC 5270
Db 3246 GCTTGTGTCTTGAAGAAAGTGAAGTGAAGAGAGATCTCAGTGA----- 3296
Qy 5271 CTGTAGAAAACTTTTCTTCTTAAATGCTTAAATCACTTCACTTCACTA---ACTT 5327
Db 3297 -----TCTGTGATTTTCAAGACTTTATCACTTTTGAAGAAATCAAT 3342

QY 5328 TGACTTTATACATGCTGTACATGAAAGTGTGAGCCCGCTTCATGCGCTCTGCGG 5387
 Db 3343 TCATATTTGCAATGGGTGGCATGTGGAAGATGATATGCTTTTCTGCTGTGCTTCA 3402
 QY 5388 AAAAGCACCATTAGGGGGAAGAAATGTATGCTGAGAAATCTGACCGGAGGAAACTGCT 5447
 Db 3403 GAAAGCA-CAGAGGAGAGCAATGTGTTCAGAGAAATCATACAGAGGAGAACTGT 3461
 QY 5448 CAGAGCTCCCCGAAGCA-----CCACAGGTGTATGATAGG 5485
 Db 3462 CAGAGCTGTGAAATAGGGTGTGTTGGAGGCAATATTCCTCTGCTGTGGGGTAA 3521
 QY 5486 AACGCTCCAGGTGGCTCATGTATATGAAAGCAAGAGGAGGAAATATGCTACAA 5545
 Db 3522 AGCAGAACGAGGTGTGATGAAAT-GCATGACAGACAGTGGGGAAGATAACTTTAA 3580
 QY 5546 AGTTTCATAGGCTC-CGGAGCTTAAAGTACAAATAGCTGC--TTGGGCTTCATACA 5602
 Db 3581 AATCTTTATAGTCTTGGAGTCTTTGAGATGAAAGAAATATCTTTTGGCTTATGTC 3640
 QY 5603 AAGGAATCTGGGAAGCAGCAAGTGAAGGGAATGAAAGGAAAGCAATCTAG 5662
 Db 3641 AAAGAGTATGGAAG-----TGAAAGGCGGAAGAAAGAGAGAAAGAG 3688
 QY 5663 AGGACTTGAACAGCTTACAAATCTCTACCAAGATTTTCTTGGAAATCTAGAGGT 5722
 Db 3689 AACCATGTATATATAGAGCAATGTGACAAAGTCTTCTGAAATATATGCAATATG 3748
 QY 5723 AGTGAATAGTGTATGAGGGGAGCTGCTTGTGCAATTTGATGATGCTGCTCT 5782
 Db 3749 ATAGTTAGAGAAATTTAGTAGAGAAAGTCTTTCATCTGAAATTTGGGTCTCT--T 3805
 QY 5783 CCATGAGGTGAAAGCGTCAACCTTTTACCTCGATGAGAGAGAAAGAGGGGTGT 5842
 Db 3806 CGATTAAGTTGGATCTCTCATCTGCAATTTGACT---TGAAGAGAAAGAAATGAT 3861
 QY 5843 TATGATCTCTACTGAGATTTTACTAGTTTACGCAATGAAACAGACTCGGGACTCT 5902
 Db 3862 TAGGACCTATATCTGTTTCTATTAATTAAGCAAGTGAAGAACTAATTTGGTATTT 3921
 QY 5903 CTTGACAAAATAAATGAAACCTGTGTTGCTGTTGTTGTTCTTTTAAAGAAAGAC 5962
 Db 3922 TTCCCAAAAAGTGAATCTTTCTTTACTGTGTGTGTAAGAAAGGTGAATAAG 3981
 QY 5963 AGGCAAGCCCGACACATGGGTGAATGGGTCTTGAAGTCAAGCTTTTGAATGAG 6022
 Db 3982 CCTTAATATATTTGGATATCATGTGTCAAGTCAATTTGATGAGATGTTTAAATAG 4041
 QY 6023 CACTCATATATGTT-----GATCATGTGAGGTGAGGGC 6058
 Db 4042 GAGTGTCCATCATTTGCTTCCCTGACACACTTGAAGAAATGCTTGTGACACAT 4101
 QY 6059 TACCTGTAGGCGGAGCCCTGTGCTGCTGCACTTAACATCTCCAGGTCTAGATCACT 6118
 Db 4102 AAAATACAGAAACATAGCTATGAGCTAAATAAGTCAATGATTAATCTACTGTTT 4161
 QY 6119 TCTGCTACTTAGCAGCTTAGAGTGAAGCAAACTTTTTC----- 6163
 Db 4162 TAAAGAAATTTATGATTTCTGTATAGGGTCAATCAAGCTCTCTGGCCATGCGGC 4221
 QY 6164 -----AACCCTAATAATTTAATGACAAAAGCTGTGTAATTTG 6205
 Db 4222 CTGTGGGCTGAGGTTGACAAAGCTCTTATATAGAAATCTGTCAATAGATTTGGAGC 4281
 QY 6206 TGGGATACAGTGTGTAATGA----- 6227
 Db 4282 TGCAAAACAGGCAAGCATATATGGGTGCACTCGGATCCCCAGATCCAGCTCACT 4341
 QY 6228 ----TCTATGTGTGATTTGCAAGTTCAATTAAGATGATTAATAGGCCCATCAACAGC 6283
 Db 4342 TCAGTCTCTGCTCTGTGTTAAGAGGGGTGCTCACTCTGCGCCACTTTTAAACAGC 4401
 QY 6284 TTTATGGGTGTAATGCAAGTATATATAGTATGATGCTGTGTGCTCTTATAGGTACAAA 6343

Db 4402 TTATATAGTGTGAGTGCACCTGAAATATGATGCTGTGTGTGCT-CTCAGTCCAGAGA 4460
 QY 6344 GGCATGATTTTAAAGTCTTGGGCAATCATATTTACTCATGTCAAAATAATATATGTT 6403
 Db 4461 GCCGTCTTTTAACTCTTTGGCAATCATATCAATTAATAAGGAT-----T 4508
 QY 6404 GATTATTAATCTTTTAAAGAGGCTGATCTGTTTGTGTGCTCAGCAAGCAATGTC 6463
 Db 4509 TACTATGAATGTTTAAATAGCTTAAACCTCGGTTCTGTCTCATCAACCTATATCTTG 4568
 QY 6464 CCAGCTCTTCTACCTGTACCACTTAAAGAAATGCTACCTGCTCAAAATTTGTTGTA 6523
 Db 4569 CAATTTCT---AATTTGTCACTTAAAGAAACATGCAATTAATCTCAAAATCTTTGCA 4625
 QY 6524 TTCTTATTTTCAATGCTTGGAGAGTGAAGATCAAGGAGATTTGGGAACTGACCTG 6583
 Db 4626 TTCTTATTTTCAAGCTTTGGAGAGAGTGGAGAGATCAAGCAATTTGAGAACTGATTTG 4685
 QY 6584 CTGTTTATGCTCTGAGAAATGCTTGGCTGTGAGCGAGAAAGACTAGAAACGAGAGAC 6643
 Db 4686 CTGTTTATGCTCTGAGAAATGCTGCTGATTTGACCAAGCAAACTGAAATGATATAC 4745
 QY 6644 TGCTCTCTCTGCTCTTCAAAAGAAACATTAAGTCCCTGAAATGACTTTT 6695
 Db 4746 TAACTCCCTTCTCTGCTGAGAAATTAATTAATGATGCTCCCAAGCAATTTT 4797

 RESULT 11
 AAD27151
 ID AAD27151 standard; DNA; 4797 BP.
 AC AAD27151;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human T cell derived inducible factor (TIF) beta genomic DNA.
 XX
 KW T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;
 KW protein therapy; STAT activation; differentiation; human; de.
 OS Homo sapiens.
 XX
 PN US631613-B1.
 XX
 PD 18-DEC-2001.
 XX
 PP 18-OCT-1999; 99US-0419568.
 XX
 PR 26-OCT-1998; 98US-0178973.
 PR 16-JUL-1999; 99US-0354243.
 XX
 PA (LUDWIG INST CANCER RES.
 XX
 PI Dumoutier L, Louhed J, Renaud J;
 XX
 DR WPI; 2002-105277/14.
 XX
 PT Nucleic acids encoding T cell derived inducible factors useful for
 PT inducing STAT activation in cells -
 XX
 PS Claim 1; Column 31-36; 24pp; English.
 CC
 CC The present invention relates to an isolated nucleic acid molecule, which
 CC encodes a T cell derived inducible factor comprising an amino acid
 CC sequence encoded by 6 defined nucleotide sequences. The nucleic acid
 CC molecules are shown to be up regulated by the cytokine interleukin-9
 CC (IL-9) and are described as T Cell Derived Inducible Factors (TIFs). The
 CC invention is used in protein therapy. The nucleic acid molecules encode
 CC proteins which induce STAT activation in cells. They can be used, for
 CC example, in the stimulation of regeneration of targeted tissues.
 CC Further, their inhibitors or antagonists can be used to retard, prevent
 CC or inhibit differentiation of other tissues. The present sequence is

CC human T1F beta genomic DNA.

XX Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;

Query Match 9.2%; Score 666; DB 24; Length 4797;

Best Local Similarity 53.8%; Pred. No. 2,7e-145;

Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

QY 2034 CTCCTCTCACTTATCACTGTGACACTGTGCGATCTGTGATGCTGTCTGTGAGAA 2093
DB CTCCTCTCCCACTCACTGCTGTGAGTAAATGTCTGCATATGCGCCCTGAGAA 88
QY 2094 ATCTATGAGTTTTCCTTATGAGGACTTTGGCCGACACTGTCTGTCTATGAGCCCT 2153
DB ATCTGTAGCTCTTCTTATGAGGACCTGTGCGACACAGCTGTCTCTCTTGTGAGCCCT 148
QY 2154 GTGGGCGGAGGAGAAATGGCGCTGCGTCAACCCGGTGCAGCTTGAAGTGCAG 2213
DB CTGGGTACAGGAGAGGACAGCTGCGCCATCAGCTCCACCTGAGGCTTGAAGTCCAA 208
QY 2214 CTTTCAGAGCCGTAATGCTCAACCGCACTTTATGCTGCGCAAGAGTACAGTGA 2273
DB CTTTCAGAGCCGCTATATACCAACCGCACTTCACTGTGCTTGAAGAGTATACATCTC 268
QY 2274 TCTCTTCTCTCATACCGCTTGCATTTCTGTGAGCACTTGCAAACTCTTGAAGGG 2333
DB AATCTGCTCTTCTCTGTGATCTACTTGAATCCAAATAGTCTTAAACTTTCTTCA 328
QY 2334 CGCTTATATCCGAGAGTCTCACTACTATGTTT-----TCTGTCTTTAGAG 2382
DB GAGCATCTCTAAGAGCTTGAAGACCCACTGTTATCCCTGAGGGATGAATTAATTTCTG 388
QY 2383 ACTCTTAAAGAGCTGGGCTTTTCTATTTCAAGGTCTCAGACCAATTTCCAT 2442
DB TTTTTCAGAGACTCTTGGGAACTGCGCTTTTCTTTTCTTGAACCTTCTCTCCAT 448
QY 2443 CTTGAGCTTTCAGAGACATATATCTGAATTTTATCTACAGAGGGCACTTT--AGAAAGCA 2500
DB TTTGGCTTATGATATCATATGATGATTTTCCCAAGAGGGCCATTCAGTAATCAT 508
QY 2501 CCCAGACTGCAATATCTTCCATTTCTGTGCTCTCTTCTGAACATCATCTCTTGGC 2560
DB CTGATGATTTTCTTCTTATGCTCTGTGATGTTCTTAAACATGACACACATCTG 568
QY 2561 TACTC-----CTGAGCCCACTGCGGACATATCATCTCTAC 2595
DB AATCTGCTTAACTTTATGATGTTGCTCTGGGAGACGGGATGGGACATGCTCAT 628
QY 2596 TTACAGGCTTTTCTTCATCTCTTGTCAACCGAGCACTTGAAGGTTTC-TCTCTTTCAG 2654
DB GTATTAATTTTCTTCTATTTGCTCAATGCTCAGACCTTATGCTTCTCTCTCCAG 688
QY 2655 GCGAGCTTTCAGATTAACAACAACAAGCTGCGCTATGGGAGAAACTGTTCGAGGA 2714
DB GCTAGCTTGGCTGATTAACAACAACAAGCTGCTCATTTGGGGAGAAACTGTTCACGGA 748
QY 2715 GTGAGTAAAGTCTCACTGTGATGAGCAAGGGC-----TAGTGGGAGAGCT 2761
DB GTGAGTAAAGTCTCACTGTGATGAGCAAGGGCCTGTGCTGCTGCTGCTGCTGCT 808
QY 2762 GGTGAGCCCTTGGAGTAG---TCTGAGGTATGACCCCTGCTGCTTCTGTGCTGCTG 2817
DB GGTGAGTATGAGTGTAGGTCTTATCCCTTATGACCTTTCTGTTTCCCTTCACTG 868
QY 2818 AGGCTAAAGTCAAGTCTATCTGATGAAGAGTGTCTCACTTCACTTGGAGAGAGTTT 2877
DB AGATGAGTGAAGCGCTCTATCTGATGAAGAGTGTCTGAACCTTCACTTGAAGAGTGC 928
QY 2878 TGTGCTCCAGTCAAGAGTTCAGAGCTTCACTGAGAGAGTGTGTAACCTTCTCTGACCA 2937
DB TGTGCTCCAGTCAAGTGTGAGTGTGAGCTTATATGAGAGAGTGTGAGTGTGCTTCTG 988
QY 2938 AACTGACATATGCTCAAGTCTCTGTGTAAGTCTGACTGTGCTACTATGCTCTCTCT 2997

DB 969 GGCTCAGAACAGGCTAAGACATGTGTAAATTTCACTCTAGGCTATGCCACTTACC 1048
QY 2998 CTTCTCTTCTATTTCCAGTAAGAACCCGAGGTCTGCGCTCTCTCTTCAACAGATGA 3057
DB CTCCTCTCCCTCTTCCACAGAGACCCCTTACCCCAACTCTCTCTCTCTCTCTCTCC 1108
QY 3058 GAGGAGCTCAGACACACACATCATATGCGCACTTGAATAGTCAACAAAGGCTTGGC 3117
DB TAACTGACAGAGAAAGATGTCTTGGCAGAGTGTATCAGAGTCA-----TTTGGG 1161
QY 3118 TTCAATTGATTAATCTTATGATTGTATGATGAGTAACTTATTTATTTATTCATGAA 3177
DB ATCATAGATATTTCTTTTCTTGTCTTGTACTGATGATCATCTTGAATTTATGATG 1221
QY 3178 AGAAATCAATCAATTTCTGATGATGAAGAAAGATGTGGAGCGAAAGAGGCTAGAT 3237
DB GGTCTGGAACCTTAAGTGTACAGAAAGCGCATGTGTTGTCTTGGAAGAAAGGCACTC 1281
QY 3238 AGAGAAACAGATCTGCTGATATGATCTTATGGGGGAGCAGGGGGCATATCAGTGA 3297
DB A-----GGTTCGTAAGATGAAGAAAGTGTGG 1309
QY 3298 GTACAGTACTTGTGGGAGAGAAATCCAGTGAATCAAGTACTTGTGGCATGAGATC 3357
DB GAAACATCTAGCTGTGAAATGATCCATTGATGATGATGTTGTGAGGGAGGGAGTGG 1369
QY 3358 CACTGATGACAACTTGTGGGGGAGGAAATGACACAGACAAAGTTGAAGGGAAG 3417
DB CATGAGAGAAATTTGAAGAGAAATGGGAAATGGGAAGGCTTAA----- 1415
QY 3418 AAGATGAGAGGCTCATGTGTGGGGGTGTGAAGTCACTCTTTCATGTATGAG 3477
DB GTGCGTGTGGGTGCGGACAGCTGTGCGCTGTGATGTATGAGGA 1460
QY 3478 AGTTAAGAAACCA-GTGTGTGATTTGATGTCTTACAGACACCCCACTATGAATAT 3536
DB AGCCCAAAATGCGAGGGGTGTGAACCTGATGCCCCCTGAACATTTGAACATATGA 1520
QY 3537 ATCCAGAGAGAGCGGAGACATGTGGAGACCTGTGCACTTATGAGGAAGGCG--GGCTTT 3594
DB AGTTGATGAGTGTGGCGCCAGTAAAGCCCTTGAAGCTTATGAGAGGCTTAAATTT 1580
QY 3595 CACAGAGAACTTATATCTATCTTGTGTACATCCACCTTATGATGAGTTACAG 3654
DB CACATGAGATGTTTATGATGATCTTGTCTTACATGACATTTCTGAGATATCAT 1640
QY 3655 TTAGGTTTCTTTCT-----ACCTTCTGTCTACTGTGGAAC 3693
DB TTAGGTTTATTTCTTACAGATTTGATTAACCTACCTGCTTTTCCAAATGCAAAAC 1700
QY 3694 TTCAAGAGATTTCCCAAGAGAGAGAGAGCTCTCTGTGAAGAGAGAGCTGATTTCA 3753
DB CTCAAGTATTTCCCAAGAGATGAAGAGAGTCTCTGTGAAGAGAGTATGATTTCTG 1760
QY 3754 GTGTCTTGAAGAGAAATAGCTCAGAAATCTAGTCAACGTGAATCTAGTCAAGC 3813
DB GCGTCAAGGGAATCAAGAGCTCAGAAATCTAGTCACTGTGAATCTAGTCAATTTG 1820
QY 3814 GGGCAAAATGACTGAAGCGCTCTATTTCCAGTGAACGTCACGTGCTCAATATACG 3873
DB TGGGCAAAATTAATAAGCTTAAATCCAGGTGAATGTACTGATCTTCAATGGGTGG 1880
QY 3874 AGTATTTGGGCTCCACCGGATTAAGTCTGTATGTA-GTCTGCTTATTTTGGAGCA 3932
DB GAGGTTCATTAAGTTTCAACACATTAAGTATGATGCTTGTATTTATTTATAGA 1940
QY 3933 CATCAGCGGTGACGACCAAGACATCCAGAAAGTCTCAGAGGCTGAAAGAGACAGTGA 3992
DB TATTGAAGTGTATGACTGTCAATATCAGAGAGATGTGCAAAAGCTGAAAGACAGTGA 2000
QY 3993 AAAGTATCTATTGGAGCAACATATCTAAGCATTTAGTAG--GAGAGGTGGGATTTTC 4050

Db	2001	AAAGGTAGACTGATTAATCTGCAATGCTAACTCATGCAATATGAGAGACAAATGTGTTT	2060
Oy	4051	TTTCTCTGCTTCCAGAGTCCCTTCTACTTTGTAACTTTATTTAGCTGTCTACTATCTG	4110
Db	2061	TTCTTTCTCTTTCTTTCTTCCCATCACTTTGTGATTTTTCATCTGATTTCTCTACACCAAG	2120
Oy	4111	GTCCATTACTGGCTTAGTGCACCTGATCTTAGCTGGTCTATAGATCTTCAATCTGTG	4170
Db	2121	GGCGATTA-----CTTTGGTGTCTGTGATGTAGATATATCTATATATCTAGATCTGAGTT	2176
Oy	4171	TCCTAATTT-----TAGAGTCAAAATTTCTGAGACTGACGAAAGCTTAGTCCAGCTC	4227
Db	2177	TCCAATCTTGCAAAATTTGAGAAATTTGAACTGGTTGGATCTTAGCTGTCTAGTAC	2236
Oy	4228	ATGAGCACTTCTCGAGAGATGCGCTTGAGACAGATCAATCTAGAAACAGACTCCCTG	4287
Db	2237	ATAACCTCAAGTTCTGGGGATGTCTCAGTGGCAGAGATAGGGCTAGAAAGCAGGTCTCTG	2296
Oy	4288	ATTCCAGCTCTGCAC-TTGCCTAGTGGCCATGTGTAACTTCTTGCTGATTAAGTAT	4346
Db	2297	AATCCCAAGCAGAGCACTTTTCCCGGTGTATACAGATTAGTTTGGTACATTAATCT	2356
Oy	4347	TTGGGAA--GCAGTTTCCACAGACCTTACATCTGAAACCAATGATTTGAAACTA	4404
Db	2357	TAGGAAATTTTCAATTCCTATTTAGCTCATGTATATCTGMAAAGTACTGTTTAAACAA	2416
Oy	4405	GAAAGCTGAGCA----CAAACTTACTAGATGATTTTGTAGCTCATTTAAACGATGCTC	4460
Db	2417	GAAAAATCCCTATGGGCAAAATTTATTTBAAGTCATTTTGAAGTATTAAATGATGCTT	2476
Oy	4461	TGAAATGTGCAAAATCAACCCAGATTAACAACAAAGAGCTGATTTGCAATATGACAA	4520
Db	2477	TGAAACTTGGAAAGATTAATCTCAGAACATGAGAAAAGCTGGACCTGCATATAGGCT	2536
Oy	4521	AGATTTGAAATCACTGTGATTTAAAGTATCATCTTAAATTAATAATAGGCTATATTA	4580
Db	2537	AATTTCTGGA-----GTAAATTAACACTTTATTTGAATTAATCAATTAATCTATCAGATA	2589
Oy	4581	TATATTTAAGATTAAACACAGAGGATGAGTACCTCCCAATTTACTTGCGCTGTTCAAA	4640
Db	2590	TTGATTAATAGTTTAAAGCAAGAGACGACCAAC--CCGATCTCTTTTAAACAGGTTCAAT	2648
Oy	4641	AGAGTAAATAATACAGTCATGATTAATTAATAGTGTCAATGAAGTATGATGGAACCC	4700
Db	2649	AGAGTAAATAATTAATAGTAAGATTTATTAATAGTTAAATGAGATCTGAATTTGTAAGCT	2708
Oy	4701	TTTCCCTACTTTTACTCTCA-----TTTCTTAGTTTTTTTTTTCTTCAACCTCTGA	4752
Db	2709	TTTTTTTTTCTCTCTCTCCCATCAAGACCTTCCATCTTAGTTTTCTTCTTCACTCCCTCA	2768
Oy	4753	TCAAGCCACTAGTAAGACACTATCTGCTGATGACTATATATATGACTTATACAGCAACAC	4812
Db	2769	ACAAATCCCTTAGGAGACATTTATCCATGATGGCTGTGTATCATTTCTATATGTGAATGAT	2828
Oy	4813	ATTGCTGTGTGGCCTCTTTGGGGAAGGGAAACAGATAGCAGAGGCTCAGGCTAGCAAT	4872
Db	2829	ACCATCATGTGGCTTATTTGGTAAAGAAAGACA--ACAATGAAAGGCTTAGACTAACAATA	2886
Oy	4873	CTGACTTCCCTTAAAGCCAGAGAGCATGTGTTATATAGCAGAAAGTGAAGGCTCTTCCGAAAG	4932
Db	2887	GTGAATCCCTCCCAAAACCGAGAGATGATTTAGAGCAGATGAAAGTGAAGCGCTCTT--GCAGG	2945
Oy	4933	TGGGTGTCTTAAATATCAGAAACAGAAAGGCTCGGTGTATGGAATTTATCAGTAAAGA-	4991
Db	2946	CAGGTACAATTAATATCTCAGAAACATBAAGGCTTCAAGTTATGGAATTTTCAAGTAAACA	3005
Oy	4992	-----TATCTAACCTTATCTCTTCTATACGAACCTTAATCGTCTTTTCTGTGTG	5042
Db	3006	GCTTAACCTTAATTCCTCCCTTTTTCCTCTTGAATTTTAAAGAAAGCTTTCTTCTCGAG	3055
Oy	5043	TGTAGGCTGATTAACACACTGTT--TTCTTTTGAAGTGTCAATGCGCTTTGTAGATTTTAA	5100
Db	3065	CATCATTTTAATGAGTGTGATCTGTCTTCTCTTGTATTAATTAAGGCTTTGTAGTTTAA	3125

QY	5101	GTGCTTCGCAGTTCTTGT--TAGAGGTTGTACCTTACA	CTTGAGGCTTGATGTGA	5158
Db	3126	TTGTGAAGCCAGTTCCTTGTATTA	TAACAATATATTAGACATGAGGGCTGAACTGA	3185
QY	5159	GCATGCCAAGGCAACACACTTTCGATATGCTGTGTAAAGGTATTTATCTATTACT--	5215	
Db	3186	GCATGCCACAGACAGGCAATGCTTTACACATCTTGCTTAAATAATTAATCTAATTCATCTT	3245	
QY	5216	-----TTGCTTTGGAAGGTGAAGCGTGTGTGGAAGAAGTACACAGAGATGTCTT	5270	
Db	3246	GCTTGTGTCTTTAGAAAAGTGAAGTGTGAGAGAGGAACTTCATATGTGA-----	3296	
QY	5271	CTGTAGGAAACCTTTTTTTTTTCCCTTAAATGCCATATATCACTTTCAGTCA--ACTT	5327	
Db	3297	-----TCTGTGATTTTCAAGACTTTATATCAATTTGAAAGATCAATT	3342	
QY	5328	TGACTTTTATACATGCTGTACATGAAGAATGTTTAGGCCGCTCATGCTCTGGG	5387	
Db	3343	TCATATTTTGCATATGGGTGGCCATGTGGAGAGTATTAATGCTTTTGTCTGTAGCTTCA	3402	
QY	5388	AAAGGACCCATATAGGGGAAGGATGTATGTGTGAATCTGACCGGACGGGAACGTG	5447	
Db	3403	GAAAGCA-CAGAGAGGAGAGGCAATGTGTTCAGAAAATCAACAGAGAGAACTGT	3461	
QY	5448	CAGAGCTCCCGGAAGACA-----CCACAGGTGTTAAGTAGG	5485	
Db	3462	CAGAGCTGTGAAATATAGGTGCTTTTGGAGGCAATTAATCCCTCTCGTTGGGGTAAA	3521	
QY	5486	AACAGTCCAGGTGGCTCATGTATATGAATGGAACAGCGAGGAAATACCTACAA	5545	
Db	3522	AGCAGAAACGAGGTGTGATGAATAT--GCATGACAGACAGTAGGGGACGATAACTTTAA	3580	
QY	5546	AGTTTCAATAGGTC--CGAGTCTTAAGATACAAATAGCTGC--TTGGGCTTATACA	5602	
Db	3561	AATCTTTATATGCTTTGGAGCTTTTGAGATGAATAAATATCTTTTGGCTTATGTCA	3640	
QY	5603	AAGGAAGCTGTGGGAAGCGACAGACTGTGAGGGAATGAAAAGGAAAAACAGATATAG	5662	
Db	3641	AAAGAGATGGAAGG-----TGAAGGGCGGAAGAAACAGGAAAAAGGAG	3688	
QY	5663	AGGACTTGAACAGTACAAATCTCTTACACAGACGATTTTCTTGAACAATCTAGAAAGT	5722	
Db	3689	AACCATGATATATATAGAGCAATGTGTACAAAGTTTTCTTGAATAATGCAAAATATG	3748	
QY	5723	AGTGATTAGTGATTCAGAGGGGACTGTGCTTGCCATTTGAATCTGGGTTTTGTCTCT	5782	
Db	3749	ATAATTAGAAGAAATTTCAAGGGAATGCTTTCACTGATTTGGGTTTCTCT--T	3805	
QY	5783	CCATTGAGGTGAAGCGTCACTTTTATACCTCGATGGAGGAGGAAAGAGGGGTGT	5842	
Db	3806	CGATTTAATTTGGGATCTCTATCTGCATTTGACT--TGAGAGAAAAGAAATGAATGT	3861	
QY	5843	TATGATCTTCACTGTGAGTTTACTAGTTTACGCAATGGAACAGACACTCGGACCTCT	5902	
Db	3862	TAGACCTATATCTGGTTTCTATTACTTAAAGCAATGGAAGAACTTATTGTGATTT	3921	
QY	5903	CTTGACAAAAAATGGAACCTGTGTGTGTCTGTGTTTCTTTGTTTAAGAAACAC	5962	
Db	3922	TTCCCAAAAAGTAAAACTTTCTTTTACTGTGTGCAAAAAGGTGAAATAGAAAAG	3981	
QY	5963	AGGCAAAAGCCGACCAATGGGTGAATGTGGGCTTTGAGTCAAGGCTTTTGAGTTGAG	6022	
Db	3982	CCTTATATGTATGTGTGAATACATGTGTCCAAAGTCAATTTGAGTAGAAGATGTTTAAATCAG	4041	
QY	6023	CACTATCATATAGTT-----GATCATGTCAAGGTGAGGGC	6058	
Db	4042	GAGTGTCAATCATTTGGCTTCCCTGACACACTTGAAGAAGATGTCTTGTAACACAT	4101	
QY	6059	TACCTGTGAGCGAGCCCTGTGTGCTTGCACCTTAAATCTCCAGGTCTCAGATCACT	6118	
Db	4102	AAATATACAAAGCAATAGCTGATAGCTAATAAAAAAGTCCATGACATTAATCTCATATGTTTT	4161	

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QY 6119 TCCTGCTACTAGACAGATTAGAGTTGAGCAACCTTTTTC----- 6163
DB 4162 TAAGAAAGTTATGAAATTTCTGTTAGGGTGCATTTCAAGCTGTCTGGGCCATGTGGCGC 4221
QY 6164 -----AACCCCACTAAATTTTAATTGACAAAAGACTGTGTAATTTTG 6205
DB 4222 CTGTGGGCTGCAGAGTTGGAACAACCTCTTATAGTATCTGTATAGATAGTTTGGAGC 4281
QY 6206 TGGGATACAGTGTGATTAATTGA----- 6227
DB 4282 TGCATAACAGGCGCAAGCAATATGGGTGCGACTCGGGATCCCCAGATCCCAAGCTCAGT 4341
QY 6228 -----TCTATGTGTGCAATTGTGCAAGTTCAATAAGATTAAAGGCCCATCAACAGC 6283
DB 4342 TCAGTCTCCTTGTCTGTGTTAAGAGAGGGGTGTCACCTCTCTCCCAAGCTTTTAAAGAGC 4401
QY 6284 TTTATGGGTGTGAAATGCAAGTAATATAGTATAGTGCCTGTGTCTTGTAGGTCAGAAA 6343
DB 4402 TTTCATTAGTGTGAGTGCACCTGAATATGATGCTGTGTGTGCTCTCTCAGTCCAGAGA 4460
QY 6344 GGCATGATTTTAAAGTCTTGGGCAAAATCATATTATCTCATGTCTAAATAATACATTATGTT 6403
DB 4461 GCCGTCAATTTTAAAGCTCTTTGGCAAAATCATACATTAAGGATTA-----T 4508
QY 6404 GATTATTAATCTTTTGAAGAGGCTGATATTGCTTTTGTGCTCAGCAAGCAAAATGTCA 6463
DB 4509 TACTATGAATGTTTTCACAAATGCTTAAACTCGGTTTCTGTCTCCATCAACCTTAATCTTG 4568
QY 6464 CCAGCTCTTTCTAACGCTGACCACTTTAGAAAATGCTACTGCTCAATTTGTTTGTGA 6523
DB 4569 CAATTTCT--AATTTGTCACCTTTAGAAAACATGGCATTAATGCTCAAAATCTTTTGCA 4625
QY 6524 TTTCTATTTTTCATAGCTTGGAGAGAGTGAAGATCAAGGCGATTGGGAACTGGAACCTG 6583
DB 4626 TTTCTATTTTTCACAGCTTGGAGAGAGTGAAGATCAAAACATTTGGAAGACTGGAATTTG 4685
QY 6584 CTGTTTATGCTCTTGAAGAAATGCTTGGCTGTGAGCGAGAAAGAACTAGAAAAGAGAAC 6643
DB 4686 CTGTTTATGCTCTTGAAGAAATGCTTGCATTTGACCAAGAGCAAAAGCTGAAAAATGAATTAAC 4745
QY 6644 TGTCTCTCTGCTCTTAAAGAAACAAATTAAGATCCCTTAAGAGACTTTT 6695
DB 4746 TAACCCCTTTCCCTCTAGAAATTAACAATTAGATGCCCAAGCCGATTTT 4797

RESULT 12
AAA28840
ID AAA28840 standard; DNA; 4796 BP.
XX
AC AAA28840;
XX
DT 04-SEP-2000 (first entry)
XX
DE Human T cell inducible factor genomic DNA.
XX
KW TIF; T cell derived inducible factor; interleukin 9; STAT; IL-9;
KW Anti-asthmatic; anti-allergic; cytosolic; inhibitor; antagonist;
KW probe; chromosome 12q15; ss.
XX
OS Homo sapiens.
XX
XX
Key Location/Qualifiers
FH 108..4717
FT /+tag= a
FT 1..257
FT exon
FT /+tag= b
FT 258..688
FT intron
FT /+tag= c
FT 689..754
FT exon
FT /+tag= d
FT 755..870
FT intron
FT /+tag= e
FT 871..1014
FT exon

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FT FT /+tag= f
FT intron 1015..1938
FT /+tag= g
FT exon 1939..2004
FT /+tag= h
FT intron 2005..3837
FT /+tag= i
FT exon 3838..4796
FT /+tag= j
XX
XX MO200024758-A1.
XX
XX 04-MAY-2000.
XX
XX 18-OCT-1999; 99MO-US24424.
XX
XX 26-OCT-1998; 98US-0178973.
XX 16-JUL-1999; 99US-0354243.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Dumoutier L, Louhed J, Renaud J;
XX
XX WPI: 2000-422495/36.
XX P-PSDB; AAY92879.
XX
XX New nucleic acid molecule encoding a T cell derived inducible factor
XX for treating asthma, an allergy or lymphoma
XX
XX Claim 1; Page 39-40; 46pp; English.
XX
XX This DNA encodes a human T cell derived inducible factor (TIF). The gene
XX was mapped to chromosome 12q15. The human TIF was identified based on
XX homology to a murine TIF, which was identified by subtraction cloning
XX from a murine lymphoma cell line BM5147 in the presence or absence of
XX interleukin 9 (IL-9). BM5147, can be grown in vitro, without the need to
XX add any cytokines to its culture medium. Many IL-9 activities are
XX mediated by activation of STAT transcription factors. The novel TIFs were
XX expressed in the presence of IL-9, but not in its absence. TIFs induce
XX STAT activation in cells. They can be used, e.g. in the stimulation of
XX regeneration of targeted tissues. Their inhibitors or antagonists can be
XX used to retard, prevent or inhibit differentiation of other tissues. The
XX TIFs and their coding sequences are useful in the treatment of asthma,
XX allergies and lymphoma (claimed). They are also useful for identifying
XX compounds that inhibit or activate T cell induced factor activity in a
XX cell (claimed).
XX
XX Sequence 4796 BP; 1339 A; 912 C; 1063 G; 1482 T; 0 other;
XX
XX
Query Match 9.2%; Score 682.4; DB 21; Length 4796;
Best Local Similarity 53.8%; Pred. No. 1.8e-144;
Matches 2642; Conservative 0; Mismatches 1876; Indels 394; Gaps 44;
QY 2034 CTCTCTCTCACTTATCAACTGTGACACTTGTGCATCTCTGATGGCTGTCTGCAGAA 2093
DB 29 CTCCTTCCCAAGACACAGCTTGTCTCAGTAGAATGTCTGCATATGCGCCCTGCAGAA 88
QY 2094 ATCTAGATGTTTTTCCCTTATGAGGACCTTGGCCGCGCAGCTGCTCTCTCAATGGCC 2153
DB 89 ATCTGAGAGCTCTTCTTATGAGGAGCCTTGACACCACTGCTCTCTCTCTTGGCCCT 148
QY 2154 GTGGGCCAGAGGCAATATGCGTGGCCGCTCAACCCCGATGACCTTGAAGTGTCCA 2213
DB 149 CTGTGTAACAGGAGAGGAGCTGCGCCATCAGCTCCCATGAGGCTTGAACAAGTCCA 208
QY 2214 CTTCAGACAGCGGTATCATGTCAACCGACCTTTATGTCTGGCCAGAGAGTACAGTGA 2273
DB 209 CTTCAGACAGCGCTATATATCAACCAACCGACCTTATGATGCTGAGAGAGTATACATTC 268
QY 2274 TCTCTTCTCTCATATCCGCTTGCATTTTCTGGAAGCACTGCAAACTCTTGAAGG 2333
DB 269 AATCTGCTCTTCTCTGTTGATCTATCTGGAATCAAAAGCTTTTAAACTTTTCTTCA 328

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QY 2334 CGCTTATCTCCGAGGTCTCACTACATAGTTT-----TCTGTCTCTTAGAG 2382
 Db 329 GAGCATCTCTAAGACCTTTAGAACCCACTGTTATCCCTGAGGGTAATAATTTCTG 388
 QY 2383 ACTCTTTAAGAGCTGGTCTTTTCTATTTCTATTTCAAGGTCAGACCACTTTCTAT 2442
 Db 389 TTTTTCAGAGACTCTTTGGGAACTGTGGCTTTTCTTTTCTTGAACCTTCTCCAT 448
 QY 2443 CTGGCCTTCAGAGACATATCTGAATTTATCTACAGAGCGCATTT--AGAAAGCCA 2500
 Db 449 TTTGGCCTTTATGATACATATGATGAATTTTCCAAAGAGCGCATCTACATATCAT 508
 QY 2501 CCCAGACTGCATACTTCTCTGCTGCTCTCTTCTTCAATCTCATCTCTTGGC 2560
 Db 509 CTGAAGATTTTCTTTCTTTATGCTCTGTGCAATGTTCTAACTCATGACACATCTG 568
 QY 2561 TACTC-----CTGAGACCACTGCGAGACATACATCTAC 2595
 Db 569 AATTCTGCTTTTAGCTTTATGATGTGTCTCTGGGAGACGGGATGGGGACATGTCTAT 628
 QY 2596 TTACAGGCTTTTCTTCATCTCTCTGTCAACCGAGCACTTAGGGTTTC-TCTCTTTCAG 2654
 Db 629 GATATAATTTTCTTCTATTTGCTCAATGTCAGACCTTAGTCTTTCTCTCTCCAG 688
 QY 2655 GCCAGCCTTCAGATTAACAACAAGCTCCGGCTCATCGGGAGAAATCTTCCGAGA 2714
 Db 689 GCTACTTGGCTGATTAACAACAAGCTTCCTCATTTGGGGAAATCTGTTCACGGA 748
 QY 2715 GTCACTGTATGCTCCACTGTGATGAGAGGCT-----TAGCTGGGGAGCT 2761
 Db 749 GTCACTGTATGCTCAAGTTGTGACAAACAGGCGCTGTGCTCATAGGATCTTGGGT 808
 QY 2762 GGTGAGACCTCTGGGATAG---TCTGACGTATGACCCCTGTGCTCTTGTCTACCTGC 2817
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 QY 2818 AGGCTAAAGATGATGCTACTGATGAAAGAGCTCTCACTTCAACCTCGAAGAGCTTC 2877
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 QY 2878 TGCTCCCCAGTCACAGACAGTCCAGCCCTACATACAGAGAGTGTACTTCCGACCA 2937
 Db 929 TGTCTCTCAATCTATAGTGTTCAGCCCTTATATCAAGAGGTGTGCTCTCCGCA 988
 QY 2938 AACTCAGCAATCAGCTCAGCTCTGTATGCTGACTGTGCTACTATGCTCTCTCT 2997
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 QY 3058 GAGAGGCTCAGACACACACATCATAGGCCACTTTGAAATGTCACAAAGCTTTGGC 3117
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 Db 1222 GGGTCTGGAACCTTAAAGTATGAGAACCGCATTTGTTGTCTTCGAAAGAGCAATC 1281
 QY 3238 AGAGAAACGATCTCTGATGATATGATCTTATGGGGGAGCAGAGGGGCGATATCCAGTGA 3297
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 QY 3358 CACTGATGACAACTTCTGTGGGGAGGGAATGGCAGAGCAAAAAGTTGAAGGAGAG 3417

Db 1370 CATGAGAGAAATTGAAGAGAAAGTGGAAATGGGAAGCTTAA----- 1415
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 Db 1416 -----GTGGTGTGTGGGTGGCAGACTGTGCTCCCTGTGATGTATGGGA 1460
 QY 3478 AGTTAAGAAAACA-GTGTGTGAGTTGATGTCTTGACAGACCCCACTATGAAATCAT 3536
 Db 1461 AGCCACAAATCGAGAGGCTGTGAACCTGATGCGCTGAACATTTGAAACTATGAAAAA 1520
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 QY 3595 CACACGAGAACTTATGCTCATCTTGTGCTACACTCCACCTTATGATGAGTTCAAC 3654
 Db 1581 CACATGAGATTTTATGTATCTTCTTCTTAAAGCATGCAATTTTCTGGAGATACAT 1640
 QY 3655 TCAGGTTTCTTTCT-----ACGTTCTTGTACTGTGGAAC 3693
 Db 1641 TGAGGTTTATTTCTTACAGAAATTTGCAATAAATACTCCGCTTTTCCACAAATGCAAC 1700
 QY 3694 TTCAAGATTTCCCAAGAGAGAGACAGCTCTTCTGTAAGGAGGAGACCTGATTTCA 3753
 Db 1701 CTCACTGATGATTTCCCAAGAGAGAGAGGCTCTTCTTAAAGGAGAGTGAATTTCTG 1760
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 Db 1881 GAGGTCATMAAGTTTCAGCAACACATTAATAATATTTATGTTTATTTTATGGA 1940
 QY 3933 CATCAGGAGTACGACACGAGACATCCAGAAATGTCAAGAGCTGAAGAGACAGTGA 3992
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Db 2829 ACCATCATAGTGGCTATTTGGTGAAGAAAGCA--ACAATGGAAGCTTATGACTATCAATA 2886
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QY 4992 -----TATCTACCTTAATCTCTCTATCGAAGCTAAATCTCTTTTCTTCTG 5042
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QY 5043 TGTAGGCTGATPAACACACTGTT--TTCTTTGAGTGTCAAGGCTTTGATGATTTTA 5100
Db 3066 CATCATTAATAGAGTACGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3125
QY 5101 GTGCTGTCCAGTCTTGT--TAGAGGTTGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5158
Db 3126 TTGTGAAGCCCAATCT 3185
QY 5159 GCATGCCAAGGACACACT 5215
Db 3186 GCATGCCAAGGACACACT 3245
QY 5216 -----TTGTCTTTGGAAGTGAAGCTGTGTGAGAAAGAACTCAAGAGATGTGCT 5270
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 DB 4745 TAACCCCTTTCCCTGCTAGAAATTAAGATGATGCCCCCAAGCAATTTT 4796
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 ID AAA28815 standard; cDNA, 1119 BP.
 AC AAA28815;
 DT 04-SEP-2000 (first entry)
 DE Murine T cell inducible factor alpha cDNA.
 KW TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;
 KW Anti-asthmatic; anti-allergic; cytoskeletal; inhibitor; antagonist; ss.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT CDS 52..591
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 XX WO200024758-A1.
 XX PD 04-MAY-2000.
 XX PE 18-OCT-1999; 99WO-US24424.
 XX FR 26-OCT-1998; 98US-0178973.
 XX PR 16-JUL-1999; 99US-0354243.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Dumoutier L, Louhed J, Renaud J;
 XX WPI: 2000-422495/36.
 XX P-PSDB: AAY92877.
 PT New nucleic acid molecule encoding a T cell derived inducible factor
 PT for treating asthma, an allergy or lymphoma
 XX Claim 1; Page 33; 46pp; English.
 CC This cDNA encodes T cell derived inducible factor (TIF) alpha identified
 CC by subtraction cloning from a murine lymphoma cell line BW5147 in the
 CC presence or absence of interleukin 9 (IL-9). BW5147, can be grown in
 CC vitro, without the need to add any cytokines to its culture medium. Many
 CC IL-9 activities are mediated by activation of STAT transcription
 CC factors. The novel TIFs were expressed in the presence of IL-9, but not
 CC in its absence. TIFs induce STAT activation in cells. They can be used,
 CC e.g. in the stimulation of regeneration of targeted tissues. Their
 CC inhibitors or antagonists can be used to retard, prevent or inhibit
 CC differentiation of other tissues. The TIFs and their coding sequences are
 CC useful in the treatment of asthma, allergies and lymphoma (claimed). They
 CC are also useful for identifying compounds that inhibit or activate T cell
 CC induced factor activity in a cell (claimed).
 XX Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;

Query Match 8.1%; Score 601.4; DB 21; Length 1119;
 Best Local Similarity 99.8%; Pred. No. 2.3e-126;
 Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6535 ATACCTGGAGAGAGTGGAGATCAAGCGATTGGGAACTGGACCTGTTTATGTC 6594
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 QY 6595 TCTGAGAAATGCTTGGCTTGAAGGAGAAAGCTAGAAAAAGAAAGACCTGCTTCT 6654
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 DB 810 ATATTTATGTCATGATGATACAGAAAAATTAATGACTTTAAAAAATGTTGAA 869
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 QY 7015 ATATGATTTATTTATAGAAACATTAATGCTGATGATGATTTATGATTAAGCAATATA 7074
 DB 990 ATATGATTTATTTATAGAAACATTAATGCTGATGATGATTTATGATTAAGCAATATA 1049
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 DB 1050 TTTATGACATTAATAGAAACATTAATGCTGATGATGATTTATGATTAAGCAATATA 1109
 QY 7135 AAA 7137
 DB 1110 AAA 1112
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 AC AAS14858;
 DT 19-DEC-2001 (first entry)
 DE Mouse cDNA encoding T cell derived inducible factor, TIFalpha.
 KW Mouse; T cell derived inducible factor; TIFalpha; ss; antiallergic;
 KW antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;
 KW cancer; lymphoma; immune system disorder; allergy; asthma;
 KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
 KW thyroiditis; melanoma; hepatoma.
 OS Mus musculus.
 FH Key Location/Qualifiers
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 FT primer_bind 106..126
 FT /*tag= b

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FT /note= "PCR primer appearing as AAS14861"
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FT C /tag=
FT /note= "PCR primer appearing as AAS14862"
PN US2001024652-A1.
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XX 27-SEP-2001.
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XX 29-DEC-2000; 2000US-0751797.
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XX 18-OCT-1999; 99US-0419568.
XX 26-OCT-1998; 98US-0178973.
XX 16-JUL-1999; 99US-0354243.
XX
PA (DUMO/) DUMOUTIER L.
PA (LOUA/) LOUAHED J.
PA (RENA/) RENAULD J.
PI Dumoutier L, Louahed J, Renauld J;
XX
XX WPI; 2001-638496/73.
XX P-PSDB; AAU09090.
XX
XX New isolated nucleic acid molecules encoding T cell inducible factors,
XX useful as markers for expression or effect of interleukin (IL)-9 in a
XX subject and diagnosing susceptibility to asthma or allergy
XX
XX Claim 1; Page 10; 26pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule, which encodes
XX a T cell derived inducible factor (TIF) which are upregulated by the
XX cytokine interleukin-9 (IL-9) and induce STAT transcription factor
XX activation. The TIF proteins (or their muteins) may be used to test IL-9
XX and/or agonists for their potency against lymphomas, immune system
XX disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
XX autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
XX or inhibit differentiation of tissue types in which they are active and
XX therefore be used to develop treatments for melanomas and hepatomas.
XX The present sequence encodes mouse TIFalpha.
XX
XX Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;
XX
XX Query Match 8.1%; Score 601.4; DB 22; Length 1119;
XX Best Local Similarity 99.8%; Pred. No. 2.3e-126;
XX Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX 6535 ATAGCTTGGAGAGAGTGAAGATCAAGCGATTGGGAACTGGACCTGCTTTATGTC 6594
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XX Db 510 AAAGCTTGGAGAGAGTGAAGATCAAGCGATTGGGAACTGGACCTGCTTTATGTC 569
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XX QY 6595 TCTGAGAAATGCTTGGCTTGAAGCGAAGAAAGCTAGAAAACGAGAACTGCTCTTCC 6654
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XX Db 750 TAGTGTCAAGTTGTCTCATAGACACGAGGTAGATCTTGATPACCAAGAAATTCATTGACA 809
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XX QY 6835 AATATTTATTTGTCACGATGATACACAGAAATAATGACTTTAAATTTGTTGAA 6894
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XX |

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Db 930 TATTTATATATATAGATTATTTATTAATAGATACATTTTATTTATGTCAGTTATTA 989
QY 7015 ATATGATTTATTTATAGAAACATTTATCTGCTATTTGATATTTAGTATTAAGCAATPATA 7074
Db 990 ATATGATTTATTTATAGAAACATTTATCTGCTATTTGATATTTAGTATTAAGCAATPATA 1049
QY 7075 TTATGACATATATCTATGGAACAGATATCTTAGGCTTTAATAAACATGATATTCAT 7134
Db 1050 TTATGACATATATCTATGGAACAGATATCTTAGGCTTTAATAAACATGATATTCAT 1109
QY 7135 AAA 7137
Db 1110 AAA 1112
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XX RESULT 15
XX AAD30627
XX ID AAD30627 standard; cDNA; 1119 BP.
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XX AC AAD30627;
XX
XX DT 21-MAY-2002 (first entry)
XX
XX DE Mouse TIF alpha cDNA.
XX
XX KW T cell derived inducible factor; TIF; interleukin-21; IL-21; mouse;
XX STAT transcription factor; acute phase protein; inflammation; ss.
XX
XX OS Mus musculus.
XX
XX FH Key Location/Qualifiers
XX FT CDS 52..591
XX FT /tag= a
XX FT /product= "Mouse TIF alpha protein"
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XX PN W0200210393-A2.
XX
XX PD 07-FEB-2002.
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XX PF 27-JUN-2001; 2001WO-US20485.
XX
XX PR 27-JUL-2000; 2000US-062617.
XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX PI Dumoutier L, Renauld J;
XX
XX DR WPI; 2002-195964/25.
XX P-PSDB; AAE19235.
XX
XX PT Stimulating expression of STAT transcription factor and inducing
XX production of acute phase protein in a cell, involves contacting a cell
XX capable of expressing STAT with T cell derived inducible factors -
XX
XX PS Example 6; Page 49; 64pp; English.
XX
XX CC The invention relates to nucleic acid molecules encoding T cell
XX derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
XX CC TIF polynucleotides are upregulated by the cytokine, IL-9. IL-TIF or
XX CC IL-21 molecules are implicated in activation of STAT transcription
XX CC factors, acute phase proteins and inflammation. The present sequence
XX CC is mouse TIF alpha cDNA.
XX
XX SQ Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;
XX
XX Query Match 8.1%; Score 601.4; DB 24; Length 1119;
XX Best Local Similarity 99.8%; Pred. No. 2.3e-126;
XX Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 6535 ATAGCTTGAGAGAGTGAAGATCAAGCCATTGGGAACTGGACCTGCTGTTATGTC 6594
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QY 6895 AGGAGTTACCTCTCATTCCTTTAGAAAAAAAGCTTATGTAACTTCATTCCATATCCAA 6954
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SUMMARIES

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ALIGNMENTS

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Sequence 8, Application US/09751797
Patent No. US20010024652A1
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
FILE REFERENCE: LUD 5543.2
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 09/419,568
PRIOR FILING DATE: 1998-10-18
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 8
LENGTH: 7445
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-751-797-8
Query Match 100.0%; Score 7445; DB 10; Length 7445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCTATCACCCTGTTATGATTTCTTATTTATTAATAAACTATTTCTTAATGAAA 60
DB 1 GTCTATCACCCTGTTATGATTTCTTATTTATTAATAAACTATTTCTTAATGAAA 60
QY 61 GCAACCAAGCAGCATTTATGATGCTGCTTCAATGAGTGAAGGATG 120
DB 61 GCAACCAAGCAGCATTTATGATGCTGCTGCAATGAGTGAAGGATG 120
QY 121 TAAGAGCGCTTTATGACATTAACCAATGTTATGTTCTTCTGCAAGCAACT 180

Db 121 TAAGAGCGGTATTAACAGATTACCAACATGTTAATGTTTCTTGGCAAGCAACT 180
 QY 181 TGAATCTATGCTTAAACAATCTTGAAGCTCTAAATATAGTCTAAGACTGAGTCCG 240
 Db 181 TGAATCTATGCTTAAACAATCTTGAAGCTCTAATATAGTCTAAGACTGAGTCCG 240
 QY 241 CTGCTGTCCAAAGAGCTCTTGAGCAAGCTCTCTCTGTTTGGCAATTTATGTTCTTGA 300
 Db 241 CTGCTGTCCAAAGAGCTCTTGAGCAAGCTCTCTCTGTTTGGCAATTTATGTTCTTGA 300
 QY 301 TGCACTCCCAACCTCTCACTCGGCTCTGTAGTGGCAACCTTCAACTTTCGCACTTA 360
 Db 301 TGCACTCCCAACCTCTCACTCGGCTCTGTAGTGGCAACCTTCAACTTTCGCACTTA 360
 QY 361 TGAATCTATGTTTAACTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
 Db 361 TGAATCTATGTTTAACTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
 QY 421 TGTTCACCAACATGATGCTGTGCAACAGTGTGCTGCTGTTGTGGGGCAAGA 480
 Db 421 TGTTCACCAACATGATGCTGTGCAACAGTGTGCTGCTGTTGTGGGGCAAGA 480
 QY 481 GCGAGAGAGGATGCTGGGACCGGATGCGATGCGATGCGATGCGATGCGATGCGATGCG 540
 Db 481 GCGAGAGAGGATGCTGGGACCGGATGCGATGCGATGCGATGCGATGCGATGCGATGCG 540
 QY 541 GGGAGTTAGACCCAGGTCCTCCAGAAAGTCCAGAAATGCTTTAAACACAGCAGGAT 600
 Db 541 GGGAGTTAGACCCAGGTCCTCCAGAAAGTCCAGAAATGCTTTAAACACAGCAGGAT 600
 QY 601 TCTCTCTCAAGCCCAACATGAGTGTCTTTAGATTCACCTTAAATAGAGATCTGATGCG 660
 Db 601 TCTCTCTCAAGCCCAACATGAGTGTCTTTAGATTCACCTTAAATAGAGATCTGATGCG 660
 QY 661 TTCACCTACGACCTCCCTCTTGCATCTTCTGCAAGAAACACAAAGCAAGAT 720
 Db 661 TTCACCTACGACCTCCCTCTTGCATCTTCTGCAAGAAACACAAAGCAAGAT 720
 QY 721 CCCCACTGCTTTCGCTCTCAAGTCTGACCTCAACAGGTCAGAGATCTCCAGTGT 780
 Db 721 CCCCACTGCTTTCGCTCTCAAGTCTGACCTCAACAGGTCAGAGATCTCCAGTGT 780
 QY 781 CCTCTTAAACATTTCCCAAGTGTCTCTTAACTTCTCAAGTGTCTCTTAACTT 840
 Db 781 CCTCTTAAACATTTCCCAAGTGTCTCTTAACTTCTCAAGTGTCTCTTAACTT 840
 QY 841 CTCACGTGCTCTTAACTTCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGA 900
 Db 841 CTCACGTGCTCTTAACTTCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTTGA 900
 QY 901 GTGATTTTCAAGCTTCCGCTCTAGTCTAGATGAGGATTTGCGTCACTAGTCTAGT 960
 Db 901 GTGATTTTCAAGCTTCCGCTCTAGTCTAGATGAGGATTTGCGTCACTAGTCTAGT 960
 QY 961 AGGCGTGTCTCCGCTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGT 1020
 Db 961 AGGCGTGTCTCCGCTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGT 1020
 QY 1021 GGAATTCAGTATCATCAATGCAAAATCCAGATTTTGTAAATTTCTCTTCAACT 1080
 Db 1021 GGAATTCAGTATCATCAATGCAAAATCCAGATTTTGTAAATTTCTCTTCAACT 1080
 QY 1081 ATCCATCTATATAGTATGTTATGAGGCTCAATTTAAATAATATATTTTGAAGCTATG 1140
 Db 1081 ATCCATCTATATAGTATGTTATGAGGCTCAATTTAAATAATATATTTTGAAGCTATG 1140
 QY 1141 TTGCAAAAGTAAATGTCAAGAAATGCAAAATGATATATTTTAAAAAAA 1200
 Db 1141 TTGCAAAAGTAAATGTCAAGAAATGCAAAATGATATATTTTAAAAAAA 1200
 QY 1201 TCTATGCTTAAATGTCTATATGATGTTCACTACGATATTTCCAAACTTAACCTTGAC 1260
 Db 1201 TCTATGCTTAAATGTCTATATGATGTTCACTACGATATTTCCAAACTTAACCTTGAC 1260

QY 1261 TTGGCTATGATTTCAACCTTTGATTTGATCTACCATTAACAGTCTGTGACAGAACAT 1320
 Db 1261 TTGGCTATGATTTCAACCTTTGATTTGATCTACCATTAACAGTCTGTGACAGAACAT 1320
 QY 1321 TCTGTGGCAATGGAGCTGTGAAGAAAGCAACCTTTTATTTAAAAAAAACAGCTA 1380
 Db 1321 TCTGTGGCAATGGAGCTGTGAAGAAAGCAACCTTTTATTTAAAAAAAACAGCTA 1380
 QY 1381 GTTATAGTTTAAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1440
 Db 1381 GTTATAGTTTAAATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1440
 QY 1441 AATTAATTCAGATTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
 Db 1441 AATTAATTCAGATTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
 QY 1501 TTTATTTTGTGCTCACTTTCTAAAGATTAAGATCTATGAAATTTGTTGGGAAATGAGTCC 1560
 Db 1501 TTTATTTTGTGCTCACTTTCTAAAGATTAAGATCTATGAAATTTGTTGGGAAATGAGTCC 1560
 QY 1561 GTGACCAAAAGCTGACCTCAATAGCTACGGGATCAAAAGGCTGCTCAATACAGAA 1620
 Db 1561 GTGACCAAAAGCTGACCTCAATAGCTACGGGATCAAAAGGCTGCTCAATACAGAA 1620
 QY 1621 TCTACTAGGCGCAAGCCATGAGCTTTCTTGAAGAAACGTTGTTAGAGATTTCTGGGATTT 1680
 Db 1621 TCTACTAGGCGCAAGCCATGAGCTTTCTTGAAGAAACGTTGTTAGAGATTTCTGGGATTT 1680
 QY 1681 GTGTGCAAAAGCACTTTGTTGGCTTCAACGCTGACGTTTAAAGAGACTTCCCATCTCT 1740
 Db 1681 GTGTGCAAAAGCACTTTGTTGGCTTCAACGCTGACGTTTAAAGAGACTTCCCATCTCT 1740
 QY 1741 CAAGGTGGGAAAGGCTTGGAGGCTGTGCTGTGAGCTCTCAATAGGTTAGGATCTTCC 1800
 Db 1741 CAAGGTGGGAAAGGCTTGGAGGCTGTGCTGTGAGCTCTCAATAGGTTAGGATCTTCC 1800
 QY 1801 AGAAGACAGACTGGAATTAATGATATGCTGATGCTATATCATTCATTCACATACCAAAAA 1860
 Db 1801 AGAAGACAGACTGGAATTAATGATATGCTGATGCTATATCATTCATTCACATACCAAAAA 1860
 QY 1861 ACCCTGTGTCTCCGATGCTATTAAGAGCAACCTTGTGCTCTCCCATCACAGCAGAG 1920
 Db 1861 ACCCTGTGTCTCCGATGCTATTAAGAGCAACCTTGTGCTCTCCCATCACAGCAGAG 1920
 QY 1921 ACACCTAAACAGGTAGAGACTGACCTCTACAGCAATTCATCTGCTGTGCTGCTGCTA 1980
 Db 1921 ACACCTAAACAGGTAGAGACTGACCTCTACAGCAATTCATCTGCTGTGCTGCTGCTA 1980
 QY 1981 CCCGACGAACATGCTCCCTGATGTTTGTGCTTGTGCTCTCACTAACAGGCTCTCCT 2040
 Db 1981 CCCGACGAACATGCTCCCTGATGTTTGTGCTTGTGCTCTCACTAACAGGCTCTCCT 2040
 QY 2041 CTCACCTTAACTATGCTTGAACCTTGTGAGATCTGATGAGGCTGTGCTGAGAAATCTATG 2100
 Db 2041 CTCACCTTAACTATGCTTGAACCTTGTGAGATCTGATGAGGCTGTGCTGAGAAATCTATG 2100
 QY 2101 AGTTTTCCTTAATGAGGACTTTGGGCGGCAAGCTGCTCTCATTTGCGCTGTGGGCG 2160
 Db 2101 AGTTTTCCTTAATGAGGACTTTGGGCGGCAAGCTGCTCTCATTTGCGCTGTGGGCG 2160
 QY 2161 CAGAGAGCAAAATGCGCTGCTCAACACCGGCTCAAGCTTGAAGTGTCAACTTCCAG 2220
 Db 2161 CAGAGAGCAAAATGCGCTGCTCAACACCGGCTCAAGCTTGAAGTGTCAACTTCCAG 2220
 QY 2221 CAGCGCTATCATGCTAACCAGCTTTATGCTGGGCAAGAGGATCAAGTGTGATCTCTTT 2280
 Db 2221 CAGCGCTATCATGCTAACCAGCTTTATGCTGGGCAAGAGGATCAAGTGTGATCTCTTT 2280
 QY 2281 CTCTGCATACGCGCTTGGCAATTTCTCTGAAGCACTTGAAGCACTTTTAAAGGCGCTTTA 2340
 Db 2281 CTCTGCATACGCGCTTGGCAATTTCTCTGAAGCACTTGAAGCACTTTTAAAGGCGCTTTA 2340

QY	2341	TCGCCGAGGCTCTACTACCTATATTTTTCTGTCTCTTTAAGACTCTTTAAGACTGCGGT	2400
Db	2341	TCGCCGAGGCTCTACTACCTATATTTTTCTGTCTCTTTAAGACTCTTTAAGACTGCGGT	2400
QY	2401	CTTTTCTATTTCCATTTCAAGGCTCAGAGCACTTTCCATCTGTGGCTTCAGAGCAC	2460
Db	2401	CTTTTCTATTTCCATTTCAAGGCTCAGAGCACTTTCCATCTGTGGCTTCAGAGCAC	2460
QY	2461	TATCTGAATTTTATCTACAGAGGCGCATTTAGAAAGCCACCACGACTCAATCTTTC	2520
Db	2461	TATCTGAATTTTATCTACAGAGGCGCATTTAGAAAGCCACCACGACTCAATCTTTC	2520
QY	2521	CATTCTCTGTGCTCTCTTCTGAACCTATACCTCTTGGCTACTCTTGAAGCCACCTGC	2580
Db	2521	CATTCTCTGTGCTCTCTTCTGAACCTATACCTCTTGGCTACTCTTGAAGCCACCTGC	2580
QY	2581	GACATATACCTCTTACTTAACAGGCTTTTCCATCTCTTGTACCCAGGACCTTAAGGT	2640
Db	2581	GACATATACCTCTTACTTAACAGGCTTTTCCATCTCTTGTACCCAGGACCTTAAGGT	2640
QY	2641	TTTTCTCTTTTCAAGGCGAGCTTGCAGATTAACAACAAGAGCTCCGCTCATCGGGAGA	2700
Db	2641	TTTTCTCTCTTTCAAGGCGAGCTTGCAGATTAACAACAAGAGCTCCGCTCATCGGGAGA	2700
QY	2701	AACCTGTTCCGAGAGTCAGTGTAACTCTCACTGTATGAGCAGAGGCTAGCTCGGGAGC	2760
Db	2701	AACCTGTTCCGAGAGTCAGTGTAACTCTCACTGTATGAGCAGAGGCTAGCTCGGGAGC	2760
QY	2761	TGCTGACCCCTCTGGGATAGTCTACGTATGACCCCTGTCTTCTTGTCTACTCTGAGG	2820
Db	2761	TGCTGACCCCTCTGGGATAGTCTACGTATGACCCCTGTCTTCTTGTCTACTCTGAGG	2820
QY	2821	CTAAGATCACTGCTACTCGTATGAAAGAGGCTCAACTTCACTGAGAGAGCTTCTGC	2880
Db	2821	CTAAGATCACTGCTACTCGTATGAAAGAGGCTCTCAACTTCACTGAGAGAGCTTCTGC	2880
QY	2881	TCCCCCAGTCAGAGGTTCCAGCCCTACATGACGAGAGTGATACCTTCTCTGACCAAC	2940
Db	2881	TCCCCCAGTCAGAGGTTCCAGCCCTACATGACGAGAGTGATACCTTCTCTGACCAAC	2940
QY	2941	TCAGCAATCAGCTCAGCTCCTGTGTAACTGTGACTCTGGGCTACTATGCTCTTCTCTT	3000
Db	2941	TCAGCAATCAGCTCAGCTCCTGTGTAACTGTGACTCTGGGCTACTATGCTCTCTCTT	3000
QY	3001	CCTCTCATTTCCAGTAAAGAACCCGAGGCTCTGCCTCTCTCTTCAAGAGATGAGGA	3060
Db	3001	CCTCTCTATTTCCAGTAAAGAACCCGAGGCTCTGCCTCTCTCTTCAAGAGATGAGGA	3060
QY	3061	GGGCTCAGCAACAACCATCATAGGCCACTTGAATAGGTCACAAAAGCTTTGGCTTC	3120
Db	3061	GGGCTCAGCAACAACCATCATAGGCCACTTGAATAGGTCACAAAAGCTTTGGCTTC	3120
QY	3121	AATTGAGTAAATACCTTTGAGTTTGTATGAGTGAAGCTTTATTTGTTTTATCCATGGAAAGA	3180
Db	3121	AATTGAGTAAATACCTTTGAGTTTGTATGAGTGAAGCTTTATTTGTTTTATCCATGGAAAGA	3180
QY	3181	AATCAACTCAATTTCTGAGATGAGAAAGATGTTGGGACGAAAAAGGCGCTGATAGA	3240
Db	3181	AATCAACTCAATTTCTGAGATGAGAAAGATGTTGGGACGAAAAAGGCGCTGATAGA	3240
QY	3241	GAACAGATCTGCTAGATATAGTACTTATGGGGGGAGCAGGGGGCGATATCTACTGAGTA	3300
Db	3241	GAACAGATCTGCTAGATATAGTACTTATGGGGGGAGCAGGGGGCGATATCTACTGAGTA	3300
QY	3301	CAAGTACTTTGGGGAGAGAAATCCACTGAGTACAAGTACTTTGGGATGGAATCCAC	3360
Db	3301	CAAGTACTTTGGGGAGAGAAATCCACTGAGTACAAGTACTTTGGGATGGAATCCAC	3360
QY	3361	TGAGTACAGATCTTTGGGGGGAGGAGATGGCAGAGCAAAAGTTGAAGGAGAGAG	3420
Db	3361	TGAGTACAGATCTTTGGGGGGAGGAGATGGCAGAGCAAAAGTTGAAGGAGAGAG	3420
QY	3421	ATGAGAGGCTCATGTGTTGGGGGTGTAAGAAAGTCACTCTTTTCCATGTATGAGAGT	3480

Db	3421	ATGGAGAGGCTCAATGATGTGGGGGTGGAAAGGTACTCTTTTCCATGTGATGGAGAGT	3480
Oy	3481	TAAGAAAAACAGGTGTGAGTTTGAATGTCTTGACAGACCCCAACTATGAAAATATATCC	3540
Db	3481	TAAGAAAAACAGGTGTGAGTTTGAATGTCTTGACAGACCCCAACTATGAAAATATATCC	3540
Oy	3541	ACGAGGACGGGGCAGACTGTGGGAGACCTTGGCATTTTGGAGAGGCGGCTTTTCAACG	3600
Db	3541	ACGAGGACGGGGCAGACTGTGGGAGACCTTGGCATTTTGGAGAGGCGGCTTTTCAACG	3600
Oy	3601	AGAAACTTATATGCTCATCTCTTGCTGCTACACTCCCACTTTGATGAGGTTCAAGTCAAGT	3660
Db	3601	AGAAACTTATATGCTCATCTCTTGCTGCTACACTCCCACTTTGATGAGGTTCAAGTCAAGT	3660
Oy	3661	TTGCTTTCTACCGTTCTTGCTACTGCTGGGAAACTTCAATGAGATTTCCCAAGACGAGGA	3720
Db	3661	TTGCTTTCTACCGTTCTTGCTACTGCTGGGAAACTTCAATGAGATTTCCCAAGACGAGGA	3720
Oy	3721	CAGCTCTTCTGTAGAGGAGGAGCCTGATTTCACTGTCCTAGAGACGAATTAAGTCTAGA	3780
Db	3721	CAGCTCTTCTGTAGAGGAGGAGCCTGATTTCACTGTCCTAGAGACGAATTAAGTCTAGA	3780
Oy	3781	GAATCTTAGGTTAAAGTGAATCTTAGGTCAACAGCGGGCAAAAATATACCTGAACGCTCTATT	3840
Db	3781	GAATCTTAGGTTAAAGTGAATCTTAGGTCAACAGCGGGCAAAAATATACCTGAACGCTCTATT	3840
Oy	3841	CCAGGTGAAGGGTCAACGTCCTCAGATATATCTGAGTATTTGGGCTCCCAACGGATTAAGAT	3900
Db	3841	CCAGGTGAAGGGTCAACGTCCTCAGATATATCTGAGTATTTGGGCTCCCAACGGATTAAGAT	3900
Oy	3901	TCTGTATGAGAGTGTGCTTTTATTTTTCAGACACATCAACGGGTGACGACCAAGATCCAG	3960
Db	3901	TCTGTATGAGAGTGTGCTTTTATTTTTCAGACACATCAACGGGTGACGACCAAGATCCAG	3960
Oy	3961	AAGAATGTCAAGAGGCTGAGAGAGACAGTGAATAAAGTATCTATTGGCAAGCCCAATATCT	4020
Db	3961	AAGAATGTCAAGAGGCTGAGAGAGACAGTGAATAAAGTATCTATTGGCAAGCCCAATATCT	4020
Oy	4021	AAGCATTTCAATAGAGAGCGTGGGAGATTTCTTTCTCGCTTCCCAAGTCCCTTCTACTTTG	4080
Db	4021	AAGCATTTCAATAGAGAGCGTGGGAGATTTCTTTCTCGCTTCCCAAGTCCCTTCTACTTTG	4080
Oy	4081	TAACATTTTATTTGACTGTGCTACTATCTGTGCTCATTAATCTGCTTAAGTGCACCTGTATC	4140
Db	4081	TAACATTTTATTTGACTGTGCTACTATCTGTGCTCATTAATCTGCTTAAGTGCACCTGTATC	4140
Oy	4141	TAGCTGGGTCTATAGATTTTCAATCTGTGCTTAAATTTGTAAGTCAAAATTTCTGGAGCT	4200
Db	4141	TAGCTGGGTCTATAGATTTTCAATCTGTGCTTAAATTTGTAAGTCAAAATTTCTGGAGCT	4200
Oy	4201	AGCAGAAAGCTTAGGTGACGAGCTCATATGACACTTGTGGAGAGATGCTTGTGACAG	4260
Db	4201	AGCAGAAAGCTTAGGTGACGAGCTCATATGACACTTGTGGAGAGATGCTTGTGACAG	4260
Oy	4261	AGTCATGTCTAGAAAGACAGATCCCTGATTTCCAGCTCTGCACTTGCTTAAGTGGCATGT	4320
Db	4261	AGTCATGTCTAGAAAGACAGATCCCTGATTTCCAGCTCTGCACTTGCTTAAGTGGCATGT	4320
Oy	4321	GTAATTAATTTGGGCTTGATTTAAGTATTTGGGAAAGCCAGTTCCACAGGACCTAATATATC	4380
Db	4321	GTAATTAATTTGGGCTTGATTTAAGTATTTGGGAAAGCCAGTTCCACAGGACCTAATATATC	4380
Oy	4381	TGAAGAACCATGACATTTGAAAATCTGAAAAGCTGGGCACAAACTTACTAGAGATGATTTTGG	4440
Db	4381	TGAAGAACCATGACATTTGAAAATCTGAAAAGCTGGGCACAAACTTACTAGAGATGATTTTGG	4440
Oy	4441	AGCTCATTTAAACGAGTGTCTGAAATGTGGCAAAATCAACCAAGATTAACAACAAAGAG	4500
Db	4441	AGCTCATTTAAACGAGTGTCTGAAATGTGGCAAAATCAACCAAGATTAACAACAAAGAG	4500
Oy	4501	CTGGAATTTGCAATATGACAGTATTTGAAATCACTGGTATTAATAGTATCATCTTAAT	4560
Db	4501	CTGGAATTTGCAATATGACAGTATTTGAAATCACTGGTATTAATAGTATCATCTTAAT	4560

D	4501	CTGATTTTGGCAATAGGCAAGTATTTAGATCACTGGTATTTAATAGCTATCATCTTTAAT	4560
Q	4561	TAAATATAGGCGCTATATATATATTTTATAGATTAAACAAGAGTGATAGCCTCCCAAT	4620
D	4561	TAAATATAGGCGCTATATATATATTTTATAGATTAAACAAGAGTGATAGCCTCCCAAT	4620
Q	4621	TTACTTGGCGCTTGTTCAAAAGAGTAAAAATATCATGATGATTAATATAGTGTGATG	4680
D	4621	TTACTTGGCGCTTGTTCAAAAGAGTAAAAATATCATGATGATTAATATAGTGTGATG	4680
Q	4681	AAAGTATAGAGTGAAGAACCCCTTCTTCACTTTTACCTTCACTTTTACCTTTTCTTTC	4740
D	4681	AAAGTATAGAGTGAAGAACCCCTTCTTCACTTTTACCTTCACTTTTACCTTTTCTTTC	4740
Q	4741	TTCAACCCCTGATCAGAGCACTAGTAAAGCACTATCTGTGTGAGCTATATATAGCTTT	4800
D	4741	TTCAACCCCTGATCAGAGCACTAGTAAAGCACTATCTGTGTGAGCTATATATAGCTTT	4800
Q	4801	ACAGCAAAACAATTTGCTGTGTGCGCTTTTGGGGAAGGGAACAGATAGCAGAGGCTC	4860
D	4801	ACAGCAAAACAATTTGCTGTGTGCGCTTTTGGGGAAGGGAACAGATAGCAGAGGCTC	4860
Q	4861	AGGCTAGCAAGTCTGATCTTGCCCTTAAAGCCAGAGGCACTGTTGATAGCAGAAAGTGAG	4920
D	4861	AGGCTAGCAAGTCTGATCTTGCCCTTAAAGCCAGAGGCACTGTTGATAGCAGAAAGTGAG	4920
Q	4921	GCTCTTGGCAAGTGGGTGTGCTTAAATATCAGAAACAGGAAGGCTCCGGTATAGGAAT	4980
D	4921	GCTCTTGGCAAGTGGGTGTGCTTAAATATCAGAAACAGGAAGGCTCCGGTATAGGAAT	4980
Q	4981	TATCAGTAAATATCTACCCCTTATCTCTCTATCTGAACTTAATGCTCTTTTCTTG	5040
D	4981	TATCAGTAAATATCTACCCCTTATCTCTCTATCTGAACTTAATGCTCTTTTCTTG	5040
Q	5041	TGTGTAGGCGTATTAACAACACTTGTCTTTTGTAGTGTTCATAGGCTTTGATATTTTA	5100
D	5041	TGTGTAGGCGTATTAACAACACTTGTCTTTTGTAGTGTTCATAGGCTTTGATATTTTA	5100
Q	5101	GTCCTCTGCCAGTCTTGTGTAGAGGGTTGTATCTTGAACCTGACCGGGCTGATGTAGG	5160
D	5101	GTCCTCTGCCAGTCTTGTGTAGAGGGTTGTATCTTGAACCTGACCGGGCTGATGTAGG	5160
Q	5161	ATGCCAAAGGCACACTTCTGAAATGCGCTGTGTAAGGATTAATTAATTAATTAATTTGTC	5220
D	5161	ATGCCAAAGGCACACTTCTGAAATGCGCTGTGTAAGGATTAATTAATTAATTAATTTGTC	5220
Q	5221	TTTGGAAAGGTGAAGCGTGTGTGAGAAAGAACTCACAGAGATGTGTCTCTGTAGGAA	5280
D	5221	TTTGGAAAGGTGAAGCGTGTGTGAGAAAGAACTCACAGAGATGTGTCTCTGTAGGAA	5280
Q	5281	ACCTTTTTCCTTAAAGGCTATATCACTTCACTCAACTTGACTTTTATAC	5340
D	5281	ACCTTTTTCCTTAAAGGCTATATCACTTCACTTCACTTGACTTTTATAC	5340
Q	5341	ATGCTGTACATGAAGAAGTGTAGGCGCGCTCTCATAGGCTCTGGGAAAGACCAATA	5400
D	5341	ATGCTGTACATGAAGAAGTGTAGGCGCGCTCTCATAGGCTCTGGGAAAGACCAATA	5400
Q	5401	GGGGAAGGAATGTTATCTGAGAAATCTGACCGGCAAGGAAACTGTGTAGAGTCTCCCGG	5460
D	5401	GGGGAAGGAATGTTATCTGAGAAATCTGACCGGCAAGGAAACTGTGTAGAGTCTCCCGG	5460
Q	5461	AAGCAACAACAGGTGTTAAGTGAAGCACTCCAGGCTGGGCTCATGTATAAATAGGA	5520
D	5461	AAGCAACAACAGGTGTTAAGTGAAGCACTCCAGGCTGGGCTCATGTATAAATAGGA	5520
Q	5521	CAGAGCAAGGGAATAGCTACAAAGTTTCATAGGCTCCGAGTCTTAAAGTACAAA	5580
D	5521	CAGAGCAAGGGAATAGCTACAAAGTTTCATAGGCTCCGAGTCTTAAAGTACAAA	5580
Q	5581	TAGCTGCTTGGGCTTCTTAAACAAGAGTCTGGGAAGGCAAGTGAAGGGAATGG	5640
D	5581	TAGCTGCTTGGGCTTCTTAAACAAGAGTCTGGGAAGGCAAGTGAAGGGAATGG	5640

[illegible]

	TYPE: DNA	ORGANISM: Homo sapiens	FEATURE: 5'
Query Match	57.0%;	Score 4245.2;	DB 10; Length 5935;
Best Local Similarity	88.3%;	Pred. No. 0;	
Matches 5039;	Conservative 0;	Mismatches 178;	Indels 487; Gaps 20;
US-09-751-797-29			
1971	TACCATGCTACCGACGAAATGCTCCCTGATGTTTGGCTTTGCTCTCACTAAC	2030	
293	TACCATGCTATCCGACGACATGTTCCCTGATGTTTGGCTTTGCTCTCTCGCTAAC	352	
2031	AGGCTCCCTCTCACTATCAACGTGTGACCTTGCGGATCTCTGATGGCTGCTCGCA	2090	
353	AGGCTCCCTCTCACTATCAACGTGTGACCTTGCGGATGGGATGGCTGCTCGCA	412	
2091	GAAATCTATGAGTTTTCCTTATGGGAGACTTTGGCCGACGTGCTCTTCATATGC	2150	
413	GAAATCTATGAGTTTTCCTTATGGGAGACTTTGGCCGACGTGCTCTTCATATGC	472	
2151	CCTGTGGGCCGAGAGGCAAAATGCGTCCCGTCAACACCCGTGCAAGCTTGAAGTGC	2210	
473	CCTGTGGGCCGAGAGGCAAAATGCGTCCCGTCAACACCCGTGCAAGCTTGAAGTGC	532	
2211	CAACTTCGAGAGCCGATCATCTGTCACACCGACCTTTATGCTGGCCAAAGAGATACGCT	2270	
533	CAACTTCGAGAGCCGATCATCTGTCACACCGACCTTTATGCTGGCCAAAGAGATACGCT	592	
2271	GCATCTGCTTCTCCATACCGCCTTGCACTTTCTCTGAAAGCACTTGCAAACTTTAG	2330	
593	GCATCTGCTTCTCCATACCGCCTTGCACTTTCTCTGAAAGCACTTGCAAACTTTAG	651	
2331	GGGCGCTTATCTCCGAGAGTCTCACTACCTATGTTTCTGCTCTTTAGAGACTTTTA	2390	
652	GGGCGCTTATCTCCGAGAGTCTCACTACCTATGTTTCTGCTCTTTAGAGACTTTTA	711	
2391	AGGACTGGGCTTTTTCTTATTTCTATTTCAATTTCAAGGTCCTGAGACCACTTCTATCTTGGGCT	2450	
712	AGGACTGGGCTTTTTCTTATTTCTATTTCAAGGTCCTGAGACCACTTCTATCTTGGGCT	771	
2451	TCAGAGACATATCTGAAATTTTATCTAACAAGGCGCACTTAAAGGACCCACGACTG	2510	
772	TCAGAGACATATCTGAAATTTTATCTAACAAGGCGCTTTAAAGGACCCACGACTG	831	
2511	CAATACCTTCAATTTCTCTGTGCTCTCTTCTGAACTCATCTCTTGGCTACTCTCTAG	2570	
832	CAATACCTTCAATTTCTCTGTGCTCTCTTCTGAACTCATCTCTTGGCTACTCTCTAG	891	
2571	ACCACCTGGGACATACATCTCTAATTACAGGCTTTTCTTCCATCTCTTGTCAACCCAGG	2630	
892	ACCACCTGGGACATACATCTCTAATTACAGGCTTTTCTTCCATCTCTTGTCAACCCAGG	951	
2631	CACTTAAGGTTTTCTCTCTTTCAGGCGACCTTGCAAGTAAACAACAAGAGAGTCCGAGTC	2690	
952	CACTTAAGGTTTTCTCTCTTTCAGGCGACCTTGCAAGTAAACAACAAGAGAGTCCGAGTC	1011	
2691	ATCGGGAGAAACTGTTCCGAGAGTCACTGTAAGTCTCTCACTGATGAGACAGGCTAG	2750	
1012	ATCGGGAGAAACTGTTCCGAGAGTCACTGTAAGTCTCTCACTGATGAGAGAGGCTAG	1072	
2751	CTGCGGAGAGCTGTGAGACCTCTGTGGAGATGCTGACGATATGACCCCTGCTCTTCTTGC	2811	
1072	CTGCGGAGAGCTGTGAGACCTCTGTGGAGATGCTGACGATATGACCCCTGCTCTTCTTGC	1133	
2811	TACCTGACAGCTAAAGATCAAGTCACTGATGAGAGAGGAGTCAATTCACCCCTGGA	2870	
1132	TACCTGACAGCTAAAGATCAAGTCACTGATGAGAGAGGAGTCAATTCACCCCTGGA	1199	
2871	GACGTTCTGCTCCCGACAGTCAAGAGTTCAGCCCTCAATGACAGAGAGTGTACTTTC	2930	
1192	GACATTTCTGCTCCCGACAGTCAAGAGTTCAGCCCTCAATGACAGAGAGTGTGTGCTTTC	1251	

[illegible][illegible]

QY 3298 GTACAGTACTTGTGGGAGAGAAATCCAGTACAGTACTTGTGGATGAGATC 3357
DB 1310 GAAAGATCTAGCTGTGGAATGATCCATTGATCTTGTGGGAGAGGATGG 1369
QY 3358 CACTGAGTACAGTACTTGTGGGAGAGAGATGACAGAGCAAAAGTTGAGGAGG 3417
DB 1370 CATGAGAGAGAAATTGAGAGAGAAAGTGGAAATGGGAAAGCTTAA----- 1415
QY 3418 AAGATGAGAGAGGCTCATGTGGGGGTGTGAAAAGTCACTCTTTTCCATGTGATGAG 3477
DB 1416 -----GTGGGTGGGTGGGCTGGGAGAGTGGCTTGGCTGTGATGTATGAGGA 1460
QY 3478 AGTTAAGAAACCA-GTGTGTGAGTTTGTATGTCTTGAACACCCCAACATAGAAACAT 3536
DB 1461 AGCCACAAATCGAGAGGCGTGTGAACTTGATCCGCTGAACATTTGAAATATATAAAA 1520
QY 3537 ATCCAGAGAGGCGGAGAGACTGTGGAGACCTGGCATTTAGAGAGGCGC--GGCTTTT 3594
DB 1521 AGTTGAGTGAAGTGGGCGCCAGTAAAGCCCTAGAGCTTACTGAAGAGGCTTAATTT 1580
QY 3595 CACACGAGAACTTTATGCTCATCTTGTGTACACCTCCACCTTGTGATGAGTTAGC 3654
DB 1581 CACATGAGATGTTTATGTACATTTCTGTCTTGAAGTGAATTTCTGGAGATAGAT 1640
QY 3655 TCAAGTTGCTTTT-----ACGTTCTTGTCTACTGTGTGAAC 3693
DB 1641 TGAAGTTTATCTCTTACAGAAATTGCAATAACTCTCCGCTTTTCCACAAAGTCAAC 1700
QY 3694 TTCACTGAGATTTCCCAAGACGAGACAGCTCTTCTGTAGAGGAGGAGCTGATTTCA 3753
DB 1701 CTCACTGAGATTTCCCAAGAGTGAAGAGGCTCTTGTAGAGGAGAGTCTGATTTCTG 1760
QY 3754 GTGTCTAGAGAAAGAAATAGCTCAGAGAACTTGAAGTCAACGTGAATCTAGTCAACG 3813
DB 1761 GCGTCAAGGAAATTCAAGAGCTCAGAGAACTTGAAGTCACTGTGAATCTAGGTCATG 1820
QY 3814 GGGCAAAATGACTGAAGCGCTTATTTCAAGTGAACGCTCACTGCTCAGATATCTG 3873
DB 1821 TGGCAAAATTAATAAGAGCTTTAATTCAGGTGAATGTACTGAACCTTCATGAGGTG 1880
QY 3874 AGATATGGGCTCCACCGGATTAAGATCTGTAGTGA-GTGTGTTTATTTTGCACA 3932
DB 1881 GAGGTATTAAGTTTCAAGCAACATTAAGATAGTATGCTTGTATTTATTTATACCA 1940
QY 3933 CATAGCGGTGACACACAGAACTTCAAGAAATGTCAAGAGGCTGAAGAGACAGTGA 3992
DB 1941 TATGAAAGGTATGATCTGCAATCCAGAGATGTGAAAAGCTGAAGACAGCTGA 2000
QY 3993 AAAGTACTATTTGGCAAGCCCAATCTAAGCCATTCAATG--GAGACGTGGGATTT 4050
DB 2001 AAAGTAGAGCTGATTAATCTCAATGTCAATGCAATGAGAGAGCAATGTGTTT 2060
QY 4051 TTTCTGCTCCAGTCCCTTCACTTGTGAACATTTTATTTGATCTGTCACTATCTG 4110
DB 2061 TTTCTTCTTCTTCTTCTCCATCACTTGTGATTTTCACTTGTCTCTTCAACAG 2120
QY 4111 GTCACTTACGCTTACGACCTGTATCTTGTGAGTGTATAGATCTTTCAATCTGTG 4170
DB 2121 GGGCATTA-----CTTGTGTCTGTGATGTGATATATATATATATGATGTCAAGT 2176
QY 4171 TCTAAATTT--GTAACTACAAATCTGAGTGTAGAGAAAGCTTACCTCACTCTC 4227
DB 2177 TCCAAATCTTGAATTTGTAGAAATCTGAACTGTGGATCTTAAAGCTTGTCTATGTC 2236
QY 4228 ATGAGCACTGTCTGGAGAGATGCTTGAACAGAGTCAATGTAGAGAGCAGATCCCG 4287
DB 2237 ATTAACCTAGATTTGGGATGTGTAGTGTGAGAGATGAGGCTTAATGACAGTCTCTG 2296
QY 4288 ATTCCAGCTGTGAC--TTGCTAGTGGCCATGTGTATTAATCTTTGGCTGTATAGAT 4346
DB 2297 AATCCAGGACGACTTTTCCCGGTGTGATACAGATTAATTTTGTGTCAATTAATCT 2356
QY 4347 TTGGGAAA--GCCAGTTCCACGAGCTTACATATCTGAAAGAACATGATTTGAAAAC 4404

DB 2357 TAGGAAAATTGAGATTCATGACTCATGTATCTGAAAGATCTTGTAAAAACA 2416
QY 4405 GAAAGCTGGCA----CAACTACTAGATATATTTTGTAGCTCATTTAAACGATGCTC 4460
DB 2417 GAAAAATGCTTATGGGCAATTTATTTGAGTATATTTTGAAGTCAATTAATGATGCTT 2476
QY 4461 TGAATGTGGCAAAATCAACCCAGAAATTAACAACAAAGAGCTGATTTGCAATAGACA 4520
DB 2477 TGAATCTGAGAAATTAATCTCAGAAATTAAGAAAGAGCTGATTTGATAGGCT 2536
QY 4521 AGTATTTAGATCACTGTATTTAATAGCTATCATCTTAATTAATATAGGCTATATA 4580
DB 2537 AATTTCTGA-----GTATTAACACTATTTGATGATATATATATATATATATAT 2589
QY 4581 TATATTTAAGATTAACAAAGAGTGTATGCTTCCCAATTTACTTGGCTGTGTTCAA 4640
DB 2590 TTGATTTATGTTTAAAGCAAGAGCAGACAAAC--CCGATCTCTTTATACAGGTTCAAT 2648
QY 4641 AGATTAATAATACAGTACATGATTAATTAATAGTCAATGAAAGTATGATGAAACCC 4700
DB 2649 AGATTAATAATTAAGTAAAGATTTATATAGTAAATGAAAGTCTGAATGTATGCT 2708
QY 4701 TTTCTTACTTTTACCTCA-----TTCTTATGTTTTTTTTTTCTTCAACCTGTA 4752
DB 2709 TTTTCTTCTCTCTCTCCATCAAGACCTTCATTTAGTTCTTCTTCACTCCCTCA 2768
QY 4753 TCAAGCAGATGAAGCCTATCTGTGTGAGCTATTAATGACTTTACAGCAAAAC 4812
DB 2769 ACAATCCCTAGGAGATTTATTCATGATGTGGGTGTGTATCAATTTATATGTAATGAT 2828
QY 4813 ATTGCTGTGGCTCTTTTGGGAGAGAAACAGATGACAGAGGCTCAGGCTGACAGT 4872
DB 2829 ACAATCAATGTGGCTTATTTGGTAAAGAAACA--ACAATGAGAGCTTATGCTTAACAATA 2886
QY 4873 CTGACTTGGCTTAAAGCAGAGGATGTGATGACAGAGAAAGTGAAGCTTTTCGACAG 4932
DB 2887 GTGACTACCCCAAAACCGAGAGATGATTAAGAGAGTGAATGACGCTT--GCAG 2945
QY 4933 TGGGTGTCTTAATTAACAGAAACAGAAAGCTCCGCTGTATGAAATTAACATGAAGA- 4991
DB 2946 CAGGTACAATTAATCTCAGAAACATGAAGGCTCCAGATGTATGAATTTTCACTAACA 3005
QY 4992 -----TATCACTTATCTCTTATGCAACCTAATGCTCTCTTTCTGTG 5042
DB 3006 GCTTAACCTTAATTCCTCTTTTCTCTTGAATTTTAAAGGTTCTTCTGAG 3065
QY 5043 TGTAGGCTGATTAACACACTTGT--TTCTTTGAGTGTGATGCTTTGTAGATTTTAA 5100
DB 3066 CATCATTTATGAGTGTGACTGTTCTTCTTGTATTAATGAAGCTTTGTAGTTTAA 3125
QY 5101 GTGCTGTCCAGTCTTGT--TAGAGGTTTGTATCTTGAACCTGTGAGCTTGTGATTA 5158
DB 3126 TTTGAGAGCCAGTCTCTGTATTAAGAACTAATATAGACATGAGAGGCTGATATTA 3185
QY 5159 GCATGCCAAAGCAGACACTTGTGAATCCCTGTGTAAGATTTTAAAGTATTAATTAAT 5215
DB 3186 GCATGCCAACAAGAGGCTTTTCAACATCTTGTCTTAAAAATTAATCTGATTTCACTT 3245
QY 5216 -----TTGCTTGGAAAGTGAAGCGTGTGAGAAAGAACTGACAGAGATGTCT 5270
DB 3246 GCTTGTGTCTTTAGAAAGTGAAGTGTGAGAGAGAAATCTCATGTGA----- 3296
QY 5271 CTGTAGAAAATTTTTTTTCCCTTAATGCTTAATATCACTTCACTCA--ACTT 5327
DB 3297 -----TCTGTGATTTTCAAGACCTTTATATCATTTTGAAGATCAATTT 3342
QY 5328 TGACTTTATATACATGCTGTCAATGAAGAGTGTGAGGCGCTCTCATGAGGCTGTGG 5387
DB 3343 TCAATTTTGCATGAGGTTCCATGTGAAGAGTGTATGCTTTTGTCTGTGACTTCA 3402
QY 5388 AAAAGCACCAATAGGGAAGAAATGTATGCTGAGAAATCTGACCGGAGGAGAACTGCT 5447

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Db 3403 GAAGCA-CAGGAGGAGGACATGTTGTCAGAGAAAGATCAACAGAGAGAACTGT 3461
QY 5448 CAGAGCTCCCGAAGCA-----CCACAGGTGTTAAGTAGG 5485
Db 3462 CAGAGCTGTGAAATAGGGTGTGTTGGAGGCAATTAATTCCTCTGTTGGGGTAAA 3521
QY 5486 AACAGTCCAGGGTGGCTCATGTAAATAGAAACAGAGGAGGAAATAGCTCAA 5545
Db 3522 AGCGAAGCAGAGGTGTAGTAAAT-GCATGACAGCAGTAGGGGACGATTAACCTTAA 3580
QY 5546 AGTTCAAGAGGTC-CGAGCTCTTAAGATACAAATAGAGTC--TTGGGCTTCATACA 5602
Db 3581 AATCTTATATGTTTGGAGCTTTGAGATAGAAAAGAAATCTTTTGGCTTAATCTCA 3640
QY 5603 AAGAACTTGGGAGGAGCAGCAGTGAAGAGGAAATGAAAAGGAAAAACAGATAG 5662
Db 3641 AAGAAATAGGAAAG-----TGAAAGGCGGAGAAAGAACAGAAAGAAAG 3688
QY 5663 AGGACTGGAACAGCTACAAATCCTTACACAGCATTTTCTTGGAAACATTAAGAGT 5722
Db 3689 AACCATGTATTAATATAGAGCAATGCTGACAAAGTCTTCTGAAATTAATGCAATATG 3748
QY 5723 AGTGGATTAGGTGATGACAGGGGACTTGTGCTTGCATTTGAATCTGGGTTTTGTCT 5782
Db 3749 ATAGATTAGAGAAATTCAGTAGGAAATGCTTTTCACTTGAATTTGGGTTTCTCT--T 3805
QY 5783 CCATTGAGGTGAAAGCGTCACTTTTAACTCCCTGATGAGAGGAGAAAGAGGGTGT 5842
Db 3806 CGATTAGTTGGGATCCTCATGCTGATTTGACT---TGGAGGAGAAAGAAATGATGT 3861
QY 5843 TAGGACTCTTACTGAGCTTTTACTAGTTTACGATAGAAACAGACACTGGGACTCT 5902
Db 3862 TAGAGCTTAATCTGCTTTCTTCTTAACTAAAGCAATGAGAAAGACTTTTGTATTT 3921
QY 5903 CTGACAAAAAATGAAACCTGTTGTCTGTGTTTCTTTTGTAAAGAAC 5962
Db 3922 TTCCACAAAAGGAAATCTTTCTTTTACTGTTTGCAAAAGGTGAAATGAAAG 3981
QY 5963 AGGCAAGCCGACCAACATGGGTGATGAGGTCTTTGAGTCAAGCTTTGAGTTAG 6022
Db 3982 CTTAATGATGATGTAATCATGCTCAAAAGTCAATTTGATGAGATGTTTAAATCAG 4041
QY 6023 CACTCATCATAGT-----GATCATGCTCAGGTGAGGGC 6058
Db 4042 GAGTGTCAATCATTTGGCTTCCCTGACCACTTGAAGAAATGCTTGTGTACACAT 4101
QY 6059 TACCTGACAGCGAGCCCTGCTGCTGCACTTAAATCTCAGGCTCAGATCACT 6118
Db 4102 AAAATACAAACAATAGCTGATGAGCTAAAGAAATCCATGATTAATCTCATCTGTT 4161
QY 6119 TCCTGCTACTTACACAGTTAGAGGTTGACAAACCTTTTCTCC-----6163
Db 4162 TAGAAAGTTTATGAAATTTCTGTTAGGGTCAATCAAGCTGCTCTGGGCATGTGGGC 4221
QY 6164 -----AACCCCAATAAATTTAATTGACAAAGACTGTGTAATTG 6205
Db 4222 CTGTGGCTGAGGTTGAGCAAGCTCTTATAGTATCTGTCAATGATAGTTTGGAGC 4281
QY 6206 TGGATTCAGTGTGATTAATGA-----6227
Db 4282 TGCAAAACAGGCCAAGCATATAGGTGCACTCGGGATCCCAAGATCCCAAGCTCACT 4341
QY 6228 -----TCTATGTGATCTTGAAGAGTTCAATAGATAGATTAATAGGCCATCAACAG 6283
Db 4342 TCAGTCTCTGCTGCTGTTAAGAAAGGGGTGTCACCTCTGCGCCAGCTTTTAAACAGC 4401
QY 6284 TTTATGGGTGTAATAGCAATATATAGTAAATGCTGTGTGCTTAAAGTCAAAA 6343
Db 4402 TTATATAGTGTAGGTGACCTGAAATGATGCTGTGTGTGCT--CTAGTCAAGAGA 4460
QY 6344 GGCATGATTTTAAAGTCTTGGGCAATCATATTTACTCATGCTTAAAGAAATCATTTAGTT 6403
Db 4461 GCGGTATTTTAAAGCTCTTTGGCAATCATCAATACTTAAAGGAT-----T 4508

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QY 6404 GATTATTAATCTTTAGAGAGGCTGATATCTTGTTTGGTGTCTAGCAAGAAATGTCA 6463
Db 4509 TACTATGAATGTTTCAAAATGCTTAAATCGGTTTCTGTCTCCATCAACCTAATCTTG 4568
QY 6464 CCAGCTCTTTCTTACTGTAACCTTTAGAAAATGCTACTGTGCTCAAAATGGTTTGA 6523
Db 4569 CAATTTCT--AATTTGTTCACTTTAGAAAACATGCAATAAATGCTCAATACTTTTGA 4625
QY 6524 TTCTATTTTCAATAGCTGAGAGAGTGGAGATCAAGCCGATGAGGAACTGGAAGCTG 6583
Db 4626 TTCTTATTTTCAACGCTTTGAGAGAGTGGAGATCAAGCAATTTGAGAACTGGAATTTG 4685
QY 6584 CTGTTATATGCTCTGAGAAATGCTTGCCTGAGCAGAGAAAGCTAGAAACGAAAGAC 6643
Db 4686 CTGTTATATGCTCTGAGAAATGCTGCATTTGACAGAGCAAAAGCTGAAATGAAATTAAC 4745
QY 6644 TGCTCTCTCTGCTCTTCTTAAAGAACATTAATCTCCTGATGACTTTT 6695
Db 4746 TAACCCCTTCTCTCTGCTAGAAATTAACATTAATGATGCCCAAGCGATTTT 4797

RESULT 4
US-09-751-797-7
; Sequence 7, Application US/09751797
; Patent No. US20010024652A1
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
; FILE REFERENCE: LUD 5543.2
; CURRENT APPLICATION NUMBER: US/09/751, 797
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 09/419, 568
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US09/178, 973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 7
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; US-09-751-797-7

Query Match 8.1%; Score 601.4; DB 10; Length 1119;
Best Local Similarity 99.8%; Pred. No. 6.2e-126;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6535 ATAGCTTGAAGAGTGAAGATCAAGGCGATTTGGGGAACTGGACCTGCTGTTATGTC 6594
Db 510 AAGCTTGAAGAGTGAAGATCAAGGCGATTTGGGGAACTGGACCTGCTGTTATGTC 569
QY 6595 TCTGAGAAATGCTTGGCTGAGCGAGAAAGCTAGAAACGAAAGACTGCTCTTCT 6654
Db 570 TCTGAGAAATGCTTGGCTGAGCGAGAAAGCTAGAAACGAAAGACTGCTCTTCT 629
QY 6655 GCGTTTAAAGAAACATTAAGATCCCTGAATGAGACTTTTAACTAAAGAAAGTAGAA 6714
Db 630 GCGTTTAAAGAAACATTAAGATCCCTGAATGAGACTTTTAACTAAAGAAAGTAGAA 689
QY 6715 GCTAAGCTCATCATATTAAGAAATTTACATGAAACCTGGCTCAGTGAAGAAAGAAA 6774
Db 690 GCTAAGCTCATCATATTAAGAAATTTACATGAAACCTGGCTCAGTGAAGAAAGAAA 749
QY 6775 TAGTGTCAAGTTGTCATGAGACAGAGGTAGACTTGTATTAACACAAAGATTCATTGACA 6834
Db 750 TAGTGTCAAGTTGTCATGAGACAGAGGTAGACTTGTATTAACACAAAGATTCATTGACA 809
QY 6835 AATTTTATGTCATGATGATCAACAGAAATTAATGATCTTTAAAGAAATTTGTTGA 6894

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Db 810 ATATTATGTGCTGATGATACACAGAAAAATATGTAATTTGTTGAA 869
QY 6895 AGAGGTTACCTGCTCATTCCTTTAGAAAAAAGCTTATGTAATTCATTTCCATATGCA 6954
Db 870 AGAGGTTACCTGCTCATTCCTTTAGAAAAAAGCTTATGTAATTCATTTCCATATGCA 929
QY 6955 TATTTTATATGTAAGTTTATTTATATATGTAATTCATTTTATGTCAGTTTATTA 7014
Db 930 TATTTTATATGTAAGTTTATTTATATATGTAATTCATTTTATGTCAGTTTATTA 989
QY 7015 ATATGATTTTATTTATAGAAACATATCTGCTATGATATTTAGTATAGGCAATATATA 7074
Db 990 ATATGATTTTATTTATAGAAACATATCTGCTATGATATTTAGTATAGGCAATATATA 1049
QY 7075 TTTATGACATATACATGTAAGAAACAAGATATCTTAGGCTTTAATAACAACATGATATCAT 7134
Db 1050 TTTATGACATATACATGTAAGAAACAAGATATCTTAGGCTTTAATAACAACATGATATCAT 1109
QY 7135 AAA 7137
Db 1110 AAA 1112

RESULT 5

US-10-084-298-3
Sequence 3, Application US/10084298
Publication No. US2003009649A1

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth
APPLICANT: Pitman, Debra
APPLICANT: Fouser, Lynette
APPLICANT: Spaulding, Vikki
APPLICANT: Xuan, Dejun
TITLE OF INVENTION: Composition and Method for Treating Inflammatory
TITLE OF INVENTION: Disorders
FILE REFERENCE: G15358 CIP
CURRENT APPLICATION NUMBER: US/10/084,298
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/270,823
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/281,353
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/131,473
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 09/561,811
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 1166
TYPE: DNA
ORGANISM: Murine
US-10-084-298-3

Query Match 8.0%; Score 598.2; DB 15; Length 1166;
Best Local Similarity 99.5%; Pred. No. 3.4e-125;
Matches 600; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6535 ATAGCTTGAGAGAGTGGAGAGATCAAGCGATTTGGGGAACCTGGACCTGTTTATGTC 6594
Db 533 AAAGCTTGAGAGAGTGGAGAGATCAAGCGATTTGGGGAACCTGGACCTGTTTATGTC 592
QY 6595 TCTGAGAAATGCTTGCGTCTGAGCGAGAAAGCTTGAGAAACGAAAGCTGCTTCCCT 6654
Db 593 TCTGAGAAATGCTTGCGTCTGAGCGAGAAAGCTTGAGAAACGAAAGCTGCTTCCCT 652
QY 6655 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGGAATTTTATCTAAGAGAAAGTGA 6714
Db 653 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGGAATTTTATCTAAGAGAAAGTGA 712
QY 6715 GCTAAGTGCATATCATTTAGAAAGATTTTCAATGAACCTGGCTGCTGAAAGAA 6774
Db 713 GCTAAGTGCATATCATTTAGAAAGATTTTCAATGAACCTGGCTGCTGAAAGAA 772

QY 6775 TAGTTCAGCTTTCATGAGACGAGAGTGAAGTATGATTAACCAAGATTCATGCA 6834
Db 773 TAGTTCAGCTTTCATGAGACGAGAGTGAAGTATGATTAACCAAGATTCATGCA 832
QY 6835 ATATTTATTTGTCAGTGTATGATACACAGAAAAATTAATGATCTTTAAAAAATTTTGA 6894
Db 833 ATATTTATTTGTCAGTGTATGATACACAGAAAAATTAATGATCTTTAAAAAATTTTGA 892
QY 6895 AGAGGTTACCTGCTCATTCCTTTAGAAAAAAGCTTATGTAATTCATTTCCATATGCA 6954
Db 893 AGAGGTTACCTGCTCATTCCTTTAGAAAAAAGCTTATGTAATTCATTTCCATATGCA 952
QY 6955 TATTTTATATGTAAGTTTATTTATATATGTAATTCATTTTATGTCAGTTTATTA 7014
Db 953 TATTTTATATGTAAGTTTATTTATATATGTAATTCATTTTATGTCAGTTTATTA 1012
QY 7015 ATATGATTTTATTTATAGAAACATATCTGCTATGATATTTAGTATAGGCAATATATA 7074
Db 1013 ATATGATTTTATTTATAGAAACATATCTGCTATGATATTTAGTATAGGCAATATATA 1072
QY 7075 TTTATGACATATACATGTAAGAAACAAGATATCTTAGGCTTTAATAACAACATGATATCAT 7134
Db 1073 TTTATGACATATACATGTAAGAAACAAGATATCTTAGGCTTTAATAACAACATGATATCAT 1132
QY 7135 AAA 7137
Db 1133 AAA 1135

RESULT 6

US-09-751-797-9
Sequence 9, Application US/09751797
Patent No. US20010024652A1

GENERAL INFORMATION:

APPLICANT: Dumoulier, Laure
APPLICANT: Renauld, Jamile
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
TITLE OF INVENTION: (TfR) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/751,797
CURRENT FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 09/419,568
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-751-797-9

Query Match 7.5%; Score 555.2; DB 10; Length 1111;
Best Local Similarity 96.0%; Pred. No. 1.9e-115;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY 6535 ATAGCTTGAGAGAGTGGAGAGATCAAGCGATTTGGGGAACCTGGACCTGTTTATGTC 6594
Db 508 AAAGCTTGAGAGAGCGAGAGATCAAGCGATTCGGGGAACCTGGACCTGTTTATGTC 567
QY 6595 TCTGAGAAATGCTTGCGTCTGAGCGAGAAAGCTTGAGAAACGAAAGCTGCTTCCCT 6654
Db 568 TCTGAGAAATGCTTGCGTCTGAGCGAGAAAGCTTGAGAAACGAAAGCTGCTTCCCT 627
QY 6655 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGGAATTTTATCTAAGAGAAAGTGA 6714
Db 628 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGGAATTTTATCTAAGAGAAAGTGA 687
QY 6715 GCTAAGTGCATATCATTTAGAAAGATTTTCAATGAACCTGGCTGCTGAAAGAA 6774
Db 772 GCTAAGTGCATATCATTTAGAAAGATTTTCAATGAACCTGGCTGCTGAAAGAA 772

Db	668	GCTAACGTCACCATCATTTAGAGATTTCACTGAACCTGGCTCAGTTGAAGAGAA	747
Oy	6775	TAGTGTCAAGTTGTCCATGAGACCCAGAGTGAAGCTTGAATCAACAAGATTCATTGACA	6834
Db	748	TAGTGTCAAGTTGTCCATGAGACCCAGAGTGAAGCTTGAATCAACAAGATTCATTGACA	807
Oy	6835	ATATTTTATTTGTCACTGATGATACAAACAGAAAAATATGTAAGCTTTAAAAAATTGTTTGA	6894
Db	808	ATATTTTATTTGTCACTGATGATACAAACAGAAAAATATGTAAGCTTTAAAAAATTGTTTGA	867
Oy	6895	AGAGGTTACCTTCATTCCTTTAGAAAAAAGCTTATGTACCTTCATTCATATCCAA	6954
Db	868	AGAGGTTACCTTCATTCCTTCNAAAGAAAGCCTATGTAACTTCATTCATATCCAA	927
Oy	6955	TATTTTATATATGTAAGTTATTTATTTATTAAGTATACATTTTATTTATGTCAATTATTA	7014
Db	928	TACTTTATATATGTAAGTTATTTATTTATTAAGTATACATTTTATTTATGTCAATTATTA	987
Oy	7015	ATATGAGATTTATTTATAGAAACATTATCTGTAATGATATTT-AGTATPAAGCAAAATAT	7073
Db	988	ATATGAGATTTATTTATAGAAAAAATTATCTGATGTTGATTTAGATATPAAGCAAAATAT	1047
Oy	7074	ATTATATGCATTAAGTATAGAAAAACAGATATCTTAGGCTTTATATAAACATGTGATATCA	7133
Db	1048	ATTATATGATTAATCACTATAGAAACAGATATCTTAGGCTTTATATAAACATGTGATATCA	1107
Oy	7134	TAAA TAAA 7137	
Db	1108	TAAA 1111	

QY 6715 GCTAACGTCATCATATTGAGAAATTTCACATGAAACCTGCTCAGTTGAAAGAAA 6774
DB 688 GCTAACGTCACCATCATATTGAGAAATTTCACATGAAACCTGCTCAGTTGAAAGAAA 747
QY 6775 TAGTGCAGGTTGTCATGAGACCAAGGTGAGCTTGATPACACAAAGTTGATGAC 6834
DB 748 TAGTGCAGGTTGTCATGAGACCAAGGTGAGCTTGATPACACAAAGTTGATGAC 807
QY 6835 AATATTTATTTGTCATGATGATCAACAGAAAAATATGATCTTTAAAAATTTGTTGAA 6894
DB 808 AATATTTATTTGTCATGATGATCAACAGAAAAATATGATCTTTAAAAATTTGTTGAA 867
QY 6895 AGAGAGTTACCTCTCATCTTCCTTTGAAAAAGCTTATGTAATCTTCATTTCCATATCCA 6954
DB 868 AGAGAGTTACCTCTCATCTTCCTTTGAAAAAGCTTATGTAATCTTCATTTCCATATCCA 927
QY 6955 TATTTATATATGATGATGATTTATTTATATGATATCTTTATTTATGTCAGTTATTA 7014
DB 928 TATTTATATATGATGATGATTTATTTATATGATATCTTTATTTATGTCAGTTATTA 987
QY 7015 AATATGATTTATTTATGAAAAACATATCTGCTATGATATTT-AGTATAAGCAAAATAT 7073
DB 988 AATATGATTTATTTATGAAAAATATCTGATGATGATTTATTTAGATATAAGCAAAATAT 1047
QY 7074 ATT 7076
DB 1048 ATT 1050

RESULT 9

US-10-084-298-1
; Sequence 1, Application US/10084298
; Publication No. US2003009649A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Piltman, Debra
; APPLICANT: Fouser, Lynette
; APPLICANT: Spaulding, Vikki
; APPLICANT: Xuan, Dejun
; TITLE OF INVENTION: Composition and Method for Treating Inflammatory
; FILE OF INVENTION: Disorders
; FILE REFERENCE: G15358 CIP
; CURRENT APPLICATION NUMBER: US/10/084,298
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/270,823
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/281,353
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/111,473
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/561,811
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-084-298-1

Query Match 2.9%; Score 217.6; DB 15; Length 1191;
Best Local Similarity 70.9%; Pred. No. 8.3e-39;
Matches 454; Conservative 0; Mismatches 149; Indels 37; Gaps 11;
QY 6535 ATAGCTTGAGAGAGATGAGAGATCAAGCGATTGGGAACTGGACCTGCTGTTATGTC 6594
DB 529 AAGAGCTTGAGAGAGATGAGAGATCAAGCAATTTGGAATGCTGATTTGCTTATGTC 588
QY 6595 TCTGAGAAATGCTTGCTGCTGAGAGAGAGAAAGCTAGAAAAACGAGAACTGCTTCT 6654
DB 589 TCTGAGAAATGCTTGCTGCTGAGAGAGAAAGCTAGAAAAATGATTAATTAACCCCTTT 648

QY 6655 GCCTTCTAAAAAGAACAAATAGATCCCTGATGACTTTT-----ACTAAGAGAAAGTG 6710
DB 649 CCTTGCTAABAAATTAACATTAATGATGCCCAAGCATTTTTTTAAACCAAGAGATG 708
QY 6711 AGAAGCTAACGTCATCATCATTTAGAAATTTACATGAAACCTGCTCAGTTGAAAAAG 6770
DB 709 GGAAGCAAACTCATCATCATGATGGGGATTCCTAATGAAACCCGCTGATTTCAAAAG 768
QY 6771 AAAATGATGCA--GTTGTCATGAGACAG--AGTATGATCTGATTAACCAAGATTC 6827
DB 769 GAAACCAATGCCATTTGTTTATTAAGACCAAGGTAGACTTTTAAAGCATATGATTT 828
QY 6828 ATTGCAATATTTATTTGTCATGATG--ATACAGAGAAAAATATGATCTTTAA 6883
DB 829 ATTGATTAATTTATTTGATGATGATGTTCTTATACAGAAACATTTATTTTAAAT 888
QY 6884 AATGTTG-----AAAGAGTTACCTCTCATTTCTTTA---GAAAAAGCTTATG 6933
DB 889 AATGCTTTTCCATTAAGAAATTAATCTTCCATTTCCCTTATGGGAAAAACCCCTATA 948
QY 6934 TAACCTCA--TTCCATATCAATATTTATATATGAAAGTTATTTATTTATATATAT 6990
DB 949 TAGCTTCAATTTCCATATCAATCTTATATTTATTAATGATTTATTTATTTATATTA 1008
QY 6991 -----CATTTATTTATGTCAGTTATTTATATGATTTATTTATAGAAACATTTATG 7045
DB 1009 GACTGATTTTATTTATATCATTTATTAATGATTTATTTATAGAAACATTTATGCA 1068
QY 7046 TATGTATA--TTAGTATAAGCAATA--ATATTTATGACATTAATGATG-----AAAC 7097
DB 1069 TATGTACTTATGATGATAGGCTAATATTTATTTATTTATTTATTTATTTATTTAT 1128
QY 7098 AAGATATCTTAGGCTTTATTAATAACATGATATATATAA 7137
DB 1129 CATGTTATTTGACCTCATTAACACTTGATATCTTAA 1168

RESULT 10

US-09-728-911-14
; Sequence 14, Application US/09728911
; Patent No. US20020012669A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenteng
; APPLICANT: Kindesvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 99-93
; CURRENT APPLICATION NUMBER: US/09/728,911
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/169,049
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 60/232,219
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/244,610
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21)...(557)
US-09-728-911-14

Query Match 2.9%; Score 215.6; DB 10; Length 1116;
Best Local Similarity 70.8%; Pred. No. 2.3e-38;
Matches 452; Conservative 0; Mismatches 149; Indels 37; Gaps 11;
QY 6535 ATAGCTTGAGAGAGATGAGAGATCAAGCGATTGGGAACTGGACCTGCTGTTATGTC 6594

Db 479 AAAGCTTGAGAGAGAGAGAGATCAAGCAATTGGAGAACTGGATTGCTTTATGTC 538
QY 6595 TCTGAGAAATGCTTGGCTGTGACCGAGAAAGAGTGAAGAAACGAGAACTGCTTCCT 6654
Db 539 TCTGAGAAATGCTTGGCTGTGACCGAGAAAGAGTGAAGAAATGAGTAAACCCCTTC 598
QY 6655 GCCTTTTAAAGAAACATTAAGATCCCTGAATGACTTTT---ACTAAGAAAGAG 6710
Db 599 CCTGTGAGAAATTAAGATTAAGATGCCCCAAGCGATTTTAAACCAAGAAAGAG 658
QY 6711 AGAGCTAAGCTGCATCATCATTAAGAAATTCACATGAACCTGCTCAGTGAAGAG 6770
Db 659 GGAAGCAAACTGCATCATGATGAGGAGATCCAAATGAACCCCTGCTAGTACAAAG 718
QY 6771 AAAATAGTCA--GTGTCCATGAGACGAG--AGGTAGACTTGATTAACACAAAGATTC 6827
Db 719 GAAACCAATGCCACTTTGTTTATTAAGACCAAGATGAGCTTTGATGATGATATTT 778
QY 6828 ATTGAACAATTTTATTTGCTGACTGATG---ATACACAGAAATAATGACTTTAAA 6883
Db 779 ATTGAACAATTTTATTTGATTAAGCTGCTGCTTCTATACAGAAACAAATTAATTTTAAAT 838
QY 6884 AATTGTTT-----GAAAGAGGTACCTCTCATTCCTTTA---GAAAAAAGCTTATG 6933
Db 839 AATTGCTTTTCCATTAAGAAATTAATTTTCCATTCCTTTAGGGGAAAAACCCCTAAA 898
QY 6934 TTAACCTCA--TTTCCATATCCAAATTTTATATATATGATTAATTTATTAAGATA- 6990
Db 899 TACTCTCACTTCCATTAATCAGTACTTATATTTAATGATTAATTTATTTATTAATA 958
QY 6991 -----CATTTATTTATGCTGATTTATTAATGATTAATTTATTAAGAAACATTAATCTGC 7045
Db 959 GACTGCATTTTATTTATATATATTTTATTAATGATTAATTTATTAAGAAACATTAATCTCA 1018
QY 7046 TATTGATA--TTTGTATTAAGGCAATA--ATATTATGCAATAATCTATG---AAAC 7097
Db 1019 TATTGCTACTTGAGTGAAGCTTAATTTATTTATTAAGCAATTAATTAAGCTATAA 1078
QY 7098 AAGATATCTTAGCTTTAATTAACATGATATATCA 7135
Db 1079 CATGTTTATTGACCTCAATTAACATGATATCTCA 1116

RESULT 11
US-10-090-365-14
; Sequence 14, Application US/10090365
; Publication No. US2003007706A1
GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindesvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Mouse Cytokine Receptor
; FILE REFERENCE: 01-08
; CURRENT APPLICATION NUMBER: US/10/090,365
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/273,035
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/279,232
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21)...(557)
US-10-090-365-14

Query Match 2.9%; Score 215.6; DB 15; Length 1116;
Best Local Similarity 70.8%; Pred. No. 2.3e-38;

Matches 452; Conservative 0; Mismatches 149; Indels 37; Gaps 11;
QY 6535 ATAGCTTGAGAGAGAGATCAAGCAATTGGAGAACTGGATTGCTTTATGTC 6594
Db 479 AAAGCTTGAGAGAGAGATCAAGCAATTGGAGAACTGGATTGCTTTATGTC 538
QY 6595 TCTGAGAAATGCTTGGCTGTGACCGAGAAAGAGTGAAGAAACGAGAACTGCTTCCT 6654
Db 539 TCTGAGAAATGCTTGGCTGTGACCGAGAAAGAGTGAAGAAATGAGTAAACCCCTTC 598
QY 6655 GCCTTTTAAAGAAACATTAAGATCCCTGAATGACTTTT---ACTAAGAAAGAG 6710
Db 599 CCTGTGAGAAATTAAGATTAAGATGCCCCAAGCGATTTTAAACCAAGAAAGAG 658
QY 6711 AGAGCTAAGCTGCATCATCATTAAGAAATTCACATGAACCTGCTCAGTGAAGAG 6770
Db 659 GGAAGCAAACTGCATCATGATGAGGAGATCCAAATGAACCCCTGCTAGTACAAAG 718
QY 6771 AAAATAGTCA--GTGTCCATGAGACGAG--AGGTAGACTTGATTAACACAAAGATTC 6827
Db 719 GAAACCAATGCCACTTTGTTTATTAAGACCAAGATGAGCTTTGATGATGATATTT 778
QY 6828 ATTGAACAATTTTATTTGCTGACTGATG---ATACACAGAAATAATGACTTTAAA 6883
Db 779 ATTGAACAATTTTATTTGATTAAGCTGCTGCTTCTATACAGAAACAAATTAATTTTAAAT 838
QY 6884 AATTGTTT-----GAAAGAGGTACCTCTCATTCCTTTA---GAAAAAAGCTTATG 6933
Db 839 AATTGCTTTTCCATTAAGAAATTAATTTTCCATTCCTTTAGGGGAAAAACCCCTAAA 898
QY 6934 TTAACCTCA--TTTCCATATCCAAATTTTATATATATGATTAATTTATTAAGATA- 6990
Db 899 TACTCTCACTTCCATTAATCAGTACTTATATTTAATGATTAATTTATTTATTAATA 958
QY 6991 -----CATTTATTTATGCTGATTTATTAATGATTAATTTATTAAGAAACATTAATCTGC 7045
Db 959 GACTGCATTTTATTTATATATTTTATTAATGATTAATTTATTAAGAAACATTAATCTCA 1018
QY 7046 TATTGATA--TTTGTATTAAGGCAATA--ATATTATGCAATAATCTATG---AAAC 7097
Db 1019 TATTGCTACTTGAGTGAAGCTTAATTTATTTATTAAGCAATTAATTAAGCTATAA 1078
QY 7098 AAGATATCTTAGCTTTAATTAACATGATATATCA 7135
Db 1079 CATGTTTATTGACCTCAATTAACATGATATCTCA 1116

RESULT 12
US-10-104-919-14
; Sequence 14, Application US/10104919
; Publication No. US2003009608A1
GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Kindesvogel, Wayne
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 01-12
; CURRENT APPLICATION NUMBER: US/10/104,919
; PRIOR FILING DATE: 2002-03-23
; PRIOR APPLICATION NUMBER: US 60/279,222
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21)...(557)
US-10-104-919-14

Query Match 2.9%; Score 215.6; DB 15; Length 1116;
 Best Local Similarity 70.8%; Pred. No. 2.3e-38;
 Matches 452; Conservative 0; Mismatches 149; Indels 37; Gaps 11;

6535 ATAGCTTGAGAGAGAGAGATCAAGCGATTGGGAACTGAGCTGTGTTATGTC 6594
 479 AAGCTTGAGAGAGAGAGATCAAGCGATTGGGAACTGAGCTGTGTTATGTC 538
 6595 TCTGAGAAATGCTGCGTGTGAGCGAGAAAGCTGAGAAACGAGAACTGCTCTTCT 6654
 539 TCTGAGAAATGCTGCGTGTGAGCGAGAAAGCTGAGAAACGAGAACTGCTCTTCT 598
 6655 GCCTCTGAGAAATGCTGCGTGTGAGCGAGAAAGCTGAGAAACGAGAACTGCTCTTCT 6710
 599 CCTGCTGAGAAATGCTGCGTGTGAGCGAGAAAGCTGAGAAACGAGAACTGCTCTTCT 658
 6711 AGAAGCTAAGCTGATCATCATTAAGAAATTCACATGAAACCTGCTGAGTGAAG 6770
 659 GGAAGCAAACTCCATCATGATGAGTGGATTCAGAAATGAAACCTGCTGAGTGAAG 718
 6771 AAAATAGTCA--GTGTCATGAGACAG--AGTAGACTGATTAACCAAGATTC 6827
 719 GAAGCAATGCCACTTTGTTATAGACCAAGAGTAGACTTTCTAGATGATATT 778
 6828 ATTGACAAATTTTATGTCAGTATG---ATACACAGAAATATGACTTTAAA 6883
 779 ATTGATTAATTTTATGTCAGTATG---ATACACAGAAATATGACTTTAAA 838
 6884 AATTGTT-----GAAAGAGTAACTCTCATCTCTTA---GAAAAAGCTTATG 6933
 839 AATTGCTTTTCCATTAAGAAATGATTAATTTTAAAGGAGGAAAAACCCCTAAA 898
 6934 TAATCTCA--TTTCCATATCCAAATTTTATATGATGATTTTATTAAGATTA- 6990
 899 TACTCTAGTTTCCATTAAGAAATGATTAATTTTAAAGGATTTTATTAATTA 958
 6991 -----CATTTATTTATGTCAGTTTATTAATGATTTTATTAAGAACTATGTC 7045
 959 GACTGCATTTTATTAATGATTTTATTAATGATTTTATTAAGAACTATGTC 1018
 7046 TATTGATA--TTAGTATAGGCAATA--ATATTATGACATACTATG---AAAC 7097
 1019 TATTGCTACTGAGTGAAGCTAATATTGATTTTATGCAATTAATTATAGACTATA 1078
 7098 AAGATATCTTAGGCTTTAATTAACATGATATCATA 7135
 1079 CATGTTATTGACCTCAATTAACATGATATCTTA 1116

RESULT 13
 US-09-870-574-1
 ; Sequence 1, Application US/09870574
 ; Patient No. US20020102723A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Auecin L.
 ; APPLICANT: Aggarwal, Sudeepa
 ; APPLICANT: Xie, Ming-Hong
 ; APPLICANT: Maruoka, Ellen M.
 ; APPLICANT: Foster, Jessica S.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: INTERLEUKIN-22 POLYPEPTIDES, NUCLEIC ACIDS ENCODING
 ; TITLE OF INVENTION: THE SAME AND METHODS FOR THE TREATMENT OF PANCREATIC DISORDERS
 ; FILE REFERENCE: P2806-1(US)
 ; CURRENT APPLICATION NUMBER: US/09/870, 574
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: US 60/169, 495
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 7
 ; SEQ ID NO 1
 ; LENGTH: 1152
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-09-870-574-1

Query Match 2.9%; Score 214.2; DB 11; Length 1152;
 Best Local Similarity 70.9%; Pred. No. 4.8e-38;
 Matches 450; Conservative 0; Mismatches 148; Indels 37; Gaps 11;

6535 ATAGCTTGAGAGAGAGAGATCAAGCGATTGGGAACTGAGCTGTGTTATGTC 6594
 516 AAGCTTGAGAGAGAGAGATCAAGCGATTGGGAACTGAGCTGTGTTATGTC 575
 6595 TCTGAGAAATGCTGCGTGTGAGCGAGAAAGCTGAGAAACGAGAACTGCTCTTCT 6654
 576 TCTGAGAAATGCTGCGTGTGAGCGAGAAAGCTGAGAAACGAGAACTGCTCTTCT 635
 6655 GCCTCTGAGAAATGCTGCGTGTGAGCGAGAAAGCTGAGAAACGAGAACTGCTCTTCT 6710
 636 CCTGCTGAGAAATGCTGCGTGTGAGCGAGAAAGCTGAGAAACGAGAACTGCTCTTCT 695
 6711 AGAAGCTAAGCTGATCATCATTAAGAAATTCACATGAAACCTGCTGAGTGAAG 6770
 696 GGAAGCAAACTCCATCATGATGAGTGGATTCAGAAATGAAACCTGCTGAGTGAAG 755
 6771 AAAATAGTCA--GTGTCATGAGACAG--AGTAGACTGATTAACCAAGATTC 6827
 756 GAAGCAATGCCACTTTGTTATAGACCAAGAGTAGACTTTTAAAGCATGATATT 815
 6828 ATTGACAAATTTTATGTCAGTATG---ATACACAGAAATATGACTTTAAA 6883
 816 ATTGATTAATTTTATGTCAGTATG---ATACACAGAAATATGACTTTAAA 875
 6884 AATTGTT-----GAAAGAGTAACTCTCATCTCTTA---GAAAAAGCTTATG 6933
 876 AATTGCTTTTCCATTAAGAAATGATTAATTTTAAAGGAGGAAAAACCCCTAAA 935
 6934 TAATCTCA--TTTCCATATCCAAATTTTATATGATGATTTTATTAAGATTA- 6990
 936 TACTCTAGTTTCCATTAAGAAATGATTAATTTTAAAGGATTTTATTAATTA 995
 6991 -----CATTTATTTATGTCAGTTTATTAATGATTTTATTAAGAACTATGTC 7045
 996 GACTGCATTTTATTAATGATTTTATTAATGATTTTATTAAGAACTATGTC 1055
 7046 TATTGATA--TTAGTATAGGCAATA--ATATTATGACATACTATG---AAAC 7097
 1056 TATTGCTACTGAGTGAAGCTAATATTGATTTTATGCAATTAATTATAGACTATA 1115
 7098 AAGATATCTTAGGCTTTAATTAACATGATATCATA 7132
 1116 CATGTTATTGACCTCAATTAACATGATATCTTA 1150

RESULT 14
 US-10-063-588-153
 ; Sequence 153, Application US/10063588
 ; Publication No. US20030130483A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Flivaroff, Ellen
 ; APPLICANT: Gerlitsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Maruoka, Ellen M.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P323081C1

PRIOR FILING DATE: 1998-09-10


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Db      876 AATTGCTTTTCCATAAAAAAGATTACTTCCATTCCTTAGGGAAAAAACCCCTAA 935
QY      6934 TAACTCA--TTCCATATCCATATTTATATATGTAAGTTATTATTATTAAGTATA- 6990
Db      936 TAGCTTCAGTGTTCATTAATCAGTACTTATATTTAATAATGTAATTATTATTATAA 995
QY      6991 ----CATTTAATTATGTCAGTTTATATATGATTTATTATAGAAAACATTATCTGC 7045
Db      996 GACTGCATTTTATTATATCATTTTATTATATGATTTATTATAGAAAACATCATTCGA 1055
QY      7046 TATTGATA-TTAGTATAAGGCAATA--ATATTATGACAATAACTATG---AAAC 7097
Db      1056 TATTGCTACTGAGTGAAGGCTAATATTGATATTATGACAATAATATTAGAGCTATA 1115
QY      7098 AAGATATCTTAGGCTTTAATAAACACATGATATC 7132
Db      1116 CATGTTATTGACCTCAATAAACCTTGATATC 1150

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Search completed: July 20, 2003, 03:46:00
 Job time : 1087.35 secs

QY 149 CTGGTACAGGAGAGACAGCTGCGCCCATCAGCTCCCACTGCAAGGTTGACAAGTCCA 208
DB 129 GTGGGCCCAAGAGCAATGCGCTGCGCCGTCACACCCGGTGCAAGCTTGAGGTGTCAA 188
QY 209 CTTCCAGCAGCCCTATATCAGCAACCGCCTTCATGCTGCTAAGGAG 258
DB 189 CTTCCAGCAGCCGTACATGCTCAACCGCCTTTATGCTGGCCAGGAG 238

Search completed: July 19, 2003, 19:48:41
Job time : 189.24 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:07:55 ; Search time 234.726 Seconds
(without alignments)
9727.122 Million cell updates/sec

Title: US-09-751-797-8

Sequence: 1 gttctaccctcgttaagat.....gatttaattatgtgtat 7445

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7445	100.0	7445	4	US-09-178-973B-8
2	7445	100.0	7445	4	US-09-419-568F-8
3	7445	100.0	7445	4	US-09-354-243B-8
4	4245.2	57.0	5935	4	US-09-178-973B-17
5	4245.2	57.0	5935	4	US-09-419-568F-29
6	4245.2	57.0	5935	4	US-09-354-243B-29
7	686	9.2	4797	4	US-09-419-568F-25
8	686	9.2	4797	4	US-09-354-243B-25
9	601.4	8.1	1119	4	US-09-178-973B-7
10	601.4	8.1	1119	4	US-09-419-568F-7
11	601.4	8.1	1119	4	US-09-354-243B-7
12	555.2	7.5	1111	4	US-09-178-973B-9
13	555.2	7.5	1111	4	US-09-419-568F-9
14	555.2	7.5	1111	4	US-09-354-243B-9
15	126	1.7	690	4	US-09-419-568F-24
16	126	1.7	690	4	US-09-354-243B-24
17	75.8	1.0	48974	4	US-08-920-422-17
18	73.8	1.0	7218	1	US-08-233-463-14
19	70	0.9	7218	1	US-08-233-463-14
20	68.8	0.9	16442	3	US-08-781-891-208
21	59.2	0.8	96050	4	US-09-245-041-5
22	57.8	0.8	10409	3	US-08-772-440-33
23	57.6	0.8	10614	1	US-08-135-511-35
24	57.6	0.8	10614	1	US-08-187-453-35
25	57.2	0.8	2272	3	US-08-147-592A-3
26	57.2	0.8	2272	3	US-08-292-694A-3
27	56.8	0.8	48974	4	US-08-920-422-17

C	28	56.8	0.8	90050	4	US-09-245-041-5	Sequence 5, Appl
	29	56.2	0.8	4765	3	US-08-936-135-21	Sequence 21, Appl
	30	56.2	0.8	4780	3	US-08-936-135-23	Sequence 23, Appl
	31	56.2	0.8	37950	4	US-09-338-907-183	Sequence 183, Appl
	32	56.2	0.8	37950	4	US-09-218-207-183	Sequence 183, Appl
	33	55	0.7	5852	1	US-07-667-106-2	Sequence 2, Appl
	34	55	0.7	17056	4	US-09-245-041-5	Sequence 3, Appl
C	35	54.8	0.7	3205	4	US-09-061-768A-3	Sequence 2, Appl
	36	54.8	0.7	5109	4	US-08-930-055A-2	Sequence 2, Appl
	37	54.8	0.7	7874	4	US-09-780-175-96	Sequence 96, Appl
	38	54.2	0.7	13011	2	US-08-791-849A-14	Sequence 14, Appl
C	39	54.2	0.7	169998	4	US-09-676-610B-24	Sequence 24, Appl
	40	53.2	0.7	6727	3	US-08-629-643A-5	Sequence 5, Appl
	41	53.2	0.7	6727	3	US-09-280-799-1	Sequence 1, Appl
	42	53.2	0.7	6727	4	US-09-155-884-5	Sequence 5, Appl
	43	53	0.7	586	4	US-09-227-357-103	Sequence 103, Appl
	44	52.6	0.7	4526	1	US-07-855-412B-4	Sequence 4, Appl
	45	52.6	0.7	4526	2	US-08-308-887A-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1									
US-09-178-973B-8									
Sequence 8, Application US/09178973B									
Patent No. 6274710									
GENERAL INFORMATION:									
APPLICANT: Dumoutier, Laure									
APPLICANT: Renauld, Jean-Christophe									
TITLE OF INVENTION: (Isolated) Nucleic Acid Molecules which Encode T Cell Inducible F									
FILE REFERENCE: LUD 5543									
CURRENT APPLICATION NUMBER: US/09/178.973B									
CURRENT FILING DATE: 1998-10-26									
NUMBER OF SEQ ID NOS: 17									
SEQ ID NO 8									
LENGTH: 7445									
TYPE: DNA									
ORGANISM: Mus musculus									
US-09-178-973B-8									
Query Match									
Best Local Similarity 100.0%; Score 7445; DB 4; Length 7445;									
Matches 7445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	GTCTATACCTGCTTAAGATTCTTCTAATTTATTAATAAACTATTCTTAATGAAA	60						
DB	1	GTCATACCTGCTTAAGATTCTTCTAATTTATTAATAAACTATTCTTAATGAAA	60						
QY	61	GCAACGACGAGTATTTAGAGTGTCTTGACGACGAGTACAGAGTGAAGG	120						
DB	61	GCAACGACGAGTATTTAGAGTGTCTTGACGACGAGTACAGAGTGAAGG	120						
QY	121	TAAAGGCGTATTTAGAGTATTAACCAATGTTATGTTCTTCTGCAAGCAACT	180						
DB	121	TAAAGGCGTATTTAGAGTATTAACCAATGTTATGTTCTTCTGCAAGCAACT	180						
QY	181	TGAATGTATGCTTAACAATCTTCAAGCTCTTAATATGCTTAACGATGAGTCCG	240						
DB	181	TGAATGTATGCTTAACAATCTTCAAGCTCTTAATATGCTTAACGATGAGTCCG	240						
QY	241	CTGCTGCAACGAGCTCTTGACGAGCTCTCTGTTGCAATTTATGTTCTTGA	300						
DB	241	CTGCTGCAACGAGCTCTTGACGAGCTCTCTGTTGCAATTTATGTTCTTGA	300						
QY	301	TCGATCCCAACCTCTACCTTCTGCTCTGATGAGGACCTTCACTTTCTGCAATTA	360						
DB	301	TCGATCCCAACCTCTACCTTCTGCTCTGATGAGGACCTTCACTTTCTGCAATTA	360						
QY	361	TGAATCCATGTTTAAATCTTTTAAATATATTCACAAATCATGATGTTGCAAGTC	420						

Db 361 TGAATCCATGTTTAACTTTTAAATAATATACACAATCATGTTTGTGCAATGC 420
Qy 421 TGTTCACCCACATGATATGTCTGTGCACCAAGTGTGCTGCTGTGTTGGGGGCAAGA 480
Db 421 TGTTCACCCACATGATATGTCTGTGCACCAAGTGTGCTGCTGTGTTGGGGGCAAGA 480
Qy 481 GCAGAGAGAGGGTGCCTTGGCACCAGAGTCAAGGATGTTGTGAGCCACATGAGGATGCT 540
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Qy 541 GGGAGTTAGACCCCAAGGTCCTCCAGAAATGACCAATGCTCTTAAACACAGCAGGCAATT 600
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RESULT 2

US-09-419-568F-8

Sequence 8, Application US/09419568F

Patent No. 6331613
 GENERAL INFORMATION:
 APPLICANT: Dumoulier, Laure
 APPLICANT: Loubet, Jamila
 APPLICANT: Renaud, Jean-Christophe
 TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
 FILE REFERENCE: LUD 5543.2
 CURRENT FILING DATE: 1999-10-18
 PRIOR FILING DATE: 1999-07-16
 PRIOR FILING DATE: 1999-07-16
 PRIOR APPLICATION NUMBER: US09/178,973
 PRIOR FILING DATE: 1998-10-26
 NUMBER OF SEQ ID NOS: 29
 SEQ ID NO 8
 LENGTH: 7445
 TYPE: DNA
 ORGANISM: Mus musculus
 FEATURE:
 US-09-419-568F-8

Query Match 100.0%; Score 7445; DB 4; Length 7445;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 7445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 121 TAAGAGGCGCTATTATAGCATTAACCAACATGTTAATGTTTCTTCTGGCAACCAACT 180
 QY 181 TGAATCTATGCTTAATAACATCTTCAAGCTCTTAATATAGTGTAAAGCATGAGTCCG 240
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 QY 301 TCGATCCCAACCTCTGACCTTGGCTCTGATGSCCACTTGAACCTTCTGATTTA 360
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 DB 481 GCAGAGAGGAGTGCCTGCGCAACGAGTCAAGATGTTGTGACCCATGAGATGCT 540
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 DB 661 TTCACTCACTGCCACTTCCCTTTGCAATCTTTCTGCAAGAGAACCAAAAGCAAGAT 720
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 DB 721 CCCCACTGCTTTGCTGCTCTCAAGTGTGCACTCTTCAAGGTCAGATTTCTCAAGTGT 780
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 DB 841 CTCGAGTCCCTCTTAACATTTTGAATGATCTCAATAGCTGAGGAGGAGAAATCTCACACA 900
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 DB 1021 GGATTCAGTGTACATATGCAATGCAAAATATCCAGATTTTGAATATCTCTTCTTCAACT 1080
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 DB 1081 ATCCATCTATATAGTATGTTATGAGGCTCAATTTAAAAAATATTTTGAAGCTTAAGC 1140
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Qy 3901 TCTGTATGATGTCTCTTTTATTTTGCAGACATACGCGGTGACGACCAATCCAG 3960
Db 3901 TCTGTATGATGTCTCTTTTATTTTGCAGACATACGCGGTGACGACCAATCCAG 3960
Qy 3961 AAGATGTCAAGAGGCTGAAGAGACAGTGAAGAAAGTACTATTGGCAAGCAAAATCT 4020
Db 3961 AAGATGTCAAGAGGCTGAAGAGACAGTGAAGAAAGTACTATTGGCAAGCAAAATCT 4020
Qy 4021 AAGCATTCAGTGAAGAGCCTGGGATTTCTTTCTCTGCTTCCAGTCCCTTCTACTTTG 4080
Db 4021 AAGCATTCAGTGAAGAGCCTGGGATTTCTTTCTCTGCTTCCAGTCCCTTCTACTTTG 4080
Qy 4081 TAAATTTTATTTAGTCTGTCTATCTATCTGTGCTATTAAGTCTAGTCAAGCTGATC 4140
Db 4081 TAAATTTTATTTAGTCTGTCTATCTATCTGTGCTATTAAGTCTAGTCAAGCTGATC 4140
Qy 4141 TAGCTGGGTCTATAGATCTTCAATCTGTCTAAATTTGATGACAAATTTGAGACT 4200
Db 4141 TAGCTGGGTCTATAGATCTTCAATCTGTCTAAATTTGATGACAAATTTGAGACT 4200

QY	4201	GGCGAAAGCTTACGTCAGCCAGCTCACTGAGCACTTGCCTGGAGAGATGGCTTGTGACAG	4250
Db	4201	AGCGAAAGCTTACGTCAGCCAGCTCACTGAGCACTTGCCTGGAGAGATGGCTTGTGACAG	4250
QY	4261	AGTCAAATGCTGAAGAAGACAGCATCCCTGATTTCCCAAGCTGTGACACTTGTGGCCATGT	4320
Db	4261	AGTCAAATGCTGAAGAAGACAGCATCCCTGATTTCCCAAGCTGTGACACTTGTGGCCATGT	4320
QY	4321	GTAATTACTTTGGCTTGAATTAGATTATTTGGGAAAGCCAGTTCCACGGAAGCTTACATATC	4380
Db	4321	GTAATTACTTTGGCTTGAATTAGATTATTTGGGAAAGCCAGTTCCACGGAAGCTTACATATC	4380
QY	4381	TGAAGAACCATGCATTTGAAAATCTGAAAGCTGGGGCAAACTTACTAGATGATTTTGG	4440
Db	4381	TGAAGAACCATGCATTTGAAAATCTGAAAGCTGGGGCAAACTTACTAGATGATTTTGG	4440
QY	4441	AGCTCATTTAAACGAGTGCCTGAAATGAGGAAATCAACCCAGATTAACAACAAAGAG	4500
Db	4441	AGCTCATTTAAACGAGTGCCTGAAATGAGGAAATCAACCCAGATTAACAACAAAGAG	4500
QY	4501	CTGATTTTGCAAATAGGACAGATATTTAGATTCACCTGGATTTAAATAGCTATCATCTTAAT	4560
Db	4501	CTGATTTTGCAAATAGGACAGATATTTAGATTCACCTGGATTTAAATAGCTATCATCTTAAT	4560
QY	4561	TAAATATATAGGCGCTATATATATATTTAAGATTAAACAAGAGTGATAGCCCTCCAAAT	4620
Db	4561	TAAATATATAGGCGCTATATATATATTTAAGATTAAACAAGAGTGATAGCCCTCCAAAT	4620
QY	4621	TTACTTGGCCCTGATTTCAAAGAGTAAATATATAGCATAGATTAATATATAGTCAATG	4680
Db	4621	TTACTTGGCCCTGATTTCAAAGAGTAAATATATAGCATAGATTAATATATAGTCAATG	4680
QY	4681	AAAGTATAGATGAGAAACCTTTCCCTTACTTTTAACTTCACTTTTCTTAACTTTTCTTTC	4740
Db	4681	AAAGTATAGATGAGAAACCTTTCCCTTACTTTTAACTTCACTTTTCTTAACTTTTCTTTC	4740
QY	4741	TTCAACCCCTGATCAAGCCACTAGTAGCAACTATCTGCTGAGCTATTTATATAGACTTT	4800
Db	4741	TTCAACCCCTGATCAAGCCACTAGTAGCAACTATCTGCTGAGCTATTTATATAGACTTT	4800
QY	4801	ACACGAACCAATTTGCTGTGTGGCTCTTTTGGGAAAGGAAACAGATACAGAGAGCTC	4860
Db	4801	ACACGAACCAATTTGCTGTGTGGCTCTTTTGGGAAAGGAAACAGATACAGAGAGCTC	4860
QY	4861	AGGCTAGCAATCTGACTTGCCTTAAACCCAGAGGATGATTTGATAGCAGAGAAGTGAAG	4920
Db	4861	AGGCTAGCAATCTGACTTGCCTTAAACCCAGAGGATGATTTGATAGCAGAGAAGTGAAG	4920
QY	4921	GCTCTTCGCAAGTGGGTGCTTAAAGTATCAGAAACAGAAAGGCTCCGATTTGAATGAT	4980
Db	4921	GCTCTTCGCAAGTGGGTGCTTAAAGTATCAGAAACAGAAAGGCTCCGATTTGAATGAT	4980
QY	4981	TATCAGTAAATATCTACCTTATCTCTTCTATGAACTTAAATCGTCTCTTTTCTTGG	5040
Db	4981	TATCAGTAAATATCTACCTTATCTCTTCTATGAACTTAAATCGTCTCTTTTCTTGG	5040
QY	5041	TGTGAGAGCTGATTAACAACACTGTGTTCTTTTGAGTGTATAGCTTTGTAGATTTTGA	5100
Db	5041	TGTGAGAGCTGATTAACAACACTGTGTTCTTTTGAGTGTATAGCTTTGTAGATTTTGA	5100
QY	5101	GTCCTCTGCAAGTCTTGTATAGAGGTTGTTCACCTTGACAACCTGGGCTTGGATGTTAGC	5160
Db	5101	GTCCTCTGCAAGTCTTGTATAGAGGTTGTTCACCTTGACAACCTGGGCTTGGATGTTAGC	5160
QY	5161	ATGCCAAAGGCAACACTTTCTGAATGCTGTGTAAAGATTATTTATTTACTTTTGTGC	5220
Db	5161	ATGCCAAAGGCAACACTTTCTGAATGCTGTGTAAAGATTATTTATTTACTTTTGTGC	5220
QY	5221	TTTGGAAAGGTGAACGCTGTGTGAGAAAGAACTCAGAGAGTGTGTTCTCTGTAGAGAA	5280
Db	5221	TTTGGAAAGGTGAACGCTGTGTGTGAGAAAGAACTCAGAGAGTGTGTTCTCTGTAGAGAA	5280
QY	5281	ACTTTTTTTTTCCCTTAAATGCTATATATCCACTTTCAGTCAACTTTGACTTTTATATAC	5340

Db	5281	ACTTTTTCCTTCCCTTAATGCTTAATTCACCTTTTCAGTCAACTTTCATTATACC	5340
Qy	5341	ATGCTGTCACTGTAAGAAGTGTTTAAGGCCGCTCTCATGCTCTGGGMAAAGCACATA	5400
Db	5341	ATGCTGTCACTGTAAGAAGTGTTTAAGGCCGCTCTCATGCTCTGGGMAAAGCACATA	5400
Qy	5401	GGGGAGGAATGTTATGCTGAGAAATCTGACCGGCAAGGAAACTGTCAGAGTCCCG	5460
Db	5401	GGGGAGGAATGTTATGCTGAGAAATCTGACCGGCAAGGAAACTGTCAGAGTCCCG	5460
Qy	5461	AAGACCCCAAGGTTAACTAGGAACAGTCCAGGGGGGCTCATGTAAATGAAATGGA	5520
Db	5461	AAGACCCCAAGGTTAACTAGGAACAGTCCAGGGGGGCTCATGTAAATGAAATGGA	5520
Qy	5521	CAGAGCGAGGAGATAAAGTACAAAGTTTATAGAGTCCGAGTCTTAAAGATACAAA	5580
Db	5521	CAGAGCGAGGAGATAAAGTACAAAGTTTATAGAGTCCGAGTCTTAAAGATACAAA	5580
Qy	5581	TAGCTGCTTGGGCTTCATTAACAAAGAAAGTCTGGGAAAGGCGCAAGTAGAGGAAATG	5640
Db	5581	TAGCTGCTTGGGCTTCATTAACAAAGAAAGTCTGGGAAAGGCGCAAGTAGAGGAAATG	5640
Qy	5641	AAAGGGAAAAACAGAAATGTAGAGACTTGAACAGCTTCAAAATCTCTACAGACGATTT	5700
Db	5641	AAAGGGAAAAACAGAAATGTAGAGACTTGAACAGCTTCAAAATCTCTACAGACGATTT	5700
Qy	5701	TTCTTGGAAACATCTAGAAAGGTAGTGATTTAGTGATGTCAGGGGACCTTCTTTGCCAT	5760
Db	5701	TTCTTGGAAACATCTAGAAAGGTAGTGATTTAGTGATGTCAGGGGACCTTCTTTGCCAT	5760
Qy	5761	TTGAATCTGGGTTTTTGTCTCTCCATTAGAGTTGAAAGCGTCAACCCTTTTACCCTCGAA	5820
Db	5761	TTGAATCTGGGTTTTTGTCTCTCCATTAGAGTTGAAAGCGTCAACCCTTTTACCCTCGAA	5820
Qy	5821	TGAGAGAGAAAGAAAGGGGTGTATGACTCTTACCCTGGAAGTTTACTAAGTTTAGGCATG	5880
Db	5821	TGAGAGAGAAAGAAAGGGGTGTATGACTCTTACCCTGGAAGTTTACTAAGTTTAGGCATG	5880
Qy	5881	GAAACAGACATCTGGGACCTCCTCTTGAACAAAAAAATGAAACCTGGTGTGTCTTGT	5940
Db	5881	GAAACAGACATCTGGGACCTCCTCTTGAACAAAAAAATGAAACCTGGTGTGTCTTGT	5940
Qy	5941	TGTTCTTTTGTTAAGAAAGCAACAGGCAAAAGCCGACCAATGGGTGTAATGGGCTCTT	6000
Db	5941	TGTTCTTTTGTTAAGAAAGCAACAGGCAAAAGCCGACCAATGGGTGTAATGGGCTCTT	6000
Qy	6001	GAGTCAAGGCTTTTGAAGTGAAGCACTCATCAATGTTGATCATGTCAGGTGAGGAGCTTA	6060
Db	6001	GAGTCAAGGCTTTTGAAGTGAAGCACTCATCAATGTTGATCATGTCAGGTGAGGAGCTTA	6060
Qy	6061	CCTGTCAAGCCGAGCCCTGCGGTGCGTCACTTAAACCTCAGAGTCTCAGTATCACTTC	6120
Db	6061	CCTGTCAAGCCGAGCCCTGCGGTGCGTCACTTAAACCTCAGAGTCTCAGTATCACTTC	6120
Qy	6121	CTGCTACTTAGCAACAGTTAGAGTGTGAGCAAACTTTTTTCCAAACCCCACTAAATTT	6180
Db	6121	CTGCTACTTAGCAACAGTTAGAGTGTGAGCAAACTTTTTTCCAAACCCCACTAAATTT	6180
Qy	6181	AATTGACAAAAGACTGTGTAAATTTGTGGGATACAGTGTGATTAATGTATGTGAT	6240
Db	6181	AATTGACAAAAGACTGTGTAAATTTGTGGGATACAGTGTGATTAATGTATGTGAT	6240
Qy	6241	TGTGCAAGGTCATTAAGATAGTTAAATAGGCCATCAACAGCTTTATGGGTGTAATG	6300
Db	6241	TGTGCAAGGTCATTAAGATAGTTAAATAGGCCATCAACAGCTTTATGGGTGTAATG	6300
Qy	6301	CAAGTAATATAGTAGATGCTGTGTGTCTTATAGTTCAGAAAGGCATGATTTTAAGGTC	6360
Db	6301	CAAGTAATATAGTAGATGCTGTGTGTCTTATAGTTCAGAAAGGCATGATTTTAAGGTC	6360
Qy	6361	TTGGGCAATCATATTATATCTATGCTTAAAAATTCATTATGTGATTTATATCTTTAG	6420
Db	6361	TTGGGCAATCATATTATATCTATGCTTAAAAATTCATTATGTGATTTATATCTTTAG	6420

Db 952 CACTTAGGGTTTCTCTCTTTTCAGGCGACGCTTGACATTAACAACACAGAGCTCCGGCTC 1011
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Db 1012 ATCGGGGAGAACTGTTCCGAGGAGTCAGTGTAAAGTCTCTCACTGTGATGACAGAGGCTAG 1071
Qy 2751 CTGCGGGAGGCTGGGAGCCCTCTGGGATAGTCTGACGATAGACCCCTGCTCTTCTGTC 2810
Db 1072 CTGCGGGAGCTGGGAGCCCTCTGGGATAGTCTGACGATAGACCCCTGCTCTTCTGTC 1131
Qy 2811 TACCTGAGGCTTAAAGATCACTGTCTACCTGTATGAAGCAGTGTCTCACTTGACCCCTGGA 2870
Db 1132 TACCTGAGGCTTAAAGATCACTGTCTACCTGTATGAAGCAGTGTCTCACTTGACCCCTGGA 1191
Qy 2871 GACCTTCTGCTCCCCCAGTCAGACAGGTTCCAGCCCTACATGACAGAGGTGTACCTTTC 2930
Db 1192 GACATTCCTGCTCCCCCAGTCAGACAGGTTCCGCGCCCTACATGACAGAGGTGTACCTTTC 1251
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Qy 2991 CCTCA 3050
Db 1312 CCTCA 1371
Qy 3051 AGAGTGAAGAGGCGCTCAGACCAACACATCATAGGCACTTGAAATAGGTCACAAG 3110
Db 1372 AGAGTGAAGAGGCGCTCAGACCAACACATCATAGGCACTTGAAATAGGTCACAAG 1431
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Db 1432 CTTTGGCTCTCAATTGAGTAATATCTTGAAGTTGTATGATGATGAGTATTTTATTTC 1491
Qy 3171 CATGGAAGAAATCACTCAAAATCTGATGATGAGAAAGATGTTGGGAAGAAAG 3230
Db 1492 CATGGAAGAAATCACTCAAAATCTGATGATGAGAAAGATGTTGGGAAGAAAG 1551
Qy 3231 CCTAGATAGAGAAACAGATCTGCTGATATATCTTAT---GGGGGAGCAGGGGCG 3286
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Db 1612 ATATCCACTGATGATCAAGTACTTGTGGGAGAGAAATCACTGATATCAATCTTGTG-- 1669
Qy 3347 GCATGAGATCCATGATACAAGTACTGTGGGGGAGGGAATGGCAGAGCAAAAGT 3406
Db 1670 -----GGGGGAAGAAATGGCAGAGCAAAAGT 1697
Qy 3407 TGAAGGGA---AGGAAGATGAGAGAGCCTCATGTGGGGGTGTGAAGTCACTCC--TT 3462
Db 1698 TGAAGGGAAGAAAGGAAGATGAGAGGCTCATGTGGGGGTGTGAAGTCACTCCCTT 1757
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Db 1758 TTCCATGTGATGAGAGATTAAGAAACCAAGTGTGTGATTTGATGTCTTCAAGACCC 1817
Qy 3523 CAACATTAAGAAATATCCAGAGAGGCGGAGACTGTGGGAGACTGGCAATTTAGGGAA 3582
Db 1818 AA-----CTATGGCAGACTGTGGGAGACTGGCAATTTAGGGAA 1855
Qy 3583 GGGCGGCTTTTTCACAGAGAACTTTATGCTCATCTGTGTCTACCTCCACCTTTG 3642
Db 1856 GGGCGGCTTTTTCACAGAGAACTTTATGCTCATCTGTGTCTACCTCCACCTTTG 1915
Qy 3643 ATGAGGTTCAAGTCAAGGTTGTTTCTTACCGTTCTTGTCTACTGTGTGAACTTCAGTGG 3702
Db 1916 ATGAGGTTCAAGTCAAGGTTGTTTCTTACCGTTCTTGTCTACTGTGTGAACTTCAGTGG 1975
Qy 3703 ATTCCCAAGAGCAGAGCAGCTTCTGTAAAGGAGGAGCTGTGATTTCAAGTGTCTAG 3762
Db 1976 ATTCCCAAGAGCAGAGCAGCTTCTGTAAAGGAGGAGCTGTGATTTCAAGTGTCTAG 2035

Qy 3763 AGAAGCAATATAGCTCAGAGAAATCAGGTCAACGTGAATCTAGATCAGACGGGCAAAAA 3822
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Db 2096 TGAAGTGAAGCCTCTATATCCAGGTGAACGGTCAAGTGTCTCAGATATATGAGGTATTGG 2155
Qy 3883 GCTCCCAACCGATTAAGATTTCTGTAGTCTGTCTTTATTTTTCAGCAATCAGCGGT 3942
Db 2156 GCTCCCAACCGATTAAGATTTCTGTAGTCTGTCTTTATTTTTCAGCAATCAGCGGT 2215
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Qy 4003 TTGGCAAGCCACAATACTAAGCCATTCAGTAGAGAGAGTGGGATTTCTTCTCTGCTTC 4062
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Db 2456 AGTCACAATCTGAGGTACAGAAAGCTTAGCTCAGCCAGTCTCATGAGCACTGTCTG 2515
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Qy 4303 CTTGCTTATGAGGCTGATGTATTAATCTTGGCTTGTATTAAGTATTTGGAAAGCACTTC 4362
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Db 3056 ATCTGCTGAGCTATTAATAGTCTTAAACAGCAAAACAATGTGTGTGCTCTTTGG 3115


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Db 3416 GTTACCTTGAACCTGGGCTTGAATGTTAGATCCAAAGGACACACTTGAATGCT 3475
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RESULT 7
US-09-419-568F-25

Sequence 25, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
LENGTH: 4797
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-419-568F-25
Query March 9.2% Score 686; DB 4; Length 4797;
Best Local Similarity 53.8%; Pred. No. 1.9e-164;
Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;
QY 2034 CTCCTCTCTCATATCACTGTTGACACTGTGCGATCTGTGATGGCTGTCTGACGAA 2093
DB 29 CTCCTCTCTCATATCACTGTTGACACTGTGCGATCTGTGATGGCTGTCTGACGAA 88
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RESULT 8
US-09-354-243B-25
; Sequence 25, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoulier, Laure
; APPLICANT: Louned, Jamila
; APPLICANT: Renaud, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa

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: TITLE OF INVENTION: (TIPS)
: TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
: FILE REFERENCE: LUD 5543.1
: CURRENT APPLICATION NUMBER: US/09/354,243B
: CURRENT FILING DATE: 1999-07-16
: PRIOR APPLICATION NUMBER: US09/178,973
: PRIOR FILING DATE: 1998-10-26
: NUMBER OF SEQ ID NOS: 29
: SEQ ID NO 25
: LENGTH: 4797
: TYPE: DNA
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: FEATURE:
: US-09-354-243B-25
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: Query Match          9.2%; Score 686; DB 4; Length 4797;
: Best Local Similarity 53.8%; Pred. No. 1,96-164;
: Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;
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DB 3403 GAAAGCA- CAGAGGAGAGAGAAATGTTGTTGAGAAAGATCAACAGAGAGAAACGT 3461
QY 5448 CAGAGCTCCCGAAGACA- -----CCACAGGTGTTAATAGG 5485
DB 3462 CAGAGCTGTGAATAGGAGTGTGAGAGCATTAATTCCTCTGTGGGGTAA 3521
QY 5486 AACAGTCCAGGGTGGCTCATGTAATGAAATGAAACAGAGAGAGAGATTAAGTAA 5545
DB 3522 AGCAGAAACGAGTGTGTAAT- GCATGACAGACAGTGAAGGAGATTAATTTAA 3580
QY 5546 AGTTTCATAGGTC- CGAGTCTTAAAGATACAAATAGTGC- TTGGGCTTCAACA 5602
DB 3581 AATCTTTATAGTCTTGAAGCTTTGAGATAGAAAAGATATCTTTTGGCTTATGCA 3640
QY 5603 AAGGAGCTGGAAGGACAGCAAGTGAAGAGGAAATGAAAAGGAAAAACAGAAATGAG 5662
DB 3641 AAGAGATGGAAGG- -----TGAAAGGCGGAAAGAAAGAGAAAGAG 3688
QY 5663 AGGACTGGAACAGTCAAAATCTCTACACAGCATTTTCTTGAAACATCTAGAAAGT 5722
DB 3689 AACCATGTATATATAGAGCAATGTGTGAACAAGGTTTCTGTAATAATGCAAAATAG 3748
QY 5723 AGTGAATAGGTGATGACAGGGGAGCTTGGCATTTGATGAGTTTGTCTCT 5782
DB 3749 ATGATTTAGAGAAATTTCAAGTGAAGGAAATGCTTTTCACTTGAATTTGGGTTCTCT- 3805
QY 5783 CCATTTAGGTTGAAAGCCTCAACCTTTTACCTCGAATGAGAGAGAAAGAGGCTGT 5842
DB 3806 CGATTTAGTTGGGATCTCATCTGCAATTTGACT- TGAGAGAGAGAAAGATGAATGT 3861
QY 5843 TATGACTCTACCTGAGATTTTACTAGTTTACGCAATGAAACAGACACTGGGACTCTCT 5902
DB 3862 TAGGACCTATATCTGGTTTCTATTAAGCAAGGAGGAAAGACTTATTTGGTATTT 3921
QY 5903 CTGACAAAAAAATGAAACCTGTGTTGTTCTGTTGTTCTTTGTTAAGAAAGAC 5962
DB 3922 TTCCACAAAGAGTAAACCTTTTCTTTTACTGTTTGTCAAAAAGGTGAAATAGAAAAG 3981
QY 5963 AGGAAAGCCGACCAATGAGGTGAAATGTGGGCTTTGAGTCAAGGCTTTTGAAGTGAAG 6022

DB 3982 CTTAATGTATGTGTAATACATGTCTCAAAAGTATGTAAGATGTTTAAATCAG 4041
QY 6023 CACTCATCAATAGTT-----GATCATGTGAGGTGAGAGGC 6058
DB 4042 GAGTGTCAATCATTTTGGCTTCCCTGAGCACTTGAAGAAATGTTCTGTGACACAT 4101
QY 6059 TACTGTGAGCGGAGCCCTGCTGCTTCCGACCTTAACATCTCCAGCTCTTATGATCT 6118
DB 4102 AAAATACAGAAACATAGCTGATGAGCTAAAAAAGTCCATGCAATTAATCTATCTGTT 4161
QY 6119 TCTGCTACTTAGACAGATTAAGATGAGGAAACCTTTTCTCC----- 6163
DB 4162 TAAGAAAGTTTATGAATTTCTGTTAGGCTGATTTCAAAAGCTGTCTGGCCATGTGGGC 4221
QY 6164 -----AACCCCACTAAATTTAATGACAAAGACTGTGTAATTTG 6205
DB 4222 CTGTGGCTGAGGTGAGACAGCTCTTATTAATTAATCTGTATAGTTATTTGGAGC 4281
QY 6206 TGGATACAGTGTGATTAATGA----- 6227
DB 4282 TGCAAAACAGGCCAAGGCATATAGGTGACCTGGGATCCCGAGATCCAGCCTCACT 4341
QY 6228 -----TCTATGCTGATTTGCAAGGTTCAATAGATTAATAGGCCCATGACAGC 6283
DB 4342 TCACTCTCTTGTCTGTGTAGAGAGGCTGTCACTCTGCCCAGCTTTAAACAGC 4401
QY 6284 TTATGAGGTGGAATGCAATATATAGTATAGTGTGCTGTGCTTATAGTACAGAA 6343
DB 4402 TTCTATGAGTGTGAGGTGACCTGAAATGATGATCCTGCTGTGGCT- CTCAGTCAAGGA 4460
QY 6344 GGCATGATTTTAAAGTCTTGGGCAATCATTTATCTCATGCTTAAATAATCATTAATGT 6403
DB 4461 GCGCTCATTTTAACTCTTTGGCAATCATTAATCAATCAATCAATCAATCAATCAAT 4508
QY 6404 GATTTATATCTTTTAAAGAGGCTGATCTGTGTTTGTGCTCAGAACCAATGTCA 6463
DB 4509 TACTATGAATGTTTAAACAAATGCTTAAACCTGCTGTCTCATCACTCACTATCTTG 4568
QY 6464 CCAGCTCTTCTAAGTGTACCACTTATAGAAATGCTACCTGCTCAATTTGTTGTA 6523
DB 4569 CAATTTCT- AATTTGTTACTTTAGAAAACATGCAATTAATCTCAATTAATCTTGA 4625
QY 6524 TTCTTATTTTCAATGCTTGAAGAGTGAAGATCAAGGAGTTGGGAACTGACCTG 6583
DB 4626 TTCTTATTTTCAAGCTTGGAGAGAGTGAAGATCAAGGAACTGGAGAACTGGAATTTG 4685
QY 6584 CTGTTATGCTCTGAGAAATGCTTGGCTCTGAGCGAGAAAGACTGAAAAACGAAAGAC 6643
DB 4686 CTGTTATGCTCTGAGAAATGCTTGGCAATTTGACCAAGCAAAACCTGAAAAATGAAATAC 4745
QY 6644 TGCTCTTCTCCGCTTCTTAAAGAACATTAAGATCCCTGAATGAGACTTTT 6695
DB 4746 TAACCCCTTCTCCCTGCTAGAAATTAACATTAAGATGCCCAAGCAATTTT 4797

RESULT 9
US-09-178-973B-7
; Sequence 7, Application US/09178973B
; Patent No. 6274710
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Leoued, Jamila
; APPLICANT: Renaud, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
; FILE REFERENCE: LUD 5543
; CURRENT APPLICATION NUMBER: US/09/178, 973B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 7
; LENGTH: 1119

TYPE: DNA
ORGANISM: Mus musculus
US-09-419-568F-7

Query Match 8.1%; Score 601.4; DB 4; Length 1119;
Best Local Similarity 99.8%; Pred. No. 3e-143;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6535 ATAGCTTGAGAGAGAGAGAGAGATCAAGCGCATTTGGGAACTGGACCTGCTTTATGTC 6594
DB 510 AAAGCTTGAGAGAGAGAGAGATCAAGCGCATTTGGGAACTGGACCTGCTTTATGTC 569
QY 6595 TCTGAGAAATGCTGCTGCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6654
DB 570 TCTGAGAAATGCTGCTGCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 629
QY 6655 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGAGACTTTTACTTAAGAGAGAGAGAG 6714
DB 630 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGAGACTTTTACTTAAGAGAGAGAGAG 689
QY 6715 GCTAACGTCATCATCATTAAGAGATTTACATGAAACCTGGCTCAGTTGAAAAAGAGAA 6774
DB 690 GCTAACGTCATCATCATTAAGAGATTTACATGAAACCTGGCTCAGTTGAAAAAGAGAA 749
QY 6775 TAGTGTCAAGTTGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6834
DB 750 TAGTGTCAAGTTGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 809
QY 6835 ATATTTTATTTGTCATGATGATACACAGAAAAATATGATCTTTAAAAAATTTGTTGA 6894
DB 810 ATATTTTATTTGTCATGATGATACACAGAAAAATATGATCTTTAAAAAATTTGTTGA 869
QY 6895 AGAGAGTACCTCTCATTCCTTTAGAAAAAGCTTAATGATCTTCCATATCCAA 6954
DB 870 AGAGAGTACCTCTCATTCCTTTAGAAAAAGCTTAATGATCTTCCATATCCAA 929
QY 6955 TATTTTATATATGATGATTTATTTATTAAGATATACATTTTATTTATGTCGTTATTA 7014
DB 930 TATTTTATATATGATGATTTATTTATTAAGATATACATTTTATTTATGTCGTTATTA 989
QY 7015 ATATGATTTTATTTATAGAAACATATCTGATTTGATTTATGATTAAGCAATTAATA 7074
DB 990 ATATGATTTTATTTATAGAAACATATCTGATTTGATTTATGATTAAGCAATTAATA 1049
QY 7075 TTTATGACATTAATCTATGAGAAACAGATATCTTAGGCTTTAATAACACATGATATCAT 7134
DB 1050 TTTATGACATTAATCTATGAGAAACAGATATCTTAGGCTTTAATAACACATGATATCAT 1109
QY 7135 AAA 7137
DB 1110 AAA 1112

RESULT 10
US-09-419-568F-7
Sequence 7, Application US/09419568F
Patent No. 631613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119

TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-419-568F-7

Query Match 8.1%; Score 601.4; DB 4; Length 1119;
Best Local Similarity 99.8%; Pred. No. 3e-143;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6535 ATAGCTTGAGAGAGAGAGAGATCAAGCGCATTTGGGAACTGGACCTGCTTTATGTC 6594
DB 510 AAAGCTTGAGAGAGAGAGAGATCAAGCGCATTTGGGAACTGGACCTGCTTTATGTC 569
QY 6595 TCTGAGAAATGCTGCTGCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6654
DB 570 TCTGAGAAATGCTGCTGCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 629
QY 6655 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGAGACTTTTACTTAAGAGAGAGAGAG 6714
DB 630 GCCTTCTAAAAAGAACATTAAGATCCCTGAATGAGACTTTTACTTAAGAGAGAGAGAG 689
QY 6715 GCTAACGTCATCATCATTAAGAGATTTACATGAAACCTGGCTCAGTTGAAAAAGAGAA 6774
DB 690 GCTAACGTCATCATCATTAAGAGATTTACATGAAACCTGGCTCAGTTGAAAAAGAGAA 749
QY 6775 TAGTGTCAAGTTGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6834
DB 750 TAGTGTCAAGTTGTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 809
QY 6835 ATATTTTATTTGTCATGATGATACACAGAAAAATATGATCTTTAAAAAATTTGTTGA 6894
DB 810 ATATTTTATTTGTCATGATGATACACAGAAAAATATGATCTTTAAAAAATTTGTTGA 869
QY 6895 AGAGAGTACCTCTCATTCCTTTAGAAAAAGCTTAATGATCTTCCATATCCAA 6954
DB 870 AGAGAGTACCTCTCATTCCTTTAGAAAAAGCTTAATGATCTTCCATATCCAA 929
QY 6955 TATTTTATATATGATGATTTATTTATTAAGATATACATTTTATTTATGTCGTTATTA 7014
DB 930 TATTTTATATATGATGATTTATTTATTAAGATATACATTTTATTTATGTCGTTATTA 989
QY 7015 ATATGATTTTATTTATAGAAACATATCTGATTTGATTTATGATTAAGCAATTAATA 7074
DB 990 ATATGATTTTATTTATAGAAACATATCTGATTTGATTTATGATTAAGCAATTAATA 1049
QY 7075 TTTATGACATTAATCTATGAGAAACAGATATCTTAGGCTTTAATAACACATGATATCAT 7134
DB 1050 TTTATGACATTAATCTATGAGAAACAGATATCTTAGGCTTTAATAACACATGATATCAT 1109
QY 7135 AAA 7137
DB 1110 AAA 1112

RESULT 11
US-09-354-243B-7
Sequence 7, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119

TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-354-243B-7

Query Match 8.1%; Score 601.4; DB 4; Length 1119;
Best Local Similarity 99.8%; Pred. No. 3e-143;
Matches 602; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6535 ATAGCTTGGAGAGAGTGGAGATCAAGGCGATTGGGAACTGACCTGCTGTTATATGTC 6534
DB 510 AAAGCTTGGAGAGAGTGGAGATCAAGGCGATTGGGAACTGACCTGCTGTTATATGTC 569
QY 6595 TCTGAGAAATGCTTGGCTGAGCGAGAGAAAGCTAGAAAAGAAAGCTGCTCTCTCT 6654
DB 570 TCTGAGAAATGCTTGGCTGAGCGAGAGAAAGCTAGAAAAGAAAGCTGCTCTCTCTCT 629
QY 6655 GCCCTTCTAAAAGAACATAGATCCCTGATGAGACTTTTCTAAAGAAAGTGAAGAA 6714
DB 630 GCCCTTCTAAAAGAACATAGATCCCTGATGAGACTTTTCTAAAGAAAGTGAAGAA 689
QY 6715 GCTAACGTCATCATCTTTAGAGATTTCACATGAAACCTGCTCAGTTGAAAAAGAAA 6774
DB 690 GCTAACGTCATCATCTTTAGAGATTTCACATGAAACCTGCTCAGTTGAAAAAGAAA 749
QY 6775 TAGGTCAAGTTGTCATGAGACCAAGAGTAGACTGATAACCAAAAGATTCATTGACA 6834
DB 750 TAGGTCAAGTTGTCATGAGACCAAGAGTAGACTGATAACCAAAAGATTCATTGACA 809
QY 6835 ATATTATTATGTCACATGATATACACAGAAAAATTAATGACTTTAAATAATGTTGAA 6894
DB 810 ATATTATTATGTCACATGATATACACAGAAAAATTAATGACTTTAAATAATGTTGAA 869
QY 6895 AGAGAGTTACCTCTCATCTCTTTAGAAAAAAAGCTTATGTAACCTTCCATATCCAA 6954
DB 870 AGAGAGTTACCTCTCATCTCTTTAGAAAAAAAGCTTATGTAACCTTCCATATCCAA 929
QY 6955 TATTTTATATATGTAAGTTTATTTATATAGTATACCTTTTATTTATGTCAGTTTATA 7014
DB 930 TATTTTATATATGTAAGTTTATTTATATAGTATACCTTTTATTTATGTCAGTTTATA 989
QY 7015 ATATGATTTATTTATAGAAACATTTATCTGCTATTTAGTATTAAGCAATATATA 7074
DB 990 ATATGATTTATTTATAGAAACATTTATCTGCTATTTAGTATTAAGCAATATATA 1049
QY 7075 TTATGACAAATACATGAGAAACAGATATCTTAGGCTTTAATAAACAATGATATCAT 7134
DB 1050 TTATGACAAATACATGAGAAACAGATATCTTAGGCTTTAATAAACAATGATATCAT 1109
QY 7135 AAA 7137
DB 1110 AAA 1112

RESULT 12

US-09-178-973B-9
Sequence 9, Application US/09178973B
Patent No. 6274710
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
FILE REFERENCE: LUD 5543
CURRENT APPLICATION NUMBER: US/09/178, 973B
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus

US-09-178-973B-9

Query Match 7.5%; Score 555.2; DB 4; Length 1111;
Best Local Similarity 96.0%; Pred. No. 1.7e-131;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY 6535 ATAGCTTGGAGAGAGTGGAGATCAAGGCGATTGGGAACTGACCTGCTGTTATATGTC 6594
DB 508 AAAGCTTGGAGAGAGTGGAGATCAAGGCGATTGGGAACTGACCTGCTGTTATATGTC 567
QY 6595 TCTGAGAAATGCTTGGCTGAGCGAGAGAAAGCTAGAAAAGAAAGCTGCTCTCTCTCT 6654
DB 568 TCTGAGAAATGCTTGGCTGAGCGAGAGAAAGCTAGAAAAGAAAGCTGCTCTCTCTCT 627
QY 6655 GCCCTTCTAAAAGAACATAGATCCCTGATGAGACTTTTCTAAAGAAAGTGAAGAA 6714
DB 628 GCCCTTCTAAAAGAACATAGATCCCTGATGAGACTTTTCTAAAGAAAGTGAAGAA 687
QY 6715 GCTAACGTCATCATCTTTAGAGATTTCACATGAAACCTGCTCAGTTGAAAAAGAAA 6774
DB 688 GCTAACGTCATCATCTTTAGAGATTTCACATGAAACCTGCTCAGTTGAAAAAGAAA 747
QY 6775 TAGGTCAAGTTGTCATGAGACCAAGAGTAGACTGATAACCAAAAGATTCATTGACA 6834
DB 748 TAGGTCAAGTTGTCATGAGACCAAGAGTAGACTGATAACCAAAAGATTCATTGACA 807
QY 6835 ATATTATTATGTCACATGATATACACAGAAAAATTAATGACTTTAAATAATGTTGAA 6894
DB 808 ATATTATTATGTCACATGATATACACAGAAAAATTAATGACTTTAAATAATGTTGAA 867
QY 6895 AGAGAGTTACCTCTCATCTCTTTAGAAAAAAAGCTTATGTAACCTTCCATATCCAA 6954
DB 868 AGAGAGTTACCTCTCATCTCTTTAGAAAAAAAGCTTATGTAACCTTCCATATCCAA 927
QY 6955 TATTTTATATATGTAAGTTTATTTATATAGTATACCTTTTATTTATGTCAGTTTATA 7014
DB 928 TATTTTATATATGTAAGTTTATTTATATAGTATACCTTTTATTTATGTCAGTTTATA 987
QY 7015 ATATGATTTATTTATAGAAACATTTATCTGCTATTTAGTATTAAGCAATATATA 7073
DB 988 ATATGATTTATTTATAGAAACATTTATCTGCTATTTAGTATTAAGCAATATATA 1047
QY 7074 ATTTAGCAATACATGAGAAACAGATATCTTAGGCTTTAATAAACAATGATATCA 7133
DB 1048 ATTTAGCAATACATGAGAAACAGATATCTTAGGCTTTAATAAACAATGATATCA 1107
QY 7134 TAAA 7137
DB 1108 TAAA 1111

RESULT 13

US-09-419-568F-9
Sequence 9, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419, 568F
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354, 243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178, 973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus

FEATURE:
US-09-419-568F-9

Query Match 7.5%; Score 555.2; DB 4; Length 1111;
Best Local Similarity 96.0%; Pred. No. 1.7e-131;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

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QY 6535 ATAGCTTGGAGAGAGAGAGATCAAGCGATTGGGGAAGTGGACCTGCTGTTATGTC 6594
DB 508 AAAGCTTGGAGAGAGAGAGATCAAGCGATTGGGGAAGTGGACCTGCTGTTATGTC 567
QY 6595 TCTGAGAAATGCTTGGCTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6654
DB 568 TCTGAGAAATGCTTGGCTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 627
QY 6655 GCCTTCTAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6714
DB 628 GCCTTCTAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 687
QY 6715 GCTAAGCTCATTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6774
DB 688 GCTAAGCTCATTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 747
QY 6775 TAGGTCAAGTGTCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6834
DB 748 TAGGTCAAGTGTCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 807
QY 6835 ATATTTTATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6894
DB 808 ATATTTTATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 867
QY 6895 AGGAGTACCTCTCATTCCTTTAGAAAAAGCTTATGTAATCTTATTCATATCCAA 6954
DB 868 AGGAGTACCTCTCATTCCTTTAGAAAAAGCTTATGTAATCTTATTCATATCCAA 927
QY 6955 TATTTTATATATGTAAGTATATTTATTTATTAAGTATATATTTATTTATGTCAGTTATTA 7014
DB 928 TATTTTATATATGTAAGTATATTTATTTATTAAGTATATATTTATTTATGTCAGTTATTA 987
QY 7015 ATATGAGATTTTATTAAGAAACATTAATCTGCTATGATATTTT-AGTATTAAGCAATATAT 7073
DB 988 ATATGAGATTTTATTAAGAAACATTAATCTGCTATGATATTTT-AGTATTAAGCAATATAT 1047
QY 7074 ATTTATGACATTAATTAAGAAACAGATATCTTATGCTTATTAATTAAGCAATGATATCA 7133
DB 1048 ATTTATGATTAATTAATTAAGAAACAGATATCTTATGCTTATTAATTAAGCAATGATATCA 1107
QY 7134 TAAA 7137
DB 1108 TAAA 1111
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RESULT 14
US-09-354-243B-9

Sequence 9, Application US/09354243B
Patent No. 6359117

GENERAL INFORMATION:

APPLICANT: Dumoutier, Laure

APPLICANT: Louhed, Jamila

APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides

TITLE OF INVENTION: (Title) The Proteins Encoded, and Uses Thereof

FILE REFERENCE: LUD 5543.1

CURRENT APPLICATION NUMBER: US/09/354,243B

CURRENT FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US09/178,973

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 9

LENGTH: 1111

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:
US-09-354-243B-9

Query Match 7.5%; Score 555.2; DB 4; Length 1111;
Best Local Similarity 96.0%; Pred. No. 1.7e-131;
Matches 580; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

```
QY 6535 ATAGCTTGAAGAGAGAGAGATCAAGCGATTGGGGAAGTGGACCTGCTGTTATGTC 6594
DB 508 AAAGCTTGAAGAGAGAGAGATCAAGCGATTGGGGAAGTGGACCTGCTGTTATGTC 567
QY 6595 TCTGAGAAATGCTTGGCTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6654
DB 568 TCTGAGAAATGCTTGGCTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 627
QY 6655 GCCTTCTAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6714
DB 628 GCCTTCTAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 687
QY 6715 GCTAAGCTCATTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6774
DB 688 GCTAAGCTCATTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 747
QY 6775 TAGGTCAAGTGTCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6834
DB 748 TAGGTCAAGTGTCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 807
QY 6835 ATATTTTATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6894
DB 808 ATATTTTATGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 867
QY 6895 AGGAGTACCTCTCATTCCTTTAGAAAAAGCTTATGTAATCTTATTCATATCCAA 6954
DB 868 AGGAGTACCTCTCATTCCTTTAGAAAAAGCTTATGTAATCTTATTCATATCCAA 927
QY 6955 TATTTTATATATGTAAGTATATTTATTTATTAAGTATATATTTATTTATGTCAGTTATTA 7014
DB 928 TATTTTATATATGTAAGTATATTTATTTATTAAGTATATATTTATTTATGTCAGTTATTA 987
QY 7015 ATATGAGATTTTATTAAGAAACATTAATCTGCTATGATATTTT-AGTATTAAGCAATATAT 7073
DB 988 ATATGAGATTTTATTAAGAAACATTAATCTGCTATGATATTTT-AGTATTAAGCAATATAT 1047
QY 7074 ATTTATGACATTAATTAAGAAACAGATATCTTATGCTTATTAATTAAGCAATGATATCA 7133
DB 1048 ATTTATGATTAATTAATTAAGAAACAGATATCTTATGCTTATTAATTAAGCAATGATATCA 1107
QY 7134 TAAA 7137
DB 1108 TAAA 1111
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RESULT 15
US-09-419-568F-24

Sequence 24, Application US/09419568F
Patent No. 6331613

GENERAL INFORMATION:

APPLICANT: Dumoutier, Laure

APPLICANT: Louhed, Jamila

APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides

TITLE OF INVENTION: (Title) The Proteins Encoded, and Uses Thereof

FILE REFERENCE: LUD 5543.2

CURRENT APPLICATION NUMBER: US/09/419,568F

CURRENT FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US09/354,243

PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: US09/178,973

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 24

LENGTH: 690

TYPE: DNA

;
; ORGANISM: Homo sapiens
;
; FEATURE:
US-09-419-568F-24

Query Match	1.7%	Score 126;	DB 4;	Length 690;
Best Local Similarity	71.7%;	Pred. No. 2.2e-22;		
Matches 165;	Conservative 0;	Mismatches 65;	Indels 0;	Gaps 0;

QY	2034	TTCTCCCTACTACTATACAAAGTTGAGACCTTGTGGAGATCTCGAATGGGCTGCTCGACAA	2093
Db	29	CTCTCTCCCACTCAACAGTTGCTCGAATTGATTTGCTGCATAGCCGCCCTTCACAA	88
QY	2094	ATCTATGAGTTTTCCCTTATGGGACCTTGGCCGACATGCCCTTCTCATTTGCCCT	2153
Db	89	ATCTGTAGACTTCTTCTTATGGGGAACCTGACCACAGCTGCGCTCTTCTTGGCCCT	148
QY	2154	GTGGGCCCAAGAGCAATGCGCTGCGCCGTCAACCCGGGTGCAGCTTGAAGTGTCCA	2213
Db	149	CTTGGTAAAGGAGAGAGAGCGCTGGGCCCATAGCTCCCACTGCAGAGCTTGCAATTC	208
QY	2214	CTTCAGAGAGCGTACATCTGTCACACCGACCTTTATGTGGCCAAAGAGG	2263
Db	209	CTTCAGAGAGCGCTTATATACCAACCGACCTTCACTGCTGACTAAGAGG	258

Search completed: July 19, 2003, 19:47:57
Job time : 308.726 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: July 19, 2003, 09:03:00 ; Search time 1155.93 Seconds

(without alignments)
17372.171 Million cell updates/sec

Title: US-09-751-797-24

Perfect score: 690
Sequence: 1 tgcacacagacagatcttcag.....gatccccaagcgattttt 690

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	690	100.0	690	6 AR201414	AR201414 Sequence
2	690	100.0	690	6 AX459971	AX459971 Sequence
3	690	100.0	690	6 HSA277247	AJ277247 Homo sapi
4	676	98.0	1152	6 AX092422	AX092422 Sequence
5	676	98.0	1152	6 AX358990	AX358990 Sequence
6	676	98.0	1152	6 AX362483	AX362483 Sequence
7	676	98.0	1152	6 AX392477	AX392477 Sequence
8	676	98.0	1152	6 AX403770	AX403770 Sequence
9	676	98.0	1152	6 AX454768	AX454768 Sequence
10	676	98.0	1152	6 AX491246	AX491246 Sequence
11	676	98.0	1167	6 AF279437	AF279437 Homo sapi
12	671	97.2	1139	6 AX054620	AX054620 Sequence
13	669	97.0	1132	6 AX048204	AX048204 Sequence
14	639	92.6	1116	6 AX151713	AX151713 Sequence
15	639	92.6	1116	6 AX179578	AX179578 Sequence
16	639	92.6	1116	6 AX468783	AX468783 Sequence
17	409.2	59.3	1119	6 AR201387	AR201387 Sequence
18	409.2	59.3	1119	6 AR201387	AR201387 Sequence
19	409.2	59.3	1119	6 AX459953	AX459953 Sequence
20	409.2	59.3	1121	10 MMU249491	AJ29491 Mus muscu
21	407.6	59.1	1111	6 AX179614	AX179614 Sequence
22	407.6	59.1	1111	6 AR165228	AR165228 Sequence
23	407.6	59.1	1111	6 AR201389	AR201389 Sequence
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26	380	55.1	537	6 AX054622	AX054622 Sequence
27	356.4	51.7	501	6 AX179581	AX179581 Sequence
28	317	45.9	418	6 AX459964	AX459964 Sequence
29	258	37.4	4797	6 AR201415	AR201415 Sequence
30	258	37.4	4797	6 AX459972	AX459972 Sequence
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32	237.4	34.4	8393	9 AF387519	AF387519 Homo sapi
33	237.4	34.4	133350	9 AC022511	AC022511 Homo sapi
34	159.4	23.1	191111	9 AC007458	AC007458 Homo sapi
35	127.6	18.5	5935	6 AR165234	AR165234 Sequence
36	127.6	18.5	5935	6 AR201417	AR201417 Sequence
37	127.6	18.5	5935	6 AX459988	AX459988 Sequence
38	127.6	18.5	5935	10 AR165227	AJ294728 Mus muscu
39	126	18.3	7445	6 AR165227	AR165227 Sequence
40	126	18.3	7445	6 AR201398	AR201398 Sequence
41	126	18.3	7445	6 AX459954	AX459954 Sequence
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44	96.8	14.0	133899	2 AC111483	AC111483 Rattus no
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ALIGNMENTS

RESULT 1
LOCUS AR201414 690 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 24 from patent US 6359117.
ACCESSION AR201414
VERSION AR201414.1 GI:20252302
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 690)
AUTHORS Dumoutier, L., Louhed, J. and Renaud, J.-C.
TITLE Isolated nucleic acid molecules which encode T cell inducible
factors (TIFs), the proteins encoded, and uses therefor
JOURNAL Patent: US 6359117-A 24 19-WAR-2002;

REFERENCE 1 (bases 1 to 690)
 AUTHORS Dumoutier, L., Van Roost, E., Colau, D. and Renauld, J. C.
 TITLE Human interleukin-10-related T cell-derived inducible factor: molecular cloning and functional characterization as an hepatocyte-stimulating factor
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (18), 10144-10149 (2000)
 MEDLINE 20420346
 PUBMED 10954742
 REFERENCE 2 (bases 1 to 690)
 AUTHORS Renauld, J. C.
 TITLE Direct Submission
 JOURNAL Submitted (10-APR-2000) Renauld J. C., UCL 74-59, Ludwig Institute for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels, BELGIUM

FEATURES
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BASE COUNT 182 a 176 c 167 g 165 t
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Query Match 100.0%; Score 690; DB 9; Length 690;
 Best Local Similarity 100.0%; Pred. No. 1.6e-180;
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 AATTGCTGCAGATAGGCGCCCTGAGAAATCTGTGAGCTCTTCCCTTAGGGGACCCCTG 120
 QY 121 CCACACAGTGCCTCTCTCTTGGCCCTCTTGGTACAGGAGAGAGAGAGAGAGAGAGAG 180
 DB 121 CCACACAGTGCCTCTCTCTTGGCCCTCTTGGTACAGGAGAGAGAGAGAGAGAGAGAG 180
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 DB 181 GCTCCACATGCAAGCTTGAAGTCAAGTCCAGTCCAGAGAGAGAGAGAGAGAGAGAG 240
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 DB 421 AGGTGAGGAG 480

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RESULT 4
 AX092422
 LOCUS AX092422 1152 bp DNA linear PAT 21-MAR-2001
 DEFINITION Sequence 153 from Patent WO0116318.
 AX092422
 ACCESSION AX092422
 VERSION AX092422.1 GI:13444525
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo;
 REFERENCE 1 (bases 1 to 1152)
 AUTHORS Baton, D. L., Pilvaroff, E., Gerritsen, M. E., Goddard, A., Godowski, P. J., Grimaldi, C. J., Gurney, A. L., Watanabe, C. K. and Wood, W. I.
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
 JOURNAL Patent: WO 0116318-A 153 08-MAR-2001;
 Gentech, Inc. (US)

FEATURES
 source location/Qualifiers
 1..1152
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 342 a 244 c 228 g 338 t
 ORIGIN

Query Match 98.0%; Score 676; DB 6; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 1.3e-176;
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTCGAAACAGGTTCTCTTCCCAAGTACCAAGTTGCTGAGTTAGAAATGTTGCAATG 74
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 DB 75 GCGGCGTGCAGAAATCTGTAGCTCTTCCCTTAGGGGAGAGAGAGAGAGAGAGAGAGAG 134
 QY 135 CTTCCTTGGCCCTCTTGTGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
 DB 135 CTTCCTTGGCCCTCTTGTGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
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 QY 254 CTTCGAAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314
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Db 361 GAAAGTCTGTTCCCTCAATCTGATAGTTCAGGCTTATATGAGAGAGTGTCCTTC 420
QY 435 CTGGCCAGGCTCAGCAACAGCTAAGCATAATGATTAAGAGTGAAGCTGCATATC 494
Db 421 CTGGCCAGGCTCAGCAACAGGCTAAGCATAATGATTAAGAGTGAAGCTGCATATC 480
QY 495 CAGAGAAATGTGCAAAAGCTGAAGAGACAGTGAAGAAAGCTTGGAGAGATGAGAGATC 554
Db 481 CAGAGAAATGTGCAAAAGCTGAAGAGACAGTGAAGAAAGCTTGGAGAGATGAGAGATC 540
QY 555 AAGCAATTTGAGAAATGATTTGCTTTATGCTCTGAGAAATGCTGATTTGACCA 614
Db 541 AAGCAATTTGAGAAATGATTTGCTTTATGCTCTGAGAAATGCTGATTTGACCA 600
QY 615 GAGCAAAAGCTGAAAAATGAATACTAACCCCTTCCCTGTAAGAAATCAATTAGATG 674
Db 601 GAGCAAAAGCTGAAAAATGAATACTAACCCCTTCCCTGTAAGAAATCAATTAGATG 660
QY 675 CCCCNAAGCGATTTT 690
Db 661 CCCCNAAGCGATTTT 676

RESULT 5
LOCUS AX358990 1152 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 243 from Patent WO0193983.
ACCESSION AX358990
VERSION AX358990.1 GI:18675396
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Gadowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0193983-A 243 13-DEC-2001;

JOURNAL

Genentech Inc. (US)

FEATURES

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1. .1152
Location/Qualifiers
/db_xref="taxon:9606"
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BASE COUNT 342 a 244 c 228 g 338 t

ORIGIN

Query Match 98.0%; Score 676; DB 6; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.3e-176;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTAGAAACAGTTCTCTTCCCAAGTACAGTGTGCTGAGTGAATGTCTGCATG 74
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QY 375 GAAGTCTGTCCTCAATCTGATGATGCTCCAGACCTTATATGAGAGAGTGGCTTC 434
Db 361 GAAGTCTGTCCTCAATCTGATGATGCTCCAGACCTTATATGAGAGAGTGGCTTC 420
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QY 615 GAGCAAAAGCTGAAAAATGAATACTAACCCCTTCCCTGTAAGAAATCAATTAGATG 674
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RESULT 6

LOCUS

AX362483 1152 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 243 from Patent WO0208288.
ACCESSION AX362483
VERSION AX362483.1 GI:18694699
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Gadowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0208288-A 243 31-JAN-2002;

JOURNAL

Genentech, Inc. (US)

FEATURES

source

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Location/Qualifiers
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BASE COUNT 342 a 244 c 228 g 338 t

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Best Local Similarity 100.0%; Pred. No. 1.3e-176;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 75 GCGCCCTGAGAAATCTGTAGACTCTTCTTATGGGAGACCTGGACACAGCTGCTC 134
Db 61 GCGCCCTGAGAAATCTGTAGACTCTTCTTATGGGAGACCTGGACACAGCTGCTC 120
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Db 661 CCCCAGGCAATTTT 676

RESULT 7
AX392477 1152 bp DNA linear PAT 23-MAR-2002
LOCUS AX392477
DEFINITION Sequence 1 from Patent WO0216611.
ACCESSION AX392477
VERSION AX392477.1 GI:19700776
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 Aggarwal, S., Foster, J. S., Goddard, A., Gurney, A. L., Maruoka, E. M.,
AUTHORS Wood, W. I., and Xie, M. H.
TITLE Interleukin-22 polypeptides, nucleic acids encoding the same and
JOURNAL methods for the treatment of pancreatic disorders
Genentech, Inc. (US)
Patent: WO 0216611-A 1 28-FEB-2002;
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Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 661 CCCCAGGCAATTTT 676

RESULT 8
AX403770 1152 bp DNA linear PAT 14-JUN-2002
LOCUS AX403770
DEFINITION Sequence 125 from Patent WO0077037.
ACCESSION AX403770
VERSION AX403770.1 GI:21437200
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 Ashkenazi, A., Baker, K., Botstein, D., Desnoyers, L., Eaton, D. L.,
AUTHORS Ferrera, N., Fong, S., Gao, W. Q., Gerber, H., Gertzel, M. E.,
Goddard, A., Godowski, P., Gurney, A., Kijavski, J. V., Mathier, D.,
Napier, M., Pan, J., Paoni, N., Roy, M., Tumas, D., Watanabe, C.,
Williams, P. M., Wood, W. I., and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
JOURNAL the same
Patent: WO 0077037-A 125 21-DEC-2000;
Genentech Inc. (US)
FEATURES
source Location/Qualifiers
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BASE COUNT 342 a 244 c 228 g 338 t

Query Match 98.0%; Score 676; DB 6; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.3e-176;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 GCCGCCCTGAGCAAAATCTGTAGAGCTCTTCTCTATGAGGAGCTGAGCTGCTC 120

Qy 135 CTTCTCTTGCCCTCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194

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Qy 195 CTTGCAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254

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Qy 315 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374

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Qy 375 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 434

Db 361 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

Qy 435 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 494

Db 421 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

Qy 495 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 554

Db 481 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

Qy 555 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 614

Db 541 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

Qy 615 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 674

Db 601 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660

Qy 675 CCCCCAAGCGATTTT 690

Db 661 CCCCCAAGCGATTTT 676

RESULT 9
AX454768 1152 bp DNA linear PAT 06-JUL-2002
LOCUS Sequence 353 from Patent WO0208284.
DEFINITION AX454768
ACCESSION AX454768.1 GI:21714008
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS 1 Baker, K.P., Ferrara, N., Gerber, H., Gertsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Masters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0208284-A 353 31-JAN-2002;
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone
(US); Gerber, Hanspeter (US); Gertsen, Mary E. (US); Goddard,
Andrew (US); Godowski, Paul J. (US); Gurney, Austin L. (US);
Hillan, Kenneth J. (US); Masters, Scott A. (US); Pan, James (US);
Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US);
Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William

FEATURES
Source 1. (US) Location/Qualifiers
1.1152
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 342 a 244 c 228 g 338 t
ORIGIN

Query Match 98.0%; Score 676; DB 6; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.3e-176;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTTGAGAAAGAGTTCTCTCCAGTACACAGTGTGCTGAGTTGATGTGTGCAATG 74

Db 1 CTTGAGAAAGAGTTCTCTCCAGTACACAGTGTGCTGAGTTGATGTGTGCAATG 60

Qy 75 GCCGCCCTGAGCAAAATCTGTAGAGCTCTTCTCTATGAGGAGAGAGAGAGAGAGAG 134

Db 61 GCCGCCCTGAGCAAAATCTGTAGAGCTCTTCTCTATGAGGAGAGAGAGAGAGAGAG 120

Qy 135 CTTCTCTTGCCCTCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194

Db 121 CTTCTCTTGCCCTCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180

Qy 195 CTTGCAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254

Db 181 CTTGCAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

Qy 255 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314

Db 241 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

Qy 315 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374

Db 301 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360

Qy 375 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 434

Db 361 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

Qy 435 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 494

Db 421 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480

Qy 495 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 554

Db 481 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

Qy 555 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 614

Db 541 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

Qy 615 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 674

Db 601 GAGGCTAGCTTGAGCTGATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660

Qy 675 CCCCCAAGCGATTTT 690

Db 661 CCCCCAAGCGATTTT 676

RESULT 10
AX491246 1152 bp DNA linear PAT 16-AUG-2002
LOCUS Sequence 353 from Patent WO020690.
DEFINITION AX491246
ACCESSION AX491246
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1

AUTHORS Baker, K. P., Ferrara, N., Gerber, H., Gerritsen, M. E., Goddard, A., Godowski, P. J., Gurney, A. L., Hillan, K. J., Marsters, S. A., Pan, J., Paoni, N. F., Stephan, J. P., Watanabe, C. K., Williams, P. M., Wood, W. I., and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

JOURNAL Patent: WO 0200690-A 353 03-JAN-2002;

FEATURES Genentech, Inc. (US)

source Location/Qualifiers

1. .1152
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 342 a 244 c 228 g 338 t

ORIGIN

Query Match 98.0%; Score 676; DB 6; Length 1167;
Best Local Similarity 100.0%; Pred. No. 1.3e-176;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAACAGGTTCTCTCCAGTCCAGTCCAGTTCGAGTTAGATTGTCTGCATG 74
DB 1 CTTGAGAACAGGTTCTCTCCAGTCCAGTCCAGTTCGAGTTAGATTGTCTGCATG 60

QY 75 GCGGCCCTGAGAAATGTGAGCTCTTCTTATGGGGACCCCTGGCCACAGCTGCTC 134
DB 61 GCGGCCCTGAGAAATGTGAGCTCTTCTTATGGGGACCCCTGGCCACAGCTGCTC 120

QY 135 CTTCTCTTGGCCCTCTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
DB 121 CTTCTCTTGGCCCTCTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180

QY 195 CTTGACAGTCCAACTTCCAGCAGCCCTATATACCAACCGACCTTCATGCTGCTAG 254
DB 181 CTTGACAGTCCAACTTCCAGCAGCCCTATATACCAACCGACCTTCATGCTGCTAG 240

QY 255 GAGGCTAGCTTGGCTGTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314
DB 241 GAGGCTAGCTTGGCTGTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

QY 315 GAGTCAATGATGATGAG 374
DB 301 GAGTCAATGATGATGAG 360

QY 375 GAGTCTGTCTCTCTCAATCTGATAGTTCAGCTTATATGAGAGAGAGAGAGAGAGAG 434
DB 361 GAGTCTGTCTCTCTCAATCTGATAGTTCAGCTTATATGAGAGAGAGAGAGAGAGAG 420

QY 435 CTGGCCAGGCTCAAGCAG 494
DB 421 CTGGCCAGGCTCAAGCAG 480

QY 495 CAGAGGATGATGAG 554
DB 481 CAGAGGATGATGAG 540

QY 555 AAAGCAATTGAGAACTGATTTGCTTTATGCTCTGAGAAATGCTGCAATTTGACCA 614
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QY 615 GAGGCAAGCTGAGAAATGAGATTAATACCCCTTCCCTGAGAAATTAATTAATGAG 674
DB 601 GAGGCAAGCTGAGAAATGAGATTAATACCCCTTCCCTGAGAAATTAATTAATGAG 660

QY 675 CCCCAGAGGATTTT 690
DB 661 CCCCAGAGGATTTT 676

RESULT 11 AF279437 1167 bp mRNA linear PRI 09-OCT-2000
LOCUS AF279437 Homo sapiens interleukin 22 (IL22) mRNA, complete cds.
DEFINITION AF279437

VERSION AF279437.1 GI:10719561

KEYWORDS Homo sapiens.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1167)
Xie, M. H., Aggarwal, S., Ho, W. H., Foster, J., Zhang, Z., Stinson, J., Wood, W. I., Goddard, A. D., and Gurney, A. L.
Interleukin (IL)-22, a novel human cytokine that signals through the interferon receptor-related proteins CRF2-4 and IL-22R
J. Biol. Chem. 275 (40), 31335-31339 (2000)

TITLE JOURNAL MEDLINE 20469498
PUBMED 10875937

REFERENCE 2 (bases 1 to 1167)
Xie, M. H., Aggarwal, S., Ho, W. H., Foster, J., Zhang, Z., Stinson, J., Wood, W. I., Goddard, A. D., and Gurney, A. L.
Direct Substitution
Submitted (16-JUN-2000) Molecular Biology, Genentech Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES Location/Qualifiers

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58. .597
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gene /codon_start=1
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/db_xref="GI:10719562"

CDS /translation="MAALOKSVSFLMGLTSLALLALVGGAAAPISHSRDLKSNFQDPTNRTFPLAKESLADNNTDVALIEBKLFHGISMSERCTMQVNFTEEVLFPQSDRFPQWQEVFPLRLSNLSLSTCHIEGDDLHQRNVQKLDYTKLGESEIRAIQELDLFMSLRNACI"

BASE COUNT 357 a 244 c 228 g 338 t

ORIGIN

Query Match 98.0%; Score 676; DB 9; Length 1167;
Best Local Similarity 100.0%; Pred. No. 1.3e-176;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAACAGGTTCTCTCCAGTCCAGTTCGAGTTAGATTGTCTGCATG 74
DB 1 CTTGAGAACAGGTTCTCTCCAGTCCAGTTCGAGTTAGATTGTCTGCATG 60

QY 75 GCGGCCCTGAGAAATGTGAGCTCTTCTTATGGGGACCCCTGGCCACAGCTGCTC 134
DB 61 GCGGCCCTGAGAAATGTGAGCTCTTCTTATGGGGACCCCTGGCCACAGCTGCTC 120

QY 135 CTTCTCTTGGCCCTCTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
DB 121 CTTCTCTTGGCCCTCTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180

QY 195 CTTGACAGTCCAACTTCCAGCAGCCCTATATACCAACCGACCTTCATGCTGCTAG 254
DB 181 CTTGACAGTCCAACTTCCAGCAGCCCTATATACCAACCGACCTTCATGCTGCTAG 240

QY 255 GAGGCTAGCTTGGCTGTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314
DB 241 GAGGCTAGCTTGGCTGTAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300

QY 315 GAGTCAATGATGATGAG 374
DB 301 GAGTCAATGATGATGAG 360

QY 375 GAGTCTGTCTCTCTCAATCTGATAGTTCAGCTTATATGAGAGAGAGAGAGAGAGAG 434
DB 361 GAGTCTGTCTCTCTCAATCTGATAGTTCAGCTTATATGAGAGAGAGAGAGAGAGAG 420

QY 435 CTGGCCAGGCTCAGAAAGGCTAAGCATGTCATTTGAGGTGATGACCTGCATATC 494
DB 421 CTGGCCAGGCTCAGAAAGGCTAAGCATGTCATTTGAGGTGATGACCTGCATATC 480
QY 495 CAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAGAAAGCTTGGAGAGAGTGCAGATC 554
DB 481 CAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAGAAAGCTTGGAGAGAGTGCAGATC 540
QY 555 AAAGCAATTTGAGAACTGATTTGCTTTATGTCCTGAGAAATGCTGCAATTTGACCA 614
DB 541 AAAGCAATTTGAGAACTGATTTGCTTTATGTCCTGAGAAATGCTGCAATTTGACCA 600
QY 615 GAGCAAGCTGAAAAATGAATPACTAACCCCTTCTCTGCTAGAAATPAACAATTAGATG 674
DB 601 GAGCAAGCTGAAAAATGAATPACTAACCCCTTCTCTGCTAGAAATPAACAATTAGATG 660
QY 675 CCCCAAGCGATTTT 690
DB 661 CCCCAAGCGATTTT 676

RESULT 12
LOCUS AX054620 1139 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 1 from Patent WO0073457.
ACCESSION AX054620
VERSION AX054620.1 GI:12228184
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1139)
AUTHORS Parham,C.L., de waal Malefyt,R. and Marehalli,N.L.
TITLE Mammalian interleukin-10 homologs: il-d110 and il-d210
JOURNAL Patent: WO 0073457-A 1 07-DEC-2000;
SHERING CORPORATION (US)
FEATURES
source location/Qualifiers
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/note="unidentified Homo sapiens"
59..598
/note="unnamed protein product"
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SNFOOPYITNRTFMIAKEXSLADNNTDRLGKLPFHVSVSERCYIMKQVNTLLE
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158..595
mat_peptide /product="unnamed"
BASE COUNT 337 a 238 c 227 g 333 t 4 others
ORIGIN

Query Match 97.2%; Score 671; DB 6; Length 1139;
Best Local Similarity 99.9%; Pred. No. 3.1e-175;
Matches 671; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 AGAAGAGTTCTCTCCCACTGACCAAGTCTCGAGTTAGAAATGCTGCAATGCGCG 78
DB 6 AGAAGAGTTCTCTCCCACTGACCAAGTCTCGAGTTAGAAATGCTGCAATGCGCG 65
QY 79 CCCTGAGAAATCTGAGAGCTCTTCTTATGAGGACCTGCGACAGAGTCCCTCTTC 138
DB 66 CCCTGAGAAATCTGAGAGCTCTTCTTATGAGGACCTGCGACAGAGTCCCTCTTC 125
QY 139 TCTTGGCCCTCTTGTGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 198
DB 126 TCTTGGCCCTCTTGTGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 185
QY 199 ACAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 258

DB 186 ACAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 245
QY 259 CTAGCTTGGCTGTATTAACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 318
DB 246 NTAGCTTGGCTGTATTAACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 305
QY 319 TCAGTATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
DB 306 TCAGTATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 365
QY 379 TGGCTTCCCTCAATCTGATAGGTTCCAGGCTTATATGAGAGAGAGAGAGAGAG 438
DB 366 TGGCTTCCCTCAATCTGATAGGTTCCAGGCTTATATGAGAGAGAGAGAGAGAG 425
QY 439 CCAGGCTCAGCAACAGAGCTAAGACATGTCATATTGAAGGTGATGACCTGCATATCCAGA 498
DB 426 CCAGGCTCAGCAACAGAGCTAAGACATGTCATATTGAAGGTGATGACCTGCATATCCAGA 485
QY 499 GGAATGTGCAAAAGCTGAGAGACACAGTGAAGAAAGCTTGGAGAGAGTGCAGATCAAAG 558
DB 486 GGAATGTGCAAAAGCTGAGAGACACAGTGAAGAAAGCTTGGAGAGAGTGCAGATCAAAG 545
QY 559 CAATGGAGAACTGAGATTTGCTTTATGTCCTGAGAAATGCTGATTTGACCAAGC 618
DB 546 CAATGGAGAACTGAGATTTGCTTTATGTCCTGAGAAATGCTGATTTGACCAAGC 605
QY 619 AAAGCTGAAAAATGAATPACTAACCCCTTCTCTGCTAGAAATPAACAATTAGATGCCCC 678
DB 606 AAAGCTGAAAAATGAATPACTAACCCCTTCTCTGCTAGAAATPAACAATTAGATGCCCC 665
QY 679 AAAGCGATTTT 690
DB 666 AAAGCGATTTT 677

RESULT 13
LOCUS AX048204 1132 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 44 from Patent WO0070049.
ACCESSION AX048204
VERSION AX048204.1 GI:11876994
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1132)
AUTHORS Tang,Y.T., Yue,H., Lal,P., Burford,N., Bandman,O., Baughn,M.R.,
Azimzai,Y., Lu,D.A. and Patterson,C.
TITLE Extracellular signaling molecules
JOURNAL Patent: WO 0070049-A 44 23-NOV-2000;
Incyte Genomics, Inc. (US)
FEATURES
source location/Qualifiers
1..1132
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 5571181CB1"
BASE COUNT 333 a 240 c 226 g 333 t
ORIGIN

Query Match 97.0%; Score 669; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 1.1e-174;
Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ACAGTTCTCTCTCCCACTGACCAAGTCTCGAGTTAGAAATGCTGCAATGCGCGCC 81
DB 1 ACAGTTCTCTCTCCCACTGACCAAGTCTCGAGTTAGAAATGCTGCAATGCGCGCC 60
QY 82 TGCAAGAAATCTGAGAGCTCTTCTTATGAGGACCTGCGACAGAGTGCCTCTTCT 141
DB 61 TGCAAGAAATCTGAGAGCTCTTCTTATGAGGACCTGCGACAGAGTGCCTCTTCT 120

OY		142	TGGGCCCTTGATGACAGAGAGAGACAGTGGGCCCATCAGTCCCACTGGAGGCTTACA	201
Dd		121	TGGCCCTCTTGATGACAGAGAGAGACAGTGGGCCCATCAGTCCCACTGGAGGCTTACA	180
OY		202	AGTCGAACCTTCAGACAGACCCCTATATCAACAACCGCACCTTCATCTGGCTTAAGAGAGCTA	261
Dd		181	AGTCGAACCTTCAGACAGACCCCTATATCAACAACCGCACCTTCATCTGGCTTAAGAGAGCTA	240
OY		262	GCTTGGCTGATTAACAACAACAAGCTTTGTCTCATTTGGGAGAACAATTGTTCCAAGAGTCA	321
Dd		241	GCTTGGCTGATTAACAACAACAAGCTTTGTCTCATTTGGGAGAACAATTGTTCCAAGAGTCA	300
OY		322	GTATGAGTGAACCGCTGCATCTGATGTAAGACAGAGTGTGAACCTTCAACCCTTGAAGAAGTGC	381
Dd		301	GTATGAGTGAACCGCTGCATCTGATGTAAGACAGAGTGTGAACCTTCAACCCTTGAAGAAGTGC	360
OY		382	TGTTCCCTCAATCTGATGTAAGTTCAGAGCTTATATATGACAGAGTGTGTCCTTCTGSCCA	441
Dd		361	TGTTCCCTCAATCTGATGTAAGTTCAGAGCTTATATATGACAGAGTGTGTCCTTCTGSCCA	420
OY		442	GGCTCAGCAACAGGCTAAAGCAGCATGTCAATTTGAAGTGAATGACTGTCTATTCAGAGGA	501
Dd		421	GGCTCAGCAACAGGCTAAAGCAGCATGTCAATTTGAAGTGAATGACTGTCTATTCAGAGGA	480
OY		502	ATGTGCAAAAAGCTGAAGAGACACAGTGAAAAAAGCTTGGAGAGAGTGAAGATCAAACAA	561
Dd		481	ATGTGCAAAAAGCTGAAGAGACACAGTGAAAAAAGCTTGGAGAGAGTGAAGATCAAACAA	540
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Dd		541	TTGAGAGA CTGATTTGTGTTTATGTCTCTGAGAAA TGCC TGCATTTGAC CAGAGCAA	600
OY		622	GCTGAAAAATGAATACTAACCCCCCTTCCCTGCTAGAAATAACAATTAGATGCCCAA	681
Dd		601	GCTGAAAAATGAATACTAACCCCCCTTCCCTGCTAGAAATAACAATTAGATGCCCAA	660
OY		682	GCGATTTTT 690	
Dd		661	GCGATTTTT 669	

RESULT 14
AX151713 1116 bp DNA linear PAT 22-JUN-2001

LOCUS AX151713

DEFINITION Sequence 14 from Patent WO0140467.

ACCESSION AX151713

VERSION AX151713.1 GI:14533647

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1116)
Pisaneselli,S.R., Xu,W., Kindsvogel,W. and Chen,Z.
Human cytokine receptor
Patent: WO 0140467-A 14 07-JUN-2001;
ZymoGenetics, Inc. (US)

FEATURES

Source Location/Qualifiers

1..1116 /organism="Homo sapiens"

/db_xref="taxon:9606"

21..560 /note="unnamed protein product"

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/db_xref="gi:14533648"

/translation="MAALQKSVSFSLMGTLATSCLLILALLVQGAAAPISHSORLDK
SNPOOPYITNRTFMFLAKESIASLADNNNTDVLRLIGELKFHGVSMSERCYLMDQVINTFLEB
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BASE COUNT 336 a 229 c 222 g 329 t

ORIGIN

Query Match	92.6%;	Score 639;	DB 6;	Length 1116;	
Best Local Similarity	100.0%;	Pred. No. 2.4e-166;			
Matches 639;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	52	TCGAGTTAGAAATGTCGTGCAMTGGCCGCCCTGCGAAGATCTGAGCTCTTTCCTTAAG	111		
Db	1	TCGAGTTAGAAATGTCGTGCAMTGGCCGCCCTGCGAAGATCTGAGCTCTTTCCTTAAG	60		
Qy	112	GGACCTGGCCACCAAGCTGCTCTCTTCTTGGCCCTCTTGGTACAGGAGGAGACACTG	171		
Db	61	GGACCTGGCCACCAAGCTGCTCTCTTCTTGGCCCTCTTGGTACAGGAGGAGACACTG	120		
Qy	172	CGGCCATACAGCTCCCACTGCAAGCTTGAACAAGTCCAACTTCCAGCAGCCCTATATCA	231		
Db	121	CGGCCATACAGCTCCCACTGCAAGCTTGAACAAGTCCAACTTCCAGCAGCCCTATATCA	180		
Qy	232	ACCGCACCCTCATGCTGGCTAAGAGAGCTAGCTTGGCTGATTAACACACAGCCTTGCT	291		
Db	181	ACCGCACCCTCATGCTGGCTAAGAGAGCTAGCTTGGCTGATTAACACACAGCCTTGCT	240		
Qy	292	TCATTTGGGGAGAACTGTTCCACGAGTCAATATAGTACAGCCGCTATCTGATGAAC	351		
Db	241	TCATTTGGGGAGAACTGTTCCACGAGTCAATATAGTACAGCCGCTATCTGATGAAC	300		
Qy	352	AGGTGCTGAACCTTCAACCTTGAAGAAAGTGTCTCCCTCAATCTGAATAGGTTCCAGCCT	411		
Db	301	AGGTGCTGAACCTTCAACCTTGAAGAAAGTGTCTCCCTCAATCTGAATAGGTTCCAGCCT	360		
Qy	412	ATAATGCGAGAGTGTGTGCTCTTCTGCGACAGGCTCAGCAACAGGCTAAGCATATGATA	471		
Db	361	ATAATGCGAGAGTGTGTGCTCTTCTGCGACAGGCTCAGCAACAGGCTAAGCATATGATA	420		
Qy	472	TTGAAGGTGATGACCTGECATATCCAGAGAAATGTGCAAAAAGCTGAAGACACAGTGA	531		
Db	421	TTGAAGGTGATGACCTGECATATCCAGAGAAATGTGCAAAAAGCTGAAGACACAGTGA	480		
Qy	532	AGCTTGGAGAGAGTGTGAGAAATCAAGCAATTGGAAGACTGGATTGCTGTTATGTCTC	591		
Db	481	AGCTTGGAGAGAGTGTGAGAAATCAAGCAATTGGAAGACTGGATTGCTGTTATGTCTC	540		
Qy	592	TGAGAAATGCTGCTGATTTGACAGAGCAAAAGCTGAAATAATGAAATTAACCCCTTTCC	651		
Db	541	TGAGAAATGCTGCTGATTTGACAGAGCAAAAGCTGAAATAATGAAATTAACCCCTTTCC	600		
Qy	652	CTGCTAGAAATTAACAATTAGATGCCCCCAAGCGATTTTT	690		
Db	601	CTGCTAGAAATTAACAATTAGATGCCCCCAAGCGATTTTT	639		
RESULT 15					
AX179578		1116 bp	DNA	linear	PAT 06-AUG-2001
LOCUS		Sequence 1 from Parent W00146422.			
DEFINITION		AX179578			
ACCESSION		AX179578.1			
VERSION		GI:15132010			
KEYWORDS					
SOURCE		human.			
ORGANISM		Homo sapiens			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE		1 (bases 1 to 1116)			
AUTHORS		Presnell,S.R. and Kindsvogel,W.			
TITLE		Cytokine zcyt108			
JOURNAL		Patent: WO 0146422-A 1 28-JUN-2001;			
		ZymoGenetics, Inc. (US)			
FEATURES		Location/Qualifiers			
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BASE COUNT 336 a 229 c 222 g 329 t
ORIGIN

Query Match 92.6%; Score 639; DB 6; Length 1116;
Best Local Similarity 100.0%; Pred. No. 2,4e-166;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TCGAGTTAGAAATGCTGCAATGGCCGCTGCAGAAATCTGTGAGCTCTTCTCTTATGG 60
Oy 52 TCGAGTTAGAAATGCTGCAATGGCCGCTGCAGAAATCTGTGAGCTCTTCTCTTATGG 111
Db 1 TCGAGTTAGAAATGCTGCAATGGCCGCTGCAGAAATCTGTGAGCTCTTCTCTTATGG 60
Oy 112 GGACCTGGCCACGAGCTGCTCTTCTCTTGGCCCTCTTGGTACAGGAGAGAGAGCTG 171
Db 61 GGACCTGGCCACGAGCTGCTCTTCTTGGCCCTCTTGGTACAGGAGAGAGAGAGCTG 120
Oy 172 GGCCCATGAGCTCCGCTGAGGCTTGAACAATCCACTCCAGCAGCCCTATATCACCA 231
Db 121 GGCCCATGAGCTCCGCTGAGGCTTGAACAATCCACTCCAGCAGCCCTATATCACCA 180
Oy 232 ACCGCACTTATGCTGCTAAGAGGCTAGCTGCTGATTAACAACAGACGTTGCTC 291
Db 181 ACCGCACTTATGCTGCTAAGAGGCTAGCTGCTGATTAACAACAGACGTTGCTC 240
Oy 292 TCATTGGGGAGAAAGTGTTCACGAGATCAGTATGAGTGAAGGCTGCTATCTGATGAGC 351
Db 241 TCATTGGGGAGAAAGTGTTCACGAGATCAGTATGAGTGAAGGCTGCTATCTGATGAGC 300
Oy 352 AGGTGCTGAACCTTCAACCTTGAAGAAGTGTTCCTCAATCTGATAGTTCCAGCCTT 411
Db 301 AGGTGCTGAACCTTCAACCTTGAAGAAGTGTTCCTCAATCTGATAGTTCCAGCCTT 360
Oy 412 ATATGCAGAGAGTGTGCTCTTCTGCGCAGGCTGAGCAAGGCTAAGCAATGTCATA 471
Db 361 ATATGCAGAGAGTGTGCTCTTCTGCGCAGGCTGAGCAAGGCTAAGCAATGTCATA 420
Oy 472 TTGAAGGTGATGACCTGCATATCCAGAGAAATGTGCAAAAGCTGAAGGACACAGTGA 531
Db 421 TTGAAGGTGATGACCTGCATATCCAGAGAAATGTGCAAAAGCTGAAGGACACAGTGA 480
Oy 532 AGCTTGAAGAGAGTGAAGATCAAAAGCAATGGAAGCTGATTTGCTGTTATGCTC 591
Db 481 AGCTTGAAGAGAGTGAAGATCAAAAGCAATGGAAGCTGATTTGCTGTTATGCTC 540
Oy 592 TGAGAAATGCTGCTTGTGACCAAGCAAAAGCTGAAAAATGATTAATACCCCTTTCC 651
Db 541 TGAGAAATGCTGCTGATTTGACCAAGCAAAAGCTGAAAAATGATTAATACCCCTTTCC 600
Oy 652 CTGCTAGAAATTAACATTAAGTGCACCAAGGATTTT 690
Db 601 CTGCTAGAAATTAACATTAAGTGCACCAAGGATTTT 639

Search completed: July 19, 2003, 16:16:17
Job time : 1156.93 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:06:30 ; Search time 604.063 Seconds

(without alignments)
18499.535 Million cell updates/sec

Title: US-09-751-797-24

Sequence: 1 tgcacaagaagaatcttcag.....gatccccaagaagcattttt 690

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estda:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estow:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vtc:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136.6	19.8	700	11	AK005228 Mus muscu
2	70.4	10.2	389	17	AQ104025 HS_3108 B
3	61.2	8.9	562	17	AZ449260 IM0247J21
4	41.2	6.0	507	10	AM074124 XM080b01.x
5	40.2	5.8	469	12	BP063392 7b89c03.x
6	40.2	5.8	510	10	AM451058 UT-H-B13-

7	40.2	5.8	522	9	A1061426
8	40.2	5.8	540	9	AU152179
9	40.2	5.8	540	14	BQ453405
10	40.2	5.8	543	10	AW830399
11	40.2	5.8	556	9	AU156874
12	40.2	5.8	594	9	AU1569808
13	40.2	5.8	621	10	AW779824
14	40.2	5.8	623	9	A1955085
15	40.2	5.8	635	10	AW378565
16	40.2	5.8	703	14	BM716928
17	40.2	5.8	715	12	BF791898
18	40.2	5.8	724	14	BQ775024
19	40.2	5.8	923	14	BQ221320
20	40.2	5.8	950	14	BQ220719
21	40.2	5.8	1004	13	BM542314
22	40.2	5.8	1033	14	BQ052523
23	40.2	5.8	1045	14	BM802921
24	40.2	5.8	1045	11	BC016144
25	39.6	5.7	4272	11	BC016144
26	39.2	5.7	648	12	BF168673
27	39.2	5.7	427	12	BG650820
28	39.2	5.7	452	12	BF008714
29	39.2	5.7	504	10	AW307469
30	39.2	5.7	514	14	BQ740862
31	39.2	5.7	536	9	A1166298
32	39.2	5.7	564	9	A1984038
33	39.2	5.7	718	10	AW167713
34	38.6	5.6	1101	17	CNS016HG
35	38.2	5.5	618	13	BM591464
36	38.2	5.5	632	13	BM601535
37	37.8	5.5	663	10	BE298070
38	37.6	5.4	442	14	BQ762256
39	37.6	5.4	530	12	BG300244
40	37.6	5.4	610	13	B1777354
41	37.6	5.4	628	14	BQ762255
42	37.6	5.4	635	13	B1957104
43	37.4	5.4	386	9	AA460144
44	37.4	5.4	442	9	A1651900
45	37.4	5.4	504	10	AW291394

ALIGNMENTS

RESULT 1	AK005228	700 bp	MRNA	linear	HTC 19-JAN-2002
LOCUS	AK005228				
DEFINITION	Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500012D04:interleukin 10-related T cell-derived inducible factor, full insert sequence.				
ACCESSION	AK005228	GI:12837639			
VERSION	AK005228.1				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (strain:C57BL/6J) adult male cerebellum cDNA to mRNA, clone_11b:RIKEN full-length enriched mouse cDNA library				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Suganara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				

REFERENCE
AUTHORS

3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Saeki, N., Carninci, P., Komori, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system -384-format
Genome Res. 10 (11), 1757-1771 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

4
Kawai, Y., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Komori, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanka, I., Saito, T., Okazaki, Y., Gotohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batilov, S., Casavant, T., Felschmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staib, F., Suzuki, R., Tomita, M., Wagner, L., Mashio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bulic, C., Flecher, C., Fujita, M., Gariboldi, M., Guetlich, S., Hill, D., Holman, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyman, B., Yoshida, K., Hasegawa, Y., Kawai, H., Kohetsuki, S. and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

5 (bases 1 to 700)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bulic, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hirooka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, Y., Kojima, Y., Komori, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Teijima, Y., Toya, T., Yamamura, T., Yamanka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-resgsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

TITLE
JOURNAL
COMMENT

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3']. cDNA was cleaved with XhoI and SclI. Cloning sites, 5' end, XhoI; 3'

FEATURES
source

end: SclI. Host: SOLR.
Location/Qualifiers

1..700
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="RANTOM:DB:1500012D04"
/db_xref="MGDI:1900981"
/db_xref="taxon:10090"
/clone="1500012D04"
/sex="male"
/tissue_type="cerebellum"
/clone_id="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1..700
/gene="Itif"
1..700
/gene="Itif"
/note="data source:MGDI, source key:MGDI:1355307, evidence:155
interleukin 10-related T cell-derived inducible factor"
/db_xref="MGDI:1355307"
/db_xref="MGDI:1355307"

BASE COUNT

255 a 105 c 133 g 207 t
Query Match 19.8%; Score 136.6; DB 11; Length 700;
Best Local Similarity 75.8%; Pred. No. 4.2e-29;
Matches 169; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

ORIGIN

468 CATTTGAAGTGTGATGACCTGCTATTCAGAGGATGTCGCAAAAGCTTAAGACACAGT 527
37 CACATCAGCGGTGAGCAGACCAACATCCAGAGATGTCAGAGGCTTAAGACACAGT 96
528 AAAAAGCTTGAGAGAGAGTGAGAGATCAAGCAATTTGAGAGTCTGCTGTTATG 587
97 AAAAAGCTTGAGAGAGAGTGAGAGATCAAGCAATTTGAGAGTCTGCTGTTATG 156
588 TCTCTGAGAAATGCTGCTGATTTGACACAGAGCAAAAGCTGAATGATTAACCCCT 647
157 TCTCTGAGAAATGCTGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 216
648 TTCCTGCTGAGAAATGAGATTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
217 CTGCTGCTGAGAAATGAGATTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 259

RESULT 2

LOCUS AO104025/c 389 bp DNA linear GSS 28-AUG-1998

DEFINITION HS_3108_B1_C01_T7 CIT Approved Human Genomic Sperm Library D Homo

ACCSSION AO104025 sapiens genomic clone Plate=3108 Col=1 Row=F, DNA sequence.

VERSION AO104025.1 GI:3478961

KEYWORDS

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 389)

MAHATAS G.G., WALLACE J.C., SMITH K., SWATZELL S., HOLZMAN T.,
KELLEY A., SHAKER, R., FURLONG, J., YOUNG, J., ZHAO, S., ADAMS, M.D. and
HOOD, L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

Contract: Mahatras CG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Sequence Tagged Connector

Site 1: Sail; Site 2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Library constructed by Life Technologies."

BASE COUNT
ORIGIN

Query Match 59 a 172 c 113 g 163 t

Query Match 6.0%; Score 41.2; DB 10; Length 507;
Matches 88; Conservativity 0; Mismatches 78; Indels 0; Gaps 0;

QY 115 CCTGGGACACAGCTGCTCTCTCTTGGCCCTCTTGTGACAGAGAGAGAGAGCTGGC 174
DB 246 CCGGAGGAGGAGCT 305
QY 175 CCATAGCTCCCTGACAGCTTGAACAGTCCCACTTCCAGCAGCCCTATATACCAAC 234
DB 306 CCGATAGCTTCGGCTGGGCTCTCCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCA 365
QY 235 GCACCTCATGCTGCTAGAGAGGCTGCTGCTGATATACCAAC 280
DB 366 CCACCTCTCTTCA 411

RESULT 5
BF063392 469 bp mRNA linear EST 16-OCT-2000
LOCUS
DEFINITION 7h89c03.x1 NCI_CGAP Col6 Homo sapiens cDNA clone IMAGE:3523140 3'
ACCESSION BF063392
VERSION BF063392.1 GI:10822302
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 469)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Glibco
High quality sequence stop: 457.

FEATURES

source

1..469
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3523140"
/clone_lib="NCI CGAP Col6"
/tissue_type="Colon Tumor, RER+"
/lab_host="DH10B"
/note="Organ: Colon; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Col6 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(clonids 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldi.

BASE COUNT
ORIGIN

49 a 159 c 102 g 159 t

Query Match

5.8%; Score 40.2; DB 12; Length 469;

Best Local Similarity 56.4%; Pred. No. 1.1;
Matches 75; Conservativity 0; Mismatches 58; Indels 0; Gaps 0;

QY 115 CCTGGGACACAGCTGCTCTCTCTTGGCCCTCTTGTGACAGAGAGAGAGAGCTGGC 174
DB 251 CCGGAGGAGGAGCT 310
QY 175 CCATAGCTCCCTGACAGCTTGAACAGTCCCACTTCCAGCAGCCCTATATACCAAC 234
DB 311 CCGATAGCTTCGGCTGGGCTCTCCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCA 370
QY 235 GCACCTCATGCT 247
DB 371 CCACCTCTCTCT 383

RESULT 6
AM451058 510 bp mRNA linear EST 17-FEB-2000
LOCUS
DEFINITION UI-H-B13-a10-0-UI.s1 NCI_CGAP Subs Homo sapiens cDNA clone
ACCESSION AM451058
VERSION AM451058.1 GI:6991834
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 510)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library Preparation: M.B. Soares Lab clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 1-63, >(GAAA
)#Simple_repeat
Seq primer: M13 Forward
POLYA-Yes.

FEATURES

source

1..510
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2736666"
/clone_lib="NCI CGAP Subs"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Subs
is a subtracted library derived from NCI CGAP Sub4. The
NCI CGAP Subs library had 3 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE clonids
1323376-1323911, 1456008-1456775, 1500552-1502855);
NCI CGAP Kids pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
(IMAGE clonids 1323912-1325831, 1471368-1472903,
1492104-1493255); NCI CGAP Lys pool 1 LLAM 3578-3582,
3851-3854 (IMAGE clonids 1444920-1417991, 1520904-1522439
); NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720,
3733-3735 (IMAGE clonids 1257096-1258631, 1469064-1470983,
1475592-1476743); NCI CGAP P72 pool 1 LLAM 2457-2459,
2758-2759, 3062-3068 (IMAGE clonids 985608-986759
1101192-1101959, 1217928-1220615); NCI CGAP Col6 pool 1
LLAM 2644-2653, 2871-2872 (IMAGE clonids 1057416-1061255
1144584-1145351). (10% of the driver population), plus a

Query Match	5.8%	Score 40.2	DB 10	Length 510
Best Local Similarity	56.4%	Pred. No. 1.1		
Matches	75	Conservative	0	Mismatches 58
				Indels 0
				Gaps 0
Qy	115	CCCTGGCCACGAGCTCCTCTTCTCTTGGCCCTCTTGATACAGGAGAGACAGCTGC	174	
Db	260	CCCCGGCCCCAGCTTCTTCTTCTTCTTGCTCTGGGGGCTCTGGCACTGGCTGCTC	319	
Qy	175	CCATCAGTCCCACTGCAGGCTTGCAAGTCCAATTCCAGACGCCATATACCAACC	234	
Db	320	CCGATGGCTTCGGCTTGGGGCTTCCACGCTTCTCTGTCTCTTGGTGGTGTCCA	379	
Qy	235	GCACCTTCATGCT	247	
Db	380	CCACCTTCTTCT	392	

FEATURES	SOURCE	Location/Qualifiers
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/db_xref="caxon:9606"		
/clone="IMAGE:1700117"		
/clone_1ib="Gessler W1lms tumor"		
/sex="pooled (6)"		
/lab_host="DH10B"		

Oy	115	CCCTGGGCACACAGGAGCTCCTCTCTCTTGGCCCTTGGTACAGAGAGAGACACTGGGC	174
Db	228	CCCCGGCCCCAGCTTCTTCTTCTTCTTCTTCTGCTCTGGGGGTCCTGGCAGCTGGCTGTTCT	287
Oy	175	CCATCAGCTCCCATCGACGCTTGACAAGTCCCACTTCCAGCAGCCCTATATCAACAAC	234
Db	288	CCGATAGCTTCCGCTTGCGGCTCTCCAGCCCTTCTGCTGCTCTCTCTGAGTGATCCCA	347
Oy	235	GCACCTTCATGCT	247
Db	348	CCACCTCTTCTCT	360

LOCUS	AU152179	540 bp	mRNA	linear	EST 05-Aug-2002
DEFINITION	AU152179 NT2RP3 Homo sapiens cDNA clone NT2RP3000357 3', mRNA				
ACCESSION	AU152179				
VERSION	AU152179.1	GI:11013700			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.)				
TITLE	HRI human cDNA project (Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Ozawa,M., Nakamura,Y., Nagai,T., Sugano,S., Isogai,T.)				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel.: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. Location/Qualifiers 1..540 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="NT2RP3000357" /clone_1id="NT2RP3" /cell_type="teratocarcinoma" /cell_line="NT2" /note="vector: pWELISFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction" 63 a 179 c 117 g 177 t 4 others				
BASE COUNT					

FEATURES	Location/Qualifiers
source	1. .594

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Best Local Similarity	56.4%;	Pred. No. 1.2;		
Matches 75;	Conservative 0;	Mismatches 58;	Indels 0;	Gaps 0;

Db 433 CCACCTTCTTCT 445

VERSION AW779824.1 GI:7794427
KEYWORDS EST.

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/INLNL, send email to:
infeelmage@inl.gov

SECRET

BASE COUNT	65 a	207 c	146 g	201 t	2 others
ORIGIN					

OY 115 CCTGGGCACACAGTGGCTCCTTCTCTTTGGGCTCTTGGTACAGGAGAGACAGCTGGC 174
Db 251 CCCGGGCCCCAGCTTCTTCTCTTCTTGGCTCTCTGGGGGTCCTGGACAGCTGGCTGTCNC 310
OY 175 CCATCAGCTCCCACTGAGGCTTACAAAGTCAACTTCACAGAGCCCTATATCACCMACC 234

RESULT 14

ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	

Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: Greg Lemmon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.llnl.gov/bbrp/image/image.html

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Insert Length: 1034 Std Error:
Seq primer: -40UP from Glbco
High quality sequence stop: 444.
Location/Qualifiers
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FEATURES
source
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 /lab_host="DH10B"
 /note="Vector: pTRT3D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not 1; Site 2: Eco RI; Plasmid DNA
 from the normalized library NCI CGAP GC4 was prepared, and
 ss circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (cloneds
 1257096-1258631, 1469064-1470993, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 65 a 205 c 144 g 207 t 2 others

ORIGIN

Query Match 5.8%; Score 40.2; DB 9; Length 623;
 Best Local Similarity 56.4%; Pred. No. 1.2; Mismatches 58; Indels 0; Gaps 0;
 Matches 75; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 115 CCTGGCCACAGCTGCTCTCTCTGCGCTTGTACAGGAGAGACAGCTGCGC 174
 DB 252 CCCCCGCCCCAGCTTCTTCTTCTGCTCTGCGGCTCTGCGACCTGGCTGCTC 311
 QY 175 CCATCAGCTCCACTGACAGCTTGACAAAGTCAACTTCACAGACCTATATCAACAAC 234
 DB 312 CCGATAGCTTCGGCTTGCGGCTCTCCAGCCCTTCTGCTGCTGCTGCTGCTGCTCA 371
 QY 235 GCACCTTCATGCT 247
 DB 372 CCACCTTCTTCT 384

RESULT 15

AM378565/c

LOCUS AM378565 695 bp mRNA linear EST 04-FEB-2000

DEFINITION PM0-HT0224-181099-001-b03 HT0224 Homo sapiens cDNA, mRNA sequence.

AM378565

AM378565.1 GI:6883224

EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 695)

HCGP <http://www.ludwig.org.br/ORESTES>.

The FAPESP/LICR Human Cancer Genome Project

Unpublished (1999)

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL.

(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM0&ct2=PM0-HT0224-181099-001-b03&ct3=1999-10-18&ct4=1>)

Seq primer: puc 18 forward

High quality sequence start: 43

High quality sequence stop: 626.

Location/Qualifiers

1..695

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_id="HT0224"

/dev stage="Adult"

/note="Organ: head neck; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 206 a 174 c 235 g 80 t

ORIGIN

Query Match 5.8%; Score 40.2; DB 10; Length 695;
 Best Local Similarity 56.4%; Pred. No. 1.3; Mismatches 58; Indels 0; Gaps 0;
 Matches 75; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 115 CCTGGCCACAGCTGCTCTCTCTGCGCTTGTACAGGAGAGACAGCTGCGC 174
 DB 423 CCCCCGCCCCAGCTTCTTCTTCTGCTCTGCGGCTCTGCGACCTGGCTGCTC 364
 QY 175 CCATCAGCTCCACTGACAGCTTGACAAAGTCAACTTCACAGACCTATATCAACAAC 234
 DB 363 CCGATAGCTTCGGCTTGCGGCTCTCCAGCCCTTCTGCTGCTGCTGCTGCTGCTCA 304
 QY 235 GCACCTTCATGCT 247
 DB 303 CCACCTTCTTCT 291

Search completed: July 19, 2003, 19:39:11
 Job time : 608.313 secs

XX MPI: 2000-422495/36.
 DR P-PSDB; AA192879.
 PT New nucleic acid molecule encoding a T cell derived inducible factor
 for treating asthma, an allergy or lymphoma
 XX
 PS Claim 1; Page 38; 46pp; English.
 XX
 CC This cDNA encodes a human T cell derived inducible factor (TIF). The gene
 CC was mapped to chromosome 12q15. The human TIF was identified based on
 CC homology to a murine TIF, which was identified by subtraction cloning
 CC from a murine lymphoma cell line BW5147 in the presence or absence of
 CC interleukin 9 (IL-9). BW5147 can be grown in vitro, without the need to
 CC add any cytokines to its culture medium. Many IL-9 activities are
 CC mediated by activation of STAT transcription factors. The novel TIFs were
 CC expressed in the presence of IL-9, but not in its absence. TIFs induce
 CC STAT activation in cells. They can be used, e.g., in the stimulation of
 CC regeneration of targeted tissues. Their inhibitors or antagonists can be
 CC used to retard, prevent or inhibit differentiation of other tissues. The
 CC TIFs and their coding sequences are useful in the treatment of asthma,
 CC allergies and lymphoma (claimed). They are also useful for identifying
 CC compounds that inhibit or activate T cell induced factor activity in a
 CC cell (claimed).
 XX
 SQ Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;
 Query Match 100.0%; Score 690; DB 21; Length 690;
 Best Local Similarity 100.0%; Pred. No. 1.8e-193;
 Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGCACAGAGAAATCTTTCGAAACAGGTTCTCTCCCGATCACCAGTTGCTGAGTTAG 60
 DB 1 TGCACAGAGAAATCTTTCGAAACAGGTTCTCTCCCGATCACCAGTTGCTGAGTTAG 60
 QY 61 AATTGCTGCAATGGCCGCGCCCTGACAGAAATCTGTGAGCTTTTCCATTAGGGGAGCCCTGG 120
 DB 61 AATTGCTGCAATGGCCGCGCCCTGACAGAAATCTGTGAGCTTTTCCATTAGGGGAGCCCTGG 120
 QY 121 CCACACAGCTGCTCTCTCTCTCTGAGCCCTGACAGAAATCTGTGAGCTTTTCCATTAGGGGAGCCCTGG 180
 DB 121 CCACACAGCTGCTCTCTCTCTCTGAGCCCTGACAGAAATCTGTGAGCTTTTCCATTAGGGGAGCCCTGG 180
 QY 181 GGTCCCATGAGAGGCTTGAAGTCCAACTTCCAGAGAGCCCTATACACCAACCGGACCT 240
 DB 181 GGTCCCATGAGAGGCTTGAAGTCCAACTTCCAGAGAGCCCTATACACCAACCGGACCT 240
 QY 241 TCATGCTGCTAAGAGGCTAGCTTGTGATTAACAACAACAGCTTCTCATTTGGGG 300
 DB 241 TCATGCTGCTAAGAGGCTAGCTTGTGATTAACAACAACAGCTTCTCATTTGGGG 300
 QY 301 AGAAAGTGTCCACGAGAGTCAAGTATGAGAGGCTCTATCTGATGAAGAGGTGCTGA 360
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 QY 361 ACTTACACCTTGAAGAGTCTTCCCAATCTGATAGTTCCAGCTTATATTCACAG 420
 DB 361 ACTTACACCTTGAAGAGTCTTCCCAATCTGATAGTTCCAGCTTATATTCACAG 420
 QY 421 AGGTGCTGCTTCTCTGAGCAGGCTCAGCAACAGGCTAAGCAATCTATTTGAAGTG 480
 DB 421 AGGTGCTGCTTCTCTGAGCAGGCTCAGCAACAGGCTAAGCAATCTATTTGAAGTG 480
 QY 481 ATGACCTGATATCCAGAGAGTGTGCAAAAGCTGAAGACACAGTGAAGAAAGCTTGGAG 540
 DB 481 ATGACCTGATATCCAGAGAGTGTGCAAAAGCTGAAGACACAGTGAAGAAAGCTTGGAG 540
 QY 541 AGAGTGAAGAGATCAAGAGATTTGGAATGCTGTTATGCTCTGAGAAAG 600
 DB 541 AGAGTGAAGAGATCAAGAGATTTGGAATGCTGTTATGCTCTGAGAAAG 600
 QY 601 CCTGATTGACAGAGCAAGCTGAAGAAATGATTAACCCCTTTCCCTGATAGAA 660
 DB 601 CCTGATTGACAGAGCAAGCTGAAGAAATGATTAACCCCTTTCCCTGATAGAA 660

DB 601 CCTGATTGACAGAGCAAGCTGAAGAAATGATTAACCCCTTTCCCTGATAGAA 660
 QY 661 ATACAAATTTAGATGCCCCCAAGCGATT 690
 DB 661 ATACAAATTTAGATGCCCCCAAGCGATT 690
 RESULT 2
 AAS14875
 ID AAS14875 standard; cDNA; 690 BP.
 AC AAS14875;
 XX 19-DEC-2001 (first entry)
 DE Human cDNA encoding T cell derived inducible factor, TIF.
 KW Human; T cell derived inducible factor; TIF; src; antiallergic;
 KW antiallergic; cytokine; interleukin-9; IL-9; STAT transcription factor;
 KW cancer; lymphoma; immune system disorder; allergy; asthma;
 KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
 KW thyroiditis; melanoma; hepatoma.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 72..611
 FT /tag= a
 FT /product= "TIF"
 FT /transl_except= (pos:159..161,aa:Glu)
 FT /transl_except= (pos:378..380,aa:Ile)
 FT /transl_except= (pos:405..407,aa:Arg)
 FT /transl_except= (pos:519..521,aa:Cys)
 PN US2001024652-A1.
 PD 27-SEP-2001.
 PF 29-DEC-2000; 2000US-0751797.
 XX 18-OCT-1999; 99US-0419568.
 PR 26-OCT-1998; 98US-0178973.
 PR 16-JUL-1999; 99US-0354243.
 XX (DUMO/) DUMOUTIER L.
 PA (LOUA/) LOUAHED J.
 PA (RENA/) RENAUD J.
 PI Dumoutier L, Louahed J, Renaud J;
 XX
 DR MPI: 2001-638496/73.
 DR P-PSDB; AAU09091.
 PT New isolated nucleic acid molecules encoding T cell inducible factors,
 PT useful as markers for expression or effect of interleukin (IL)-9 in a
 PT subject and diagnosing susceptibility to asthma or allergy
 XX
 PS Claim 1; Page 17; 26pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule, which encodes
 CC a T cell derived inducible factor (TIF) which are upregulated by the
 CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor
 CC activation. The TIF proteins (or their mutants) may be used to test IL-9
 CC ant/agonists for their potency against lymphomas, immune system
 CC disorders, diabetes and thyroiditis. TIF molecules promote regeneration
 CC or inhibit differentiation of tissue types in which they are active and
 CC therefore be used to develop treatments for melanomas and hepatomas.
 CC The present sequence encodes human TIF.
 SQ Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;
 Query Match 100.0%; Score 690; DB 22; Length 690;


```

QY 601 CTGCAATTGACGAGCAAGCTGAAATGATATCTAACCCCTTCCCTGCTAGAA 660
DB 601 CCGCATTACCAAGCAAGCTGAAATGATATCTAACCCCTTCCCTGCTAGAA 660
QY 661 ATACCAATTAGATGCCCCCAAGCGATTTT 690
DB 661 ATACCAATTAGATGCCCCCAAGCGATTTT 690

RESULT 4
AAD27150 standard; DNA; 690 BP.
AC AAD27150;
XX
XX 09-APR-2002 (first entry)
XX
XX Human T cell derived inducible factor (TIF) beta cDNA.
XX
XX T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;
XX protein therapy; STAT activation; differentiation; human; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 72..611
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XX FT /product= "Human TIF beta"
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XX FT /transl_except= (pos:378..380, aa:Ile)
XX FT /transl_except= (pos:405..407, aa:Arg)
XX FT /transl_except= (pos:519..521, aa:Cys)
XX
XX US631613-B1.
XX
XX 18-DEC-2001.
XX
XX 18-OCT-1999; 99US-0419568.
XX
XX 26-OCT-1998; 98US-0178973.
XX
XX 16-JUL-1999; 99US-0354243.
XX
XX (LUDWIG) INST CANCER RES.
XX
XX Dumoutier L, Louhed J, Renaud J;
XX
XX WPI; 2002-105277/14.
XX
XX P-PSDB; AAE16554.
XX
XX Nucleic acids encoding T cell derived inducible factors useful for
XX inducing STAT activation in cells -
XX
XX Claim 1; Column 31-32; 24pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule, which
XX encodes a T cell derived inducible factor comprising an amino acid
XX sequence encoded by 6 defined nucleotide sequences. The nucleic acid
XX molecules are shown to be up regulated by the cytokine interleukin-9
XX (IL-9) and are described as T Cell Derived Inducible Factors (TIFs). The
XX invention is used in protein therapy. The nucleic acid molecules encode
XX proteins which induce STAT activation in cells. They can be used, for
XX example, in the stimulation of regeneration of targeted tissues.
XX Further, their inhibitors or antagonists can be used to retard, prevent
XX or inhibit differentiation of other tissues. The present sequence is
XX human TIF beta cDNA.
XX
XX Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;
XX
XX Query Match 100.0%; Score 690; DB 24; Length 690;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-193;
XX Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TGACAGAGAGATCTTCAGAAACAGTTCTCTTCCCAAGTACCAAGTTGCTGAGTAG 60
DB 1 TGACAGAGAGATCTTCAGAAACAGTTCTCTTCCCAAGTACCAAGTTGCTGAGTAG 60
QY 61 AATTGCTGCAATGAGCGCCCTGACAGAAATCTGTAGAGCTCTTCCCTTATGAGGACCTGG 120
DB 61 AATTGCTGCAATGAGCGCCCTGACAGAAATCTGTAGAGCTCTTCCCTTATGAGGACCTGG 120
QY 121 CCACAGCTGCTCCTCTTCTCTTGGCCCTCTTGGTACAGGAGAGAGAGCTGCGCCATCA 180
DB 121 CCACAGCTGCTCCTCTTCTCTTGGCCCTCTTGGTACAGGAGAGAGAGCTGCGCCATCA 180
QY 181 GCTCCACATGCAAGGCTTGAAGAAGTCCAACTTCAGAGAGCCCTATACCAACCGACCT 240
DB 181 GCTCCACATGCAAGGCTTGAAGAAGTCCAACTTCAGAGAGCCCTATACCAACCGACCT 240
QY 241 TCATGCTGCTAAGAGAGCTAGCTGCTGATATACAAACAGAGCTTGGCTGATGAGG 300
DB 241 TCATGCTGCTAAGAGAGCTAGCTGCTGATATACAAACAGAGCTTGGCTGATGAGG 300
QY 301 AGAACTGTTCCACGAGTCAAGTATGATGAGAGGCTGCTATCTGATGAAAGCAGTCTGA 360
DB 301 AGAACTGTTCCACGAGTCAAGTATGATGAGAGGCTGCTATCTGATGAAAGCAGTCTGA 360
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DB 361 ACTTACCTTGAAGAAGTCTGCTTCCCTCAATCTATAGTTCCAGCCTTATATGACAG 420
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DB 541 AAGGTGAGAGATCAAAAGCAATTTGAGAACTGATTTGCTTTATGCTCTGAGAAATG 600
QY 601 CCTGCAATTGACCAAGCAAGCTGAAAAATGATTAATACTAACCCCTTCCCTGCTAGAA 660
DB 601 CCTGCAATTGACCAAGCAAGCTGAAAAATGATTAATACTAACCCCTTCCCTGCTAGAA 660
QY 661 ATACCAATTAGATGCCCCCAAGCGATTTT 690
DB 661 ATACCAATTAGATGCCCCCAAGCGATTTT 690

RESULT 5
AAF92134 standard; cDNA; 1152 BP.
XX
XX AAF92134;
XX
XX 15-MAY-2001 (first entry)
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XX Human FRO10096 cDNA.
XX
XX Human; PRO protein; mapping; ss.
XX
XX Homo sapiens.
XX
XX WO200116318-A2.
XX
XX 08-MAR-2001.
XX
XX 24-AUG-2000; 2000WO-US23328.
XX
XX 01-SEP-1999; 99WO-US20111.
XX
XX 15-SEP-1999; 99WO-US21090.
XX
XX 07-DEC-1999; 99US-0169495.
XX
XX 09-DEC-1999; 99US-0170262.

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	PR	11-JAN-2000; 2000US-0175481.
	PR	18-FEB-2000; 2000WO-US04341.
	PR	18-FEB-2000; 2000WO-US04342.
	PR	22-FEB-2000; 2000WO-US04414.
	PR	01-MAR-2000; 2000WO-US05601.
	PR	03-MAR-2000; 2000US-0187202.
	PR	25-APR-2000; 2000US-0193937.
	PR	22-MAY-2000; 2000WO-US14042.
	PR	05-JUN-2000; 2000US-0209832.
	XX	
	PA	(GETH) GENENTECH INC.
	XX	
	P1	Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
	P1	Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
	XX	
	DR	WPI: 2001-183260/18.
	DR	P-PSDB: AAB87602.
	PT	Eighty four nucleic acids encoding PRO polypeptides, useful in
	PT	molecular biology, including use as hybridization probes, and in
	PT	chromosome and gene mapping.
	XX	
	PS	Claim 2; Fig 153; 278bp; English.
	CC	
	CC	The present sequence is the coding sequence for a human PRO polypeptide
	CC	(secreted and transmembrane). The PRO protein, and PRO agonists, PRO
	CC	antagonists or anti-PRO antibodies are useful for preparation of a
	CC	medicament useful in the treatment of a condition which is responsive to
	CC	the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
	CC	protein may also be employed as molecular weight markers for protein
	CC	electrophoresis. The PRO coding sequence has applications in molecular
	CC	biology, including use as hybridisation probes, and in chromosome and
	CC	gene mapping.
	XX	
	SO	Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;
	Query Match	98.0%; Score 676; DB 22; Length 1152;
	Best Local Similarity	100.0%; Pzed. No. 3.le-189;
	Matches 676; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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OY	75	GCCGCCCTGCAGAAATCTGTAGACTCTTTCCTTAATGGGAGCCCTGGCCACGAGCTGCTC 134
Db	61	GCCGCCCTGCAGAAATCTGTAGACTCTTTCCTTAATGGGAGCCCTGGCCACGAGCTGCTC 120
OY	135	CTTCTCTTGGCCCTCTTGTGTACAGGAGAGACAGCTGGCCCATCAGCTCCCATCTGCAGG 194
Db	121	CTTCTCTTGGCCCTCTTGTGTACAGGAGAGACAGCTGGCCCATCAGCTCCCATCTGCAGG 180
OY	195	CTTGACAAGTCCAATCTTCAGAGAGCCCTAATACCAAACCCGACCTTATCTGGCTTAG 254
Db	181	CTTGACAAGTCCAATCTTCAGAGAGCCCTAATACCAAACCCGACCTTATCTGGCTTAG 240
OY	255	GAGGCTAGCTTGGCTGATTAACAACAACAAGCTTCTCATTTGGGGAAAACTGTTCAC 314
Db	241	GAGGCTAGCTTGGCTGATTAACAACAACAAGCTTCTCATTTGGGGAAAACTGTTCAC 300
OY	315	GGAGTCAGTATGAGTGAAGCGCTGTATCTGATGAAGAAGAGTCTGAACCTTGA 374
Db	301	GGAGTCAGTATGAGTGAAGCGCTGTATCTGATGAAGAAGAGTCTGAACCTTGA 360
OY	375	GAAAGTCTTTCCTTCATCTGATAGTTCCAGGCTTAAATACAGAGAGTGGTGCCTTC 434
Db	361	GAAAGTCTTTCCTTCATCTGATAGTTCCAGGCTTAAATACAGAGAGTGGTGCCTTC 420
OY	435	CTGGCCAGGCTCAGCAACAAGGCTAAGACATCTCATTTGAAGTGAATGACCTGCATATC 494
Db	421	CTGGCCAGGCTCAGCAACAAGGCTAAGACATCTCATTTGAAGTGAATGACCTGCATATC 480
OY	495	CAGAGAAATGTGCAAAAGCTGAAGCACAGTGA AAAAGCTTGAGAGATGAGAGATC 554

Accession	Gene	Protein	Location/Qualifiers
Db	481	CAGAGGAATGTGCAAAAGCTGAGAGCACAGTGAAGAAAGCTTGAGAGAGTGAGAGATG	540
Qy	555	AAACGAATGTGAGAACTGCATTTGCTGTTATGTCTGAGAAATGCCCGCATTTGACCA	614
Db	541	AAACGAATGTGAGAACTGCATTTGCTGTTATGTCTGAGAAATGCCCGCATTTGACCA	600
Qy	615	GAGCAAACTGAAAAATATTAATACTAACCCCTTCCCTGCTAGAAATTAACAATTGATG	674
Db	601	GAGCAAACTGAAAAATATTAATACTAACCCCTTCCCTGCTAGAAATTAACAATTGATG	660
Qy	675	CCCCAAGCGATTTT 690	
Db	661	CCCCAAGCGATTTT 676	
RESULT 6			
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ID	AAAC87053	standard, cDNA, 1152 BP.	
AC	AAAC87053;		
XX			
DT	20-APR-2001	(first entry)	
XX			
DE		Nucleotide sequence of human polypeptide PRO10096.	
XX			
KM	Human, secreted protein, transmembrane protein; PRO196; PRO444; PRO183;		
KM	PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;		
KM	PRO1183; PRO1742; PRO1419; PRO499; PRO1710; PRO246; PRO353; PRO1316;		
KM	PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;		
KM	PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;		
KW	PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;		
KW	ss.		
XX			
OS	Homo sapiens.		
XX			
FX			
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XX			
PN	WO200077037-A2.		
XX			
PD	21-DEC-2000.		
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PF	22-MAY-2000; 2000WO-US14042.		
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PR	15-JUN-1999; 99US-013695.		
PR	20-JUL-1999; 99US-0145070.		
PR	26-JUL-1999; 99US-0145698.		
PR	17-AUG-1999; 99US-0149396.		
PR	01-SEP-1999; 99WO-US20111.		
PR	08-SEP-1999; 99WO-US20594.		
PR	15-SEP-1999; 99WO-US21090.		
PR	15-SEP-1999; 99WO-US21547.		
PR	30-NOV-1999; 99WO-US28313.		
PR	01-DEC-1999; 99WO-US28301.		
PR	02-DEC-1999; 99WO-US28565.		
PR	07-DEC-1999; 99US-0169495.		
PR	05-JAN-2000; 2000WO-US00219.		
PR	18-FEB-2000; 2000WO-US04341.		
PR	18-FEB-2000; 2000WO-US04342.		
PR	22-FEB-2000; 2000WO-US04414.		
PR	01-MAR-2000; 2000WO-US05601.		
PR	02-MAR-2000; 2000WO-US05841.		
PR	20-MAR-2000; 2000WO-US07377.		
PR	30-MAR-2000; 2000WO-US08439.		
PR	15-MAY-2000; 2000WO-US13358.		
PR	17-MAY-2000; 2000WO-US13705.		
XX			
PA	(GEN) GENENTECH INC.		
XX			

P1 Ashkenazi AJ, Baker KP, Botstein DA, Desnovers L, Eaton DL,
P2 Perrera N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
P3 Godawari FU, Gunney AL, Kljavin IJ, Mather JP, Napier MA, Pan J,
P4 Paoli NF, Roy MA, Stewart TA, Tumas D, Watanebe CK, Williams PM,
P5 Wood WT, Zhang Z;
XX MPI, 2001-050091/06.
DR P-PSDB, AAB31210.

PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
XX of related polypeptides -
XX
XX

Claim 2; Fig 63; 244pp; English.

XX The present sequence encodes a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides, designated
CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO242, PRO288,
CC PRO365, PRO3161, PRO31308, PRO1189, PRO1772, PRO1419, PRO4999, PRO1170,
CC PRO248, PRO333, PRO31318, PRO1009, PRO29940, PRO533, PRO301, PRO187,
CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO533, PRO301, PRO187,
CC PRO6004, PRO350, PRO2650 and PRO8309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding these
CC polypeptides are useful in the recombinant production of the
CC polypeptides, as a hybridisation probe to screen libraries to isolate
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
replace a defective gene.

Query Match	98.0%	Score 676	DB 22	Length 1152
Best Local Similarity	100.0%	Pred. No. 3	Le-189	
Matches 676	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	15	CTTCAGAAACAGGTTCTCTCCCGACATCAGAGTGTGAGATTTGAATTTGTCCGAATG	74
Db	1	CTTCAGAAACAGGTTCTCTCCCGACATCAGAGTGTGAGATTTGAATTTGTCCGAATG	60
QY	75	GCCGCCCTGCAGAAATCTGTAGCTTTTCTTATGAGGAGCCCTGAGCCACAGCTGCCTC	134
Db	61	GCCGCCCTGCAGAAATCTGTAGCTTTTCTTATGAGGAGCCCTGAGCCACAGCTGCCTC	120
QY	135	CTTCTCTTGAGCCCTCTTGTTACAGGAGAGAGAGTGGGCCCATACAGTCCCATCTGCAG	197
Db	121	CTTCTCTTGAGCCCTCTTGTTACAGGAGAGAGAGTGGGCCCATACAGTCCCATCTGCAG	180
QY	195	CTTTGACAGTCCAACTTCCAGCAGCCCTATATCAACAAACCGACCTTCTAGTGGCTAAG	254
Db	181	CTTTGACAGTCCAACTTCCAGCAGCCCTATATCAACAAACCGACCTTCTAGTGGCTAAG	240
QY	255	GAGGCTAGGCTGGCTGATATACAAACACAGAGTTGCTTCATTTGGGAGAAAATCTGTTCA	314
Db	241	GAGGCTAGGCTGGCTGATATACAAACACAGAGTTGCTTCATTTGGGAGAAAATCTGTTCA	300
QY	315	GGAATCAGTATAGTAGAGCGCGCTGATCTGATGAAGCAGGTGCTGAATTCACCTTGAA	374
Db	301	GGAATCAGTATAGTAGAGCGCGCTGATCTGATGAAGCAGGTGCTGAATTCACCTTGAA	360
QY	375	GAAATGCTGTCCCTCAATCTGATAGAGTTCCAGCCCTTATATGACAGAGTGTGCTCTTC	434
Db	361	GAAATGCTGTCCCTCAATCTGATAGAGTTCCAGCCCTTATATGACAGAGTGTGCTCTTC	420
QY	435	CTGGCAGGCTCAGCAACAGGCTAAGCACAATGTCAATATTGAAGTGTGACTTGCAATC	494
Db	421	CTGGCAGGCTCAGCAACAGGCTAAGCACAATGTCAATATTGAAGTGTGACTTGCAATC	480
QY	495	CAGAGCAATGTSCAAAGAGCTGAAGGACACAGTGAAAAGCTTGGAGAGAGTGGAGATC	554
Db	481	CAGAGCAATGTSCAAAGAGCTGAAGGACACAGTGAAAAGCTTGGAGAGAGTGGAGATC	540

QY	555	AAAGCAATTGGAGAACTGATTTGCTGTTATGTCCTGAGAAATGCGTCATTTGACCA	61
Db	541	AATGCAATTGGAGAACTGATTTGCTGTTATGTCCTGAGAAATGCGTCATTTGACCA	600
QY	615	GAGCAAAAGCTGAAAAATGATACTAACCCCTTCCTGCTGAGAAATACAAATTAGATG	674
Db	601	GAGCAAAAGCTGAAAAATGATACTAACCCCTTCCTGCTGAGAAATACAAATTAGATG	660
QY	675	CCCCAAAGGATTTT	690
Db	661	CCCCAAAGGATTTT	676
RESULT 7			
ID	ABL95737	standard; cDNA, 1152 BP.	
XX	ABL95737;		
AC			
XX			
XX	19-JUL-2002	(first entry)	
DT			
XX			
DE			
XX			
XX			
KW	Human; angiogenesis related cDNA PRO10096 SEQ ID NO: 353.		
KW	Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;		
KW	atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;		
KW	cardiac; cystostatic; antiangiogenic; hypotensive; vulnerary;		
KW	antiarteriosclerotic; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200208264-A2.		
XX			
PD	31-JAN-2002.		
XX			
XX	09-JUL-2001; 2001WO-US21735.		
PR	20-JUL-2000; 2000US-219556P.		
PR	25-JUL-2000; 2000US-220624P.		
PR	25-JUL-2000; 2000US-220664P.		
PR	28-JUL-2000; 2000WO-US20710.		
PR	02-AUG-2000; 2000US-222695P.		
PR	17-AUG-2000; 2000WO-US43657.		
PR	23-AUG-2000; 2000WO-US23522.		
PR	24-AUG-2000; 2000WO-US23328.		
PR	07-SEP-2000; 2000US-230978P.		
PR	15-SEP-2000; 2000US-000000P.		
PR	18-SEP-2000; 2000US-0664610.		
PR	24-OCT-2000; 2000US-242922P.		
PR	08-NOV-2000; 2000US-0709238.		
PR	08-NOV-2000; 2000WO-US30952.		
PR	10-NOV-2000; 2000WO-US30873.		
PR	01-DEC-2000; 2000WO-US32678.		
PR	20-DEC-2000; 2000US-0747259.		
PR	20-DEC-2000; 2000WO-US34956.		
PR	22-JAN-2001; 2001US-0767609.		
PR	28-FEB-2001; 2001US-0796498.		
PR	28-FEB-2001; 2001WO-US06520.		
PR	01-MAR-2001; 2001WO-US06666.		
PR	09-MAR-2001; 2001US-0802706.		
PR	14-MAR-2001; 2001US-0808689.		
PR	22-MAR-2001; 2001US-0816744.		
PR	05-APR-2001; 2001US-0828366.		
PR	10-MAY-2001; 2001US-0854208.		
PR	10-MAY-2001; 2001US-0854280.		
PR	25-MAY-2001; 2001US-0866038.		
PR	25-MAY-2001; 2001US-0866034.		
PR	25-MAY-2001; 2001WO-US17092.		
PR	30-MAY-2001; 2001US-0870574.		
PR	30-MAY-2001; 2001WO-US17443.		
PR	01-JUN-2001; 2001WO-US17800.		
PR	20-JUN-2001; 2001WO-US19692.		

CC identity to a 101 amino acid interleukin (IL)-22 sequence. The invention
CC is useful for detecting IL-22R (IL-22 receptor) or IL-10Rbeta polypeptide
CC in a sample which involves contacting sample with an IL-22 polypeptide
CC and determining the formation of an IL-22R/IL-22 polypeptide conjugate or
CC an IL-10Rbeta/IL-22 polypeptide conjugate. Preferably, the IL-22
CC polypeptide is labelled with a detectable label or is attached to a solid
CC support. The polypeptide is also useful for linking a bioactive molecule,
CC e.g. toxin, radiolabel or antibody that causes the death of the cell, to
CC a cell expressing IL-22R polypeptide or IL-10Rbeta polypeptide which
CC involves contacting the cell with IL-22 polypeptide that is bound to the
CC bioactive molecule and allowing binding of the IL-22 polypeptide with
CC IL-22R or IL-10Rbeta polypeptide thus linking the bioactive molecules to
CC the cell. The molecules of the invention can also be used for modulating
CC biological activity of cell expressing IL-22R or IL-10Rbeta polypeptide,
CC whereby the cell is killed and the antibody of the invention is useful
CC for inhibiting IL-22 induced expression of PAPI (pancreatitis associated
CC protein) by pancreatic cells. The antibody is also useful for treating a
CC pancreatic disorder such as acute or chronic pancreatitis, pancreatic
CC carcinoma including acinar cell carcinoma or mixed cell population
CC pancreatic carcinoma and for reducing the activated or inflamed condition
CC of the pancreas in a mammal. The present nucleic acid sequence encodes
CC the human interleukin 22 (IL-22) protein of the invention. This sequence
CC is a clone designated DNA125185-2806.
CC
XX
SQ Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;

Query Match 98.0%; Score 676; DB 24; Length 1152;
Best Local Similarity 100.0%; Pred. No. 3,1e-189;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAAAGGTTCTCCCTCCCAAGTCACCAAGTCTGAGTGAATGTCGTGATG 74
DB 1 CTTGAGAAAGGTTCTCCCTCCCAAGTCACCAAGTCTGAGTGAATGTCGTGATG 60
QY 75 GCCGCCCTCAGAAATCTGTGAGCTCTTCCCTTATGAGGAGACCTGGCCACCAAGTCCCTC 134
DB 61 GCCGCCCTCAGAAATCTGTGAGCTCTTCCCTTATGAGGAGACCTGGCCACCAAGTCCCTC 120
QY 135 CTTCTCTTGGCCCTCTTGTGACAGGAGAGAGAGCTGCCCATCATGCTCCCACTGCAGG 194
DB 121 CTTCTCTTGGCCCTCTTGTGACAGGAGAGAGAGCTGCCCATCATGCTCCCACTGCAGG 180
QY 195 CTTGCAAGTCCAACTTCCAGAGAGCTTATCACCACCAACCGACCTTATGCTGCTAG 254
DB 181 CTTGCAAGTCCAACTTCCAGAGAGCTTATCACCACCAACCGACCTTATGCTGCTAG 240
QY 255 GAGGCTAGCTGCTGATACAAACAGAGCTTCTGCTGATGAGGAGAACTGTTCCAG 314
DB 241 GAGGCTAGCTGCTGATACAAACAGAGCTTCTGCTGATGAGGAGAACTGTTCCAG 300
QY 315 GGAGTCAAGTATGAGTGAAGGCTGCTATCTGATGAAGCAGAGCTGTAACCTTCA 374
DB 301 GGAGTCAAGTATGAGTGAAGGCTGCTATCTGATGAAGCAGAGCTGTAACCTTCA 360
QY 375 GAAGTCTGCTTCCCTCAATCTATAGTCCAGCTTATATGACAGAGGTGTCCTTC 434
DB 361 GAAGTCTGCTTCCCTCAATCTATAGTCCAGCTTATATGACAGAGGTGTCCTTC 420
QY 435 CTGGCAGGCTCAGCAACAGGCTAAGCAGATGTCTATTTAGAGTGAAGTGAATATC 494
DB 421 CTGGCAGGCTCAGCAACAGGCTAAGCAGATGTCTATTTAGAGTGAAGTGAATATC 480
QY 495 CAGAGGAATGTGCAAAAAGCTGAAGACACAGTGAAGAAAGCTTGAAGAGAGAGATC 554
DB 481 CAGAGGAATGTGCAAAAAGCTGAAGACACAGTGAAGAAAGCTTGAAGAGAGATC 540
QY 555 AAAGCAATGAGAACTGATTTGCTGTTATGCTCTGAGAAAGTCCCTGCATTTGACCA 614
DB 541 AAAGCAATGAGAACTGATTTGCTGTTATGCTCTGAGAAAGTCCCTGCATTTGACCA 600
QY 615 GAGCAAGCTGAAAAATGATACTAACCCCTTCCCTGCTAGAAATTAACAATTAGATG 674
DB 601 GAGCAAGCTGAAAAATGATACTAACCCCTTCCCTGCTAGAAATTAACAATTAGATG 660

QY 675 CCCCAAGCGATTTT 690
DB 661 CCCCAAGCGATTTT 676

RESULT 9
ABL88248
ID ABL88248 standard; cDNA; 1152 BP.

ABL88248;

16-MAY-2002 (first entry)

Human PRO10096 cDNA sequence SEQ ID NO:353.

Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
vulnerable; arteriosclerotic; PRO agonist; PRO antagonist; trauma;
gene therapy; cardiovascular disorder; endochelial disorder; cancer;
angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
age-related macular degeneration; arterial restenosis; angina;
rheumatoid arthritis; myocardial infarction; thrombophlebitis;
lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
wound healing; chromosome mapping; gene mapping; gene; ss.

Homo sapiens.

WO200200690-A2.

03-JAN-2002.

20-JUN-2001; 2001WO-US19692.

23-JUN-2000; 2000US-213637P.

20-JUL-2000; 2000US-219556P.

25-JUL-2000; 2000US-220624P.

25-JUL-2000; 2000US-220664P.

28-JUL-2000; 2000WO-US207110.

02-AUG-2000; 2000US-222695P.

17-AUG-2000; 2000US-0643657.

23-AUG-2000; 2000WO-US23522.

24-AUG-2000; 2000WO-US23328.

07-SEP-2000; 2000US-230378P.

18-SEP-2000; 2000US-0664610.

18-SEP-2000; 2000US-0665350.

24-OCT-2000; 2000US-242922P.

08-NOV-2000; 2000US-0709238.

08-NOV-2000; 2000WO-US30952.

10-NOV-2000; 2000WO-US30873.

01-DEC-2000; 2000WO-US32678.

20-DEC-2000; 2000US-0747259.

20-DEC-2000; 2000WO-US34956.

22-JAN-2001; 2001US-0767609.

28-FEB-2001; 2001US-0796498.

28-FEB-2001; 2001WO-US06520.

01-MAR-2001; 2001WO-US06666.

09-MAR-2001; 2001US-0802706.

14-MAR-2001; 2001US-0808689.

22-MAR-2001; 2001US-0816744.

05-APR-2001; 2001US-0828366.

10-MAY-2001; 2001US-0854280.

10-MAY-2001; 2001US-0854280.

25-MAY-2001; 2001US-0866034.

25-MAY-2001; 2001US-0866034.

30-MAY-2001; 2001WO-US17092.

30-MAY-2001; 2001US-0870574.

30-MAY-2001; 2001WO-US17443.

01-JUN-2001; 2001WO-US17800.

(GETH) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gorrissen ME, Goddard A,
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2002-090516/12.
DR P-PSDB; ABB84993.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT interaction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 2; Fig 353; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial stenosis,
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridisation probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
SQ Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;
Query Match 98.0%; Score 676; DB 24; Length 1152;
Best Local Similarity 100.0%; Pred. No. 3.1e-189;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CTTGAGAACAGAGTTCTCTCCAGTACAGAGTTCTGAGTGAATGTTCTGCAATG 74
DB 1 CTTGAGAACAGAGTTCTCTCCAGTACAGAGTTCTGAGTGAATGTTCTGCAATG 60
QY 75 GCGCGCCCTGCAAGAAATCTGTAGCTCTTCTTATGGGGAACCTGGCCACGCTGCTC 134
DB 61 GCGCGCCCTGCAAGAAATCTGTAGCTCTTCTTATGGGGAACCTGGCCACGCTGCTC 120
QY 135 CTTGCTTGGCCCTCTTGTATACAGAGAGAGAGCTGGCCCATGCTCCCATGCAAG 194
DB 121 CTTGCTTGGCCCTCTTGTATACAGAGAGAGAGCTGGCCCATGCTCCCATGCAAG 180
QY 195 CTTGCAAGAGTCCAACTTCAGAGGCTTATATACCAACGACCTTATGCTGCTAAG 254
DB 181 CTTGCAAGAGTCCAACTTCAGAGGCTTATATACCAACGACCTTATGCTGCTAAG 240
QY 255 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTCTTATGGGGAAGAACTGTTCCAC 314
DB 241 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTCTTATGGGGAAGAACTGTTCCAC 300
QY 315 GGAGTCAGATAGAGAGAGGCTGATCTGATGAAGAGAGGCTGAACCTGAACTGAA 374
DB 301 GGAGTCAGATAGAGAGAGGCTGATCTGATGAAGAGAGGCTGAACCTGAACTGAA 360
QY 375 GAAAGTGTCTTCCCTCAATCTGATAGGTTCCAGCCTTATATCAGAGAGGTGTCCTTC 434
DB 361 GAAAGTGTCTTCCCTCAATCTGATAGGTTCCAGCCTTATATCAGAGAGGTGTCCTTC 420
QY 435 CTGGCCAGGCTTACAGCAAGGCTTAAGACATGTCATATTGAAGGTGATGCTGCTTATC 494
DB 421 CTGGCCAGGCTTACAGCAAGGCTTAAAGCATATGTAAGGTGATGATCCTGCAATAC 480
QY 495 CAGAGAAATGTGCAAAAGCTGAAGGACAGTGAAGAAACCTTGAAGAGAGTGAAGATC 554
DB 481 CAGAGAAATGTGCAAAAGCTGAAGGACAGTGAAGAAACCTTGAAGAGTGAAGATC 540
QY 555 AAAGCAATTGGAAGCTGATTTGCTTTATGCTCTGAGAAGAAATGCTGCAATTTGACCA 614
DB 541 AAAGCAATTGGAAGCTGATTTGCTTTATGCTCTGAGAAGAAATGCTGCAATTTGACCA 600
QY 615 GAGCAAAAGCTGAAGAAATGAATACTAACCCCTTCCCTGCTAGAATAACAATTGATG 674

DB 601 GAGCAAAAGCTGAAGAAATGAATACTAACCCCTTCCCTGCTAGAATAACAATTGATG 660
QY 675 CCCCCAAGCGATTTT 690
DB 661 CCCCCAAGCGATTTT 676
RESULT 10.
ABK33657
ID ABRK33657 standard; cDNA; 1152 BP.
XX
AC ABRK33657;
XX
DT 08-MAY-2002 (first entry)
XX
DE cDNA encoding human PRO protein, Seq ID No 243.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
OS
XX Homo sapiens.
XX
XX WO200208288-A2.
XX
XX 31-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US21066.
XX
XX 20-JUL-2000; 2000US-21955EP.
XX 25-JUL-2000; 2000US-220585P.
XX 25-JUL-2000; 2000US-220605P.
XX 25-JUL-2000; 2000US-220607P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220638P.
XX 25-JUL-2000; 2000US-220664P.
XX 25-JUL-2000; 2000US-220666P.
XX 26-JUL-2000; 2000US-220893P.
XX 28-JUL-2000; 2000WO-US20710.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 15-SEP-2000; 2000US-000000P.
XX 10-NOV-2000; 2000WO-US30873.
XX 28-NOV-2000; 2000US-253646P.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 28-FEB-2001; 2001WO-US06520.
XX 10-MAY-2001; 2001US-0854280.
XX 25-MAY-2001; 2001WO-US17092.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
XX
XX P-PSDB; AAU83713.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumours
XX as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
XX tumour or liver tumour -
XX
XX
XX Claim 2; Figure 243; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung

CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK3356-ABK3365 represent human
CC PRO protein coding sequences of the invention.

XX Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;

Query Match 98.0%; Score 676; DB 24; Length 1152;

Best Local Similarity 100.0%; Pred. No. 3.1e-189;

Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAACAGGTTCTCTCCAGTCACAGTTGCTGAGTATGATTTGCTGCAATG 74
DB 1 CTTGAGAACAGGTTCTCTCCAGTCACAGTTGCTGAGTATGATTTGCTGCAATG 60
QY 75 GCCGCCCTGCAGAAATCTGTGAGCTTTCTTATGGGAGACCTGCGCCACAGCTGCTC 134
DB 61 GCCGCCCTGCAGAAATCTGTGAGCTTTCTTATGGGAGACCTGCGCCACAGCTGCTC 120
QY 135 CTTCTCTGGCCCTCTTGTATACAGGAGAGAGAGCTGCGCCATCAGCTCCACATGACAG 194
DB 121 CTTCTCTGGCCCTCTTGTATACAGGAGAGAGAGCTGCGCCATCAGCTCCACATGACAG 180
QY 195 CTTGACAAAGTCCAACTTCAGAGAGCCCTATATACCAACCGGACCTTCACTGCTGCTAG 254
DB 181 CTTGACAAAGTCCAACTTCAGAGAGCCCTATATACCAACCGGACCTTCACTGCTGCTAG 240
QY 255 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTCTCATTTGGGAGAGAACTGTTCAC 314
DB 241 GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTCTCATTTGGGAGAGAACTGTTCAC 300
QY 315 GGAGTCAGATAGAGAGAGGCTGCTATCTGATGAAGCGAGTCTGAACTTCACTTGA 374
DB 301 GGAGTCAGATAGAGAGAGGCTGCTATCTGATGAAGCGAGTCTGAACTTCACTTGA 360
QY 375 GAAGTGTCTGTTCCCTCAATCTGATAGGTTCCAGCCCTTATATGACAGAGGTGTCCTTC 434
DB 361 GAAGTGTCTGTTCCCTCAATCTGATAGGTTCCAGCCCTTATATGACAGAGGTGTCCTTC 420
QY 435 CTGCGCAGGCTCAGCAACAGGCTAAGCATGTCAATTTGAAGGTGATGACCTGCATATC 494
DB 421 CTGCGCAGGCTCAGCAACAGGCTAAGCATGTCAATTTGAAGGTGATGACCTGCATATC 480
QY 495 CAGAGGAAATGTCGCAAAAGCTGAAGACACAGTGAAGAAAGCTTGGAGAGGTGAGAGATC 554
DB 481 CAGAGGAAATGTCGCAAAAGCTGAAGACACAGTGAAGAAAGCTTGGAGAGGTGAGAGATC 540
QY 555 AAAGCAATTTGAGAACTGGATTGCTTTATGTCTCTGAGAAATGCTGCACTTTGACCA 614
DB 541 AAAGCAATTTGAGAACTGGATTGCTTTATGTCTCTGAGAAATGCTGCACTTTGACCA 600
QY 615 GAGCAAACTGAAAAATGATTAATTAACCTTCTGCTAGAAATTAACATTTAGATG 674
DB 601 GAGCAAACTGAAAAATGATTAATTAACCTTCTGCTAGAAATTAACATTTAGATG 660
QY 675 CCCCAAGGAGTATTTT 690
DB 661 CCCCAAGGAGTATTTT 676

RESULT 11

AAF28841

ID AAF28841 standard; DNA; 1139 BP.

AC AAF28841;

XX

DT 25-APR-2001 (first entry)

XX Human interleukin-10 homologue IL-D110 DNA sequence.

DE Anti-inflammatory; immunosuppressive; cytoprotective; antirheumatic; human;
XX antiarthritis; dermatological; thyromimetic; gene therapy; inflammation;
KW interleukin 10 homologue; IL-D110; IL-D210; cytokine; tumour therapy;
KW haematopoietic cell; probe; immunogen; systemic lupus erythematosus;
KW rheumatoid arthritis; Hashimoto's autoimmune response; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 59..598

FT /tag= a

FT /product= "IL-D110"

FT /transl_except= (pos:245..247,aa:Xaa)

FT /note= "Xaa=unknown"

FT sig_peptide 59..157

FT /tag= b

FT mat_peptide 158..595

FT /tag= c

PN MO200073457-A1.

PD 07-DEC-2000.

PF 26-MAY-2000; 2000MO-US14729.

PR 27-MAY-1999; 99US-0322806.

PA (SCHE) SCHERING CORP.

PI Parham CL, De Waal Malefyt R, Marshalli NL;

DR WPT: 2001-061539/07.

DR P-PSDB; AAB371122.

XX New interleukin-D110 genes and polypeptides useful for treating
PT conditions associated with abnormal physiology, particularly e.g.
PT inflammatory or autoimmune disorders -

PS Claim 3; Page 51-52; 62pp; English.

XX This sequence represents the gene sequence for a human interleukin 10
CC homologue IL-D110. The invention also relates to another IL-10 homologue
CC ID-210 (AAF28842). The IL-D110 is useful for treating conditions
CC associated with abnormal physiology or development, including
CC inflammatory conditions, either acute or chronic. The new cytokine
CC also plays a role in the regulation or development of haematopoietic
CC cells, e.g. lymphoid or myeloid cells, which affect immunological
CC responses, such as inflammation and/or autoimmune disorders. These may
CC also be used in drug screening to identify compounds having binding
CC affinity to or other relevant biological effects on IL-D110 functions.

CC in anti-tumour therapy, as probes for detecting IL-D110 levels in samples
CC from patients suspected of having an abnormal condition, e.g. autoimmune
CC or inflammatory, in raising or screen antibodies, as immunogen, in
CC diagnostic assays, and in detecting, isolating or identifying a DNA clone
CC encoding IL-D110 or IL-D210 from a natural source. IL-D110 antagonists
CC may be used to block immune responses, e.g. in situations as inflammatory
CC or autoimmune responses, including rheumatoid arthritis, systemic lupus
CC erythematosus, or Hashimoto's autoimmune responses.

XX Sequence 1139 BP; 337 A; 238 C; 227 G; 333 T; 4 other;

Query Match 97.2%; Score 671; DB 22; Length 1139;

Best Local Similarity 99.9%; Pred. No. 9.2e-188;

Matches 671; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 AGAACAGTTCTCTCTCCAGTCACAGTTGCTGAGTATGATTTGCTGCAATGCGCG 78
DB 6 AGAACAGTTCTCTCTCTCCAGTCACAGTTGCTGAGTATGATTTGCTGCAATGCGCG 65

```
QY 79 CCTGACGAAATCTGTAGACTCTTCTTATAGGGAGACCTGGCCACAGCTGCTCTTC 138
DB 66 CCTGACGAAATCTGTAGACTCTTCTTATAGGGAGACCTGGCCACAGCTGCTCTTC 125
QY 139 TCTTGGCCCTTGTGTACAGGAGAGAGAGAGCTGGCCCATCATGCTCCCACTGACAGCTTG 198
DB 126 TCTTGGCCCTTGTGTACAGGAGAGAGAGAGCTGGCCCATCATGCTCCCACTGACAGCTTG 185
QY 199 ACAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 258
DB 186 ACAAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 245
QY 259 CTACTGCTGCTGATTAACAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 318
DB 246 CTACTGCTGCTGATTAACAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 305
QY 319 TCAATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
DB 306 TCAATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 365
QY 379 TGCTGCTCCCTCAATCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 438
DB 366 TGCTGCTCCCTCAATCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 425
QY 439 CCAGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 498
DB 426 CCAGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 485
QY 499 GGAATGTGCAAAAGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 558
DB 486 GGAATGTGCAAAAGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 545
QY 559 CAATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 618
DB 546 CAATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605
QY 619 AAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 678
DB 606 AAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 665
QY 679 AAAGGATTTT 690
DB 666 AAAGGATTTT 677

RESULT 12
AAC84310
ID AAC84310 standard; cDNA, 1132 BP.
XX
AC AAC84310;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human EXCS encoding cDNA (clone ID 5571181C81).
XX
KW Extracellular signaling molecule; EXCS; anti-inflammatory; human;
KW immunosuppressive; cytotoxic; neuroprotective; gastroenteric;
KW virulence; antibacterial; anti-HIV; human immunodeficiency virus;
KW antineoplastic; cerebroprotective; neurotropic; antileukemic; antifungal;
KW anticonvulsant; tranquilizer; neuroleptic; vasodilator; gynecological;
KW keratolytic; protozoicide; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200070049-A2.
XX
PD 23-NOV-2000.
XX
PF 19-MAY-2000; 2000WO-US13975.
XX
PR 19-MAY-1999; 99US-0134949.
PR 15-JUL-1999; 99US-0144270.
PR 30-JUL-1999; 99US-0146700.
```

```
PR 04-OCT-1999; 99US-0157508.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
PI Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;
PI Azimzai Y, Lu DM, Patterson C;
DR MPI: 2001-025021/03.
DR P-PSDB: AAB48074.
XX
XX New human extracellular signaling nucleic acids and polypeptides useful
PT for diagnosing, treating and preventing infections and
PT gastrointestinal, neurological, reproductive, and
PT autoimmune/inflammatory disorders -
XX
XX Claim 4; Page 108; 114pp; English.
XX
XX The invention provides human extracellular signaling molecules (EXCS)
CC and polynucleotides which identify and encode EXCS. EXCS can be
CC expressed by standard recombinant methodology. The amino acid and nucleic
CC acid sequences of EXCS are useful for diagnosing, treating and
CC preventing infections and gastrointestinal (peptic ulcer, dysphagia,
CC pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular
CC disease, stroke), reproductive (infertility, ovulatory defects,
CC endometriosis), autoimmune/inflammatory (actinic keratosis, acquired
CC immunodeficiency syndrome (AIDS), Addison's disease), and cell
CC proliferative disorders including cancers (of the breast, adrenal gland,
CC bone). They may also be used to treat fatal familial insomnia,
CC nutritional and metabolic diseases of the nervous system, myopathies,
CC mental disorders (anxiety, schizophrenia, mood), as well as infections
CC caused by parasites (malaria, leishmania, trypanosoma), viral
CC (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,
CC staphylococcus, bacillus), and fungal (aspergillus, blastomycosis,
CC dermatophytes) agents. The nucleic acids, polypeptides, antagonists,
CC agonists, pharmaceutical compositions, and antibodies may also be used
CC for treating or preventing disorders associated with increased or
CC decreased expression or activity of EXCS. EXCS polynucleotides may also
CC be used to detect and quantify gene expression in biopsied tissues in
CC which expression of EXCS may be correlated with the disease, to determine
CC presence or excess expression of EXCS, to monitor regulation of EXCS
CC levels during therapeutic intervention, to detect the presence of
CC associated disorders, as targets in microarray, to generate hybridization
CC probes, and to detect differences in gene sequences among normal, carrier
CC or affected individuals. Antibodies may also be used in diagnosing
CC disorders, in monitoring patients being treated with EXCS agonists,
CC antagonists or inhibitors. Sequences AAC84293-084318 represent nucleic
CC acid molecules encoding the EXCS of the invention.
XX
XX Sequence 1132 BP; 333 A; 240 C; 226 G; 333 T; 0 other;
XX
XX Query Match 97.0%; Score 669; DB 22; Length 1132;
XX Best Local Similarity 100.0%; Pred. No. 3; Ee-187;
XX Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 22 ACAGGTTCTCTTCCCGACGATGCTGCTGATTAAGTTCGTAATGCGCCGCC 81
DB 1 ACAGGTTCTCTTCCCGACGATGCTGCTGATTAAGTTCGTAATGCGCCGCC 60
QY 82 TGCAAAATCTGTAGAGCTTTCTTATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 141
DB 61 TGCAAAATCTGTAGAGCTTTCTTATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 142 TGGCCCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 201
DB 121 TGGCCCTTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 202 AGTCAATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 261
DB 181 AGTCAATCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 262 GCTTGCTGATTAACAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 321
DB 241 GCTTGCTGATTAACAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
```

QY 322 GTATGAGTGAAGCGCTGCTATCTGATGAAGAGAGTCTGAACCTTACCCCTTGAAGAAGTGC 381
 Db 301 GTATGAGTGAAGCGCTGCTATCTGATGAAGAGAGTCTGAACCTTACCCCTTGAAGAAGTGC 360
 QY 382 TGTTCCTCAATCTGATGAGTTCAGCCTTATATGACAGAGAGTGTGCTTCCTGAGCCA 441
 Db 361 TGTTCCTCAATCTGATGAGTTCAGCCTTATATGACAGAGAGTGTGCTTCCTGAGCCA 420
 QY 442 GGCCTCAGCAACAGGCTTAGACATGTCATATTTGAAGGTGATGACCTGCAATATCCAGAGGA 501
 Db 421 GGCCTCAGCAACAGGCTTAGACATGTCATATTTGAAGGTGATGACCTGCAATATCCAGAGGA 480
 QY 502 ATGTGCAAAAGCTGAAGGACACAGTGAATAAGCTTGGAGAGATGAGATCAAAAGCA 561
 Db 481 ATGTGCAAAAGCTGAAGGACACAGTGAATAAGCTTGGAGAGATGAGATCAAAAGCA 540
 QY 562 TTGGAGAACTGATTTGCTGTTATGCTCTGAGAAATGCTGATTTGACACAGAGCAAA 621
 Db 541 TTGGAGAACTGATTTGCTGTTATGCTCTGAGAAATGCTGATTTGACACAGAGCAAA 600
 QY 622 GCTGAAAAATGAATTAACCTAACCCCTTTCTCTGAGAAATTAACAAATTGATGCCCCCAA 681
 Db 601 GCTGAAAAATGAATTAACCTAACCCCTTTCTCTGAGAAATTAACAAATTGATGCCCCCAA 660
 QY 682 GCGATTTT 690
 Db 661 GCGATTTT 669

RESULT 13

AAC81773
 ID AAC81773 standard; cDNA, 1177 BP.

AAC81773;

23-FEB-2001 (first entry)

Human GIL-19/AE289 protein coding sequence.

Human; GIL-19/AE289; IL-10; interleukin-10; nutrition;
 cell proliferation; immune stimulation; immune suppression;
 haematopoiesis regulation; tissue growth; inflammation; cancer; ss.

Homo sapiens.

WO200065027-A2.

02-NOV-2000.

28-APR-2000; 2000WO-US11479.

28-APR-1999; 99US-0131473.

(GENY) GENETICS INST INC.

Jacobus K, Fouser L, Spaulding V, Xuan D;

WPI; 2000-687325/67.

P-PsDB; AAB36292.

Human GIL-19 protein that shows a high degree of homology to IL

(interleukin-10, useful in upregulation of humoral immune responses,

as an antiinflammatory agent and as a modulator of immune responses

associated with injury -

Claim 1; Page 59; 60pp; English.

CC tumour inhibition. In addition, it also has uses in the treatment of
 CC inflammation and in nutrition.
 XX
 SQ Sequence 1177 BP; 362 A; 245 C; 232 G; 338 T; 0 other;
 Query Match 97.0%; Score 669; DB 21; Length 1177;
 Best Local Similarity 100.0%; Pred. No. 3.7e-187;
 Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 ACAGGTTCCCTTCCCACTACACAGTGTGAGTGAATTTGTGAAATGCGCCGCC 81.
 Db 15 AAGAGTTCTCTTCCCACTACACAGTGTGAGTGAATTTGTGAAATGCGCCGCC 74
 QY 82 TGCAGAAATCTGTGAGCTCTTTCTTATGAGGAGACCTGCGCAACAGCTCCTCTCT 141
 Db 75 TGCAGAAATCTGTGAGCTCTTTCTTATGAGGAGACCTGCGCAACAGCTCCTCTCT 134
 QY 142 TGGCCCTCTTGGTACAGGAGAGAGAGAGTGGCCCATCAGTCCCATGAGGCTTGACA 201
 Db 135 TGGCCCTCTTGGTACAGGAGAGAGAGAGTGGCCCATCAGTCCCATGAGGCTTGACA 194
 QY 202 AGTCCCACTTCAGAGAGCCCTATATCACACGACCTTCAATGCTGGGTAAAGAGGCTA 261
 Db 195 AGTCCCACTTCAGAGAGCCCTATATCACACGACCTTCAATGCTGGGTAAAGAGGCTA 254
 QY 262 GCTTGCTGATTAACAACAGACAGTCTGCTCATTTGGGAGAACTGTTCCACGAGATCA 321
 Db 255 GCTTGCTGATTAACAACAGACAGTCTGCTCATTTGGGAGAACTGTTCCACGAGATCA 314
 QY 322 GTATGAGTGAAGCGCTGCTATCTGATGAAGAGAGTGTGAACTTCAACCTTGAAGAAGTGC 381
 Db 315 GTATGAGTGAAGCGCTGCTATCTGATGAAGAGAGTGTGAACTTCAACCTTGAAGAAGTGC 374
 QY 382 TGTTCCTCAATCTGATGAGTTCAGCCTTATATGACAGAGTGTGCTTCCTGAGCCA 441
 Db 375 TGTTCCTCAATCTGATGAGTTCAGCCTTATATGACAGAGTGTGCTTCCTGAGCCA 434
 QY 442 GGCCTCAGCAACAGGCTTAGACATGTCATATTTGAAGGTGATGACCTGCAATATCCAGAGGA 501
 Db 435 GGCCTCAGCAACAGGCTTAGACATGTCATATTTGAAGGTGATGACCTGCAATATCCAGAGGA 494
 QY 502 ATGTGCAAAAGCTGAAGGACACAGTGAATAAGCTTGGAGAGATGAGATCAAAAGCA 561
 Db 495 ATGTGCAAAAGCTGAAGGACACAGTGAATAAGCTTGGAGAGATGAGATCAAAAGCA 554
 QY 562 TTGGAGAACTGATTTGCTGTTATGCTCTGAGAAATGCTGATTTGACACAGAGCAAA 621
 Db 555 TTGGAGAACTGATTTGCTGTTATGCTCTGAGAAATGCTGATTTGACACAGAGCAAA 614
 QY 622 GCTGAAAAATGAATTAACCTAACCCCTTTCTCTGAGAAATTAACAAATTGATGCCCCCAA 681
 Db 615 GCTGAAAAATGAATTAACCTAACCCCTTTCTCTGAGAAATTAACAAATTGATGCCCCCAA 674
 QY 682 GCGATTTT 690
 Db 675 GCGATTTT 683

RESULT 14

AAD09719

AAD09719 standard; cDNA; 1116 BP.

AAD09719;

10-SEP-2001 (first entry)

Human cytokine, ZCYTO18 cDNA.

Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;

cancer; inflammation; gene therapy; chromosome 12; ss.

Homo sapiens.

```

FH Key Location/Qualifiers
FT CDS 21..560
FT /tag= a
FT /product= "Human ZCYTO18 protein #1"
FT sig_peptide 21..119
FT /tag= b
FT /product= "Human mature ZCYTO18 protein #1"
FT mat_peptide 120..557
FT /tag= c
FT /product= "Human mature ZCYTO18 protein #1"
FT CDS 57..560
FT /tag= d
FT /product= "Human ZCYTO18 protein #2"
FT sig_peptide 57..119
FT /tag= e
FT /product= "Human mature ZCYTO18 protein #2"
FT mat_peptide 120..557
FT /tag= f
FT /product= "Human mature ZCYTO18 protein #2"
XX WO200146422-A1.
XX 28-JUN-2001.
XX PF 22-DEC-2000; 2000WO-US35308.
XX PR 23-DEC-1999; 99US-0471767.
XX PR 01-DEC-2000; 2000US-0250841.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX P1 Presnell SR, Kindsvogel W;
XX WPI; 2001-408648/43.
XX DR P-PsDB; AAE04538, AAE04539.
XX PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -
XX PS Claim 2; Page 140-142; 167pp; English.
XX CC The patent discloses novel human cytokine, ZCYTO18 protein and its
XX CC corresponding DNA. ZCYTO18 protein induces proliferation of cells
XX CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity
XX CC in K562 cells. ZCYTO18 DNA is useful for detecting a genetic
XX CC abnormality in a patient. ZCYTO18 DNA and its antibodies are useful
XX CC for detecting cancer and inflammation. ZCYTO18 protein is useful for
XX CC killing cancer cells. It is useful for increasing platelets in a
XX CC patient or injured tissue. It is also used in gene therapy.
XX CC The present sequence is a cDNA encoding novel human cytokine, ZCYTO18
XX CC protein. ZCYTO18 DNA is located at the 12q15 region of chromosome 12.
XX SQ Sequence 1116 BP; 336 A; 229 C; 222 G; 329 T; 0 other;
XX
XX Query Match 92.6%; Score 639; DB 22; Length 1116;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-178;
XX Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 52 TCGAGTTAAGTGTGCAATGCGCGCCCTGCAGAAATCTGAGCTCTTCTTATGG 111
XX 1 TCGAGTTAAGTGTGCAATGCGCGCCCTGCAGAAATCTGAGCTCTTCTTATGG 60
XX
XX QY 112 GGAACCTGGCAACAGCTGCTCTTCTTGGCCCTTGTGACAGGAGAGAGAGCTG 171
XX 61 GGAACCTGGCAACAGCTGCTCTTCTTGGCCCTTGTGACAGGAGAGAGAGAGCTG 120
XX
XX QY 172 CGGCCATCAGCTCCCACTGAGGCTTGACAAGTCCAACTTCCAGAGCCCTATATACCA 231
XX 121 CGGCCATCAGCTCCCACTGAGGCTTGACAAGTCCAACTTCCAGAGCCCTATATACCA 180
XX
XX QY 232 ACCGACCTTCAGCTGGGCTAAGAGGCTAGCTTGCTGATTAACAACAGAGAGCTTGGTC 291
XX 181 ACCGACCTTCAGCTGGGCTAAGAGGCTAGCTTGCTGATTAACAACAGAGAGCTTGGTC 240
XX
XX QY 292 TCATTGGGAGAAACTGTTCACAGAGTCAAGTGAAGTGAAGCGCTGATCTGATGAAGC 351
XX

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DB 241 TCATTGGGAGAAACTGTTCACAGAGTCAAGTGAAGTGAAGCGCTGATCTGATGAAGC 300
QY 352 AGTGCTGAACCTTCAACCTTGAAGAAGTGTTCCTCCATCTGATAGTTCCAGCCTT 411
DB 301 AGTGCTGAACCTTCAACCTTGAAGAAGTGTTCCTCCATCTGATAGTTCCAGCCTT 360
QY 412 ATATGACAGAGAGTGTGCTTCTTCCAGGCTCAGCAGACAGGCTAAGACATGTCTATA 471
DB 361 ATATGACAGAGAGTGTGCTTCTTCCAGGCTCAGCAGACAGGCTAAGACATGTCTATA 420
QY 472 TTGAAGTGAATGACCTGATATCCAGAGAAATGTGCAAAAGCTGAAGACACAGTGAATA 531
DB 421 TTGAAGTGAATGACCTGATATCCAGAGAAATGTGCAAAAGCTGAAGACACAGTGAATA 480
QY 532 AGCTTGAAGAGAGTGAAGATCAAAAGCAATTGGAGAACTGATTTGCTGTTATGTCTC 591
DB 481 AGCTTGAAGAGAGTGAAGATCAAAAGCAATTGGAGAACTGATTTGCTGTTATGTCTC 540
QY 592 TGAGAAATGCTGCACTTTGACCCAGAGCAAGCTGAAAATGATPACTAACCCCTTCC 651
DB 541 TGAGAAATGCTGCACTTTGACCCAGAGCAAGCTGAAAATGATPACTAACCCCTTCC 600
QY 652 CTGCTAGAAATPACAAATTGATGCCCCCAAGGATTTT 690
DB 601 CTGCTAGAAATPACAAATTGATGCCCCCAAGGATTTT 639
XX
XX RESULT 15
XX ID AAF83741 standard; cDNA; 1116 BP.
XX AC AAF83741;
XX XX
XX AC AAF83741;
XX XX
XX DR 23-JUL-2001 (first entry)
XX PT Human IL-TIF polypeptide encoding cDNA.
XX PS
XX KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cyostatic;
XX KW antirheumatic; antiallergic; antiaschemic; antiheterosclerotic;
XX KW immunosuppressive; chromosome 6q24.1-25.2; human; ss.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT CDS 21..560
XX FT /tag= a
XX FT /product= "IL-TIF"
XX
XX WO200140467-A1.
XX PN
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US32703.
XX PR 03-DEC-1999; 99US-0169049.
XX PR 13-SEP-2000; 2000US-0232219.
XX PR 31-OCT-2000; 2000US-0244610.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX DR WPI; 2001-356158/37.
XX DR P-PsDB; AAE62664.
XX PT New soluble cytokine receptor polypeptides and polynucleotides, useful
XX PT for diagnosing and treating cancer and inflammatory conditions -
XX PS Example 17; Page 193-195; 210pp; English.
XX CC The invention relates to a human cytokine receptor polypeptide,
XX CC designated zcytor16. The zcytor16 polypeptide can be expressed by
XX CC standard recombinant methodology and can bind to IL-TIF (undefined). The

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Sequence 1116 BP; 336 A; 229 C; 222 G; 329 T; 0 other;

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Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Db 601 CTGCTAGAAATAACAATTAGATGCCCAAGCGATTTT 639

Qy	13	CTTCAGAACAGGTTCTCTCTTCCCAAGTACCAAGTTGCTCGAGTTAGAATTGTCTGCAATG	74
Db	1	CTTCAGAACAGGTTCTCTCTTCCCAAGTACCAAGTTGCTCGAGTTAGAATTGTCTGCAATG	60
Qy	75	GGCGCCCTGCAGAAATCTGTAGAGCTTCTCTTATGGGAGAACCCGGCCACACAGTGGCTC	134
Db	61	GGCGCCCTGCAGAAATCTGTAGAGCTTCTCTTATGGGAGAACCTGGCCACACAGTGGCTC	120
Qy	135	CTTCTCTTGGCCCTCTTGGTACAGAGGAGAGACACTGCGCCATCAGCTCCACCTGCAGG	194
Db	121	CTTCTCTTGGCCCTCTTGGTACAGAGGAGAGACACTGCGCCATCAGCTCCACCTGCAGG	180
Qy	195	CTTGACAAAGTCCAACTTCACAGCCCTTATATCAACAACGACCTTCATGCTGGCTAAG	254
Db	181	CTTGACAAAGTCCAACTTCACAGCCCTTATATCAACAACGACCTTCATGCTGGCTAAG	240
Qy	255	GAGGCTAGTGTGGCTGATTAACAACAACAAGCTTGTCTCATTTGGGGAGAACTGTTCCAC	314
Db	241	GAGGCTAGTGTGGCTGATTAACAACAACAAGCTTGTCTCATTTGGGGAGAACTGTTCCAC	300
Qy	315	GGAGTCAGATAGTAGAGCGGCTGCATATGATGTAAGACAGGCGCTGAACCTCACCCTTGAA	374
Db	301	GGAGTCAGATAGTAGAGCGGCTGCATATGATGTAAGACAGGCGCTGAACCTTCCTTGA	360
Qy	375	GAAAGTCTGTTCCCTCAATCTGATAGTTTCCAGCCCTTATATGCAGAGAGTGTGGCCCTC	434
Db	361	GAAAGTCTGTTCCCTCAATCTGATAGTTTCCAGCCCTTATATGCAGAGAGTGTGGCCCTC	420
Qy	435	CTGGCCAGGCTCAGCAACAGGCTAAGCAGATGTCAATTTGAAGGTGATCCTTGCATATC	494
Db	421	CTGGCCAGGCTCAGCAACAGGCTAAGCAGATGTCAATTTGAAGGTGATCCTTGCATATC	480
Qy	495	CAGAGAAATGTCGCAAAACCTGAAGACACAGTGAAGAAAAGTTGAGAGATGGAGAGATC	554
Db	481	CAGAGAAATGTCGCAAAACCTGAAGACACAGTGAAGAAAAGTTGAGAGATGGAGAGATC	540
Qy	555	AAAGCAATTTGAGAACTGGATTTGCTGTTATGTCTCTGAGAAATGCGCTCATTTGACCA	614
Db	541	AAAGCAATTTGAGAACTGGATTTGCTGTTATGTCTCTGAGAAATGCGCTCATTTGACCA	600
Qy	615	GAGCAAAAGCTGAAAAATGAATTAACAACCCCTTTCCTGCTGAGAAATTAACAATTAAGATG	674
Db	601	GAGCAAAAGCTGAAAAATGAATTAACAACCCCTTTCCTGCTGAGAAATTAACAATTAAGATG	660
Qy	675	CCCCAAAGGATTTT 690	
Db	661	CCCCAAAGGATTTT 676	

```

RESULT 3
US-10-063-588-153
Sequence 153, Application US/10063588
Publication No. US20030130483A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,588
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA

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ORGANISM: Homo Sapien
US-10-063-588-153

US-10-063-588-153

Query Match	98.0%;	Score 676;	DB 14;	Length 1152;
Best Local Similarity	100.0%;	Prod No	9 19-206.	

Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY	15	CTTCGAAACAGGTTCTCCCTCCCGAGTCACAGATGGCTGAGTTAAATGTCTGCAATG	74
Db	1	CTTGAAACAGGTTCTCCCTCCCGAGTCACAGATGGCTGAGTTAAATGTCTGCAATG	60
QY	75	GCCGCGCTTCGCAAAATCTGTAGCTCTTTCCTTATGSGGACCTCGGCACACAGCTGCTC	134
Db	61	GCCGCGCTTCGCAAAATCTGTAGCTCTTTCCTTATGSGGACCTCGGCACACAGCTGCTC	120
QY	135	CTTCTCTTGGCCCTCTTGGTACAGGAGGAGCAGCTGCGCCCATCAGCTCCACTGCAAG	194
Db	121	CTTCTCTTGGCCCTCTTGGTACAGGAGGAGCAGCTGCGCCCATCAGCTCCACTGCAAG	180
QY	195	CTTGCAAAGTCCAACTTCAGCAGCCCTTATATCACCACACCGACCTTCATGCTGGCTAAG	254
Db	181	CTTGCAAAGTCCAACTTCAGCAGCCCTTATATCACCACACCGACCTTCATGCTGGCTAAG	240
QY	255	GAGGCTAGCTGGGCGTATACAAACAGACGTTGCTGCTATTGSGGAGAAACTGTTCCAC	314
Db	241	GAGGCTAGCTGGGCGTATACAAACAGACGTTGCTGCTATTGSGGAGAAACTGTTCCAC	300
QY	315	GGAGTCAGTATAGTAGGCGGCTGCTATCTGATGAAACAGATGCTGAACTTCACCTTGAA	374
Db	301	GGAGTCAGTATAGTAGGCGGCTGCTATCTGATGAAACAGATGCTGAACTTCACCTTGAA	360
QY	375	GAAGTGTCTGTTCCCTTCATCTGTATAGTTCACGCTTATATGAGAGAGTGGTCCCTTC	434
Db	361	GAAGTGTCTGTTCCCTTCATCTGTATAGTTCACGCTTATATGAGAGAGTGGTCCCTTC	420
QY	435	CTGGCGCAGGCTCAGCAACAGGCTTAAGCACATGTCATATTGAAGGTATGACTCGCATATC	494
Db	421	CTGGCGCAGGCTCAGCAACAGGCTTAAGCACATGTCATATTGAAGGTATGACTCGCATATC	480
QY	495	CAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAGAAAGCTTGGAGAGAGTGAAGATC	554
Db	481	CAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAGAAAGCTTGGAGAGAGTGAAGATC	540
QY	555	AAAGCAATTGAGAACTGATTTGCTGTTATGCTCTGAGAAATGCGTSCATTTGACCA	614
Db	541	AAAGCAATTGAGAACTGATTTGCTGTTATGCTCTGAGAAATGCGTSCATTTGACCA	600
QY	615	GAGCAAAAGCTGAAAAATGAATTAATAACCCCTTTCCTGCTAGAAATAACAATTAGATG	674
Db	601	GAGCAAAAGCTGAAAAATGAATTAATAACCCCTTTCCTGCTAGAAATAACAATTAGATG	660
QY	675	CCCCCAAGGATTTT 690	
Db	661	CCCCCAAGGATTTT 676.	

RESULT 4
US-10-006-867-153

; Sequence 153, Application US/10006867

Publication No. US20020119130A1

; GENERAL INFORMATION:

; GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.

APPLICANT: Filvarotti, Ellen
APPLICANT: Garitsen Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETET
TITLE OF INVENTION: ACTS

TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1

FILE REFERENCE: F34230X1C1

1	CURRENT APPLICATION NUMBER: US/10/006,683
2	CURRENT FILING DATE: 2001-12-06
3	PRIOR APPLICATION NUMBER: 60/063435
4	PRIOR FILING DATE: 1997-10-29
5	PRIOR APPLICATION NUMBER: 60/064215
6	PRIOR FILING DATE: 1997-10-29
7	PRIOR APPLICATION NUMBER: 60/082797
8	PRIOR FILING DATE: 1998-04-22
9	PRIOR APPLICATION NUMBER: 60/083495
10	PRIOR FILING DATE: 1998-04-29
11	PRIOR APPLICATION NUMBER: 60/085579
12	PRIOR FILING DATE: 1998-05-15
13	PRIOR APPLICATION NUMBER: 60/087759
14	PRIOR FILING DATE: 1998-06-02
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50	PRIOR FILING DATE: 1998-06-26
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53	PRIOR APPLICATION NUMBER: 60/096012
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63	PRIOR APPLICATION NUMBER: 60/097971
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65	PRIOR APPLICATION NUMBER: 60/097979
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68	PRIOR FILING DATE: 1998-09-01
69	PRIOR APPLICATION NUMBER: 60/099741
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71	PRIOR APPLICATION NUMBER: 60/099763
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73	PRIOR APPLICATION NUMBER: 60/099792

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PRIOR FILING DATE: 1999-01-20

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PRIOR APPLICATION NUMBER: 60/144791
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PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
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PRIOR FILING DATE: 2000-01-11
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PRIOR FILING DATE: 1998-08-25
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PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380142

Query Match 98.0%; Score 676; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 9, 1e-206; Gaps 0;
Matches 676; Conservative 0; Mismatches 0; Indels 0;

QY 15 CTTGAGAACAGGTTCTCTCCAGTCAGGTTGGAATTGTTGCAATG 74
DB 1 CTTGAGAACAGGTTCTCTCCAGTCAGGTTGGAATTGTTGCAATG 60
QY 75 GCGGCCCTGCAGAAATCTGTAGCTCTTTCTTATGGGAGCCCTGACCAAGCTGCTC 134
DB 61 GCGGCCCTGCAGAAATCTGTAGCTCTTTCTTATGGGAGCCCTGACCAAGCTGCTC 120
QY 135 CTTCTCTGGCCCTCTGTGTAAGGAGAGAGAGCTGCGCCATAGCTCCAGTCAGG 194
DB 121 CTTCTCTGGCCCTCTGTGTAAGGAGAGAGAGCTGCGCCATAGCTCCAGTCAGG 180
QY 195 CTTGACAAAGTCCAACTTCAGAGGCTTATATCAACCAACGACCTTCATGCTGCTAAG 254
DB 181 CTTGACAAAGTCCAACTTCAGAGGCTTATATCAACCAACGACCTTCATGCTGCTAAG 240
QY 255 GAGGCTAGCTTGGCTGATTAACAACAACAAGCTTCTTCATTTGGGAGAAACTGTTCCAC 314
DB 241 GAGGCTAGCTTGGCTGATTAACAACAACAAGCTTCTTCATTTGGGAGAAACTGTTCCAC 300
QY 315 GAGGCTAGTATGAGTGAAGGCTGCTATCTGATGAAGAGTGTGAACCTTCACCTTGA 374
DB 301 GAGGCTAGTATGAGTGAAGGCTGCTATCTGATGAAGAGTGTGAACCTTCACCTTGA 360
QY 375 GAGGCTGTGTTCCCTCAATCTGATAGTTCCAGGCTTATATGACAGAGAGTGTGCTTC 434
DB 361 GAGGCTGTGTTCCCTCAATCTGATAGTTCCAGGCTTATATGACAGAGAGTGTGCTTC 420
QY 435 CTGGCCAGGCTCAGCAACAGGCTAAGCATGTATATTGAAGTGATGACTGTGATATC 494

Db 421 CTGGCCAGGCTACGACACGGCTTAAGCATCTCATATTGAAGTGATGACCTGCAATTC 480
QY 495 CAGAGGAATGTGCACAAAGCTGAGAGACACAGTGAACAAAGCTTGAAGAGTGAAGATC 554
Db 481 CAGAGGAATGTGCACAAAGCTGAGAGACACAGTGAACAAAGCTTGAAGAGTGAAGATC 540
QY 555 AAAGCAATGTGAGAACTGGATTGCTGTTTAACTCTGAGAAATGCTGCAATTTGACCA 614
Db 541 AAAGCAATGTGAGAACTGGATTGCTGTTTAACTCTGAGAAATGCTGCAATTTGACCA 600
QY 615 GAGCAAAAGTGAACAAATGAACTAAACCCCTTCCCTGAGAAATGCAATTAAGATG 674
Db 601 GAGCAAAAGTGAACAAATGAACTAAACCCCTTCCCTGAGAAATGCAATTAAGATG 660
QY 675 CCCCAAGCGATTTT 690
Db 661 CCCCAAGCGATTTT 676
RESULT 5
US-10-066-500-125
Sequence 125, Application US/10066500
Publication No. US20020177165A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerltsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kljavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P130R1C7
CURRENT APPLICATION NUMBER: US/10/066,500
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
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PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 98.0%; Score 676; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 9.1e-206;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTAGAACAGCTTCTCTCCAGTCACAGCTGCTCGAGTTAGATTGTCGCAATG 74
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QY 75 GCGCCCTGACAGAAATGAGAGCTTTCTTATGAGGACCTGGGACACAGCTGCTC 134
DB 61 GCGCCCTGACAGAAATGAGAGCTTTCTTATGAGGACCTGGGACACAGCTGCTC 120
QY 135 CTTCTTGGCCCTCTTGTACAGAGGAGAGAGCTGCGCATCAGCTCCACTGCAAG 194
DB 121 CTTCTTGGCCCTCTTGTACAGAGGAGAGAGCTGCGCATCAGCTCCACTGCAAG 180
QY 195 CTTGACAACTGCACTTCCAGAGCCTTATATCAACACGACCTTCAATGCTGCTAG 254
DB 181 CTTGACAACTGCACTTCCAGAGCCTTATATCAACACGACCTTCAATGCTGCTAG 240
QY 255 GAGGCTAGCTGCTGCTATACACAGAGCTTCTCATTTGGGGAGAACTGTCAC 314
DB 241 GAGGCTAGCTGCTGCTATACACAGAGCTTCTCATTTGGGGAGAACTGTCAC 300
QY 315 GAGTCAGTATGAGTGAAGCCCTGCTATGATGAGAGAGGTGTAACCTTCACTTGA 374
DB 301 GAGTCAGTATGAGTGAAGCCCTGCTATGATGAGAGAGGTGTAACCTTCACTTGA 360
QY 375 GAAGTCTGTTCCCTCAATGATGATGATGATGATGATGATGATGATGATGATG 434
DB 361 GAAGTCTGTTCCCTCAATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 435 CTGGCCAGCTGACCAAGCTTAAAGCAATGATGATGATGATGATGATGATGATG 494
DB 421 CTGGCCAGCTGACCAAGCTTAAAGCAATGATGATGATGATGATGATGATGATG 480
QY 495 CAGAGAACTGCAAAAGCTGAAGGACAGAGCAAGGAAAGCTTGGAGAGAGTGAATC 554
DB 481 CAGAGAACTGCAAAAGCTGAAGGACAGAGCAAGGAAAGCTTGGAGAGAGTGAATC 540
QY 555 AAAGCAATTGAGAACTGATTTGCTTTATGCTTGAAGAAATGCTGATTTGACA 614
DB 541 AAAGCAATTGAGAACTGATTTGCTTTATGCTTGAAGAAATGCTGATTTGACA 600
QY 615 GAGCAAAAGTGAATAAATACTAACCCCTTCCCTGTAGAAATTAACATTTAGATG 674
DB 601 GAGCAAAAGTGAATAAATACTAACCCCTTCCCTGTAGAAATTAACATTTAGATG 660
QY 675 CCCCAAGCGATTTT 690
DB 661 CCCCAAGCGATTTT 676

RESULT 6
US-10-063-547-153
Sequence 153, Application US/10063547
Publication No. US20020182638A1
GENERAL INFORMATION:
APPLICANT: Bacon, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerdttsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gunney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3230R1C1
 CURRENT APPLICATION NUMBER: US/10/063,547
 CURRENT FILING DATE: 2002-05-02
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 170
 SEQ ID NO 153
 LENGTH: 1152
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-063-547-153

Query Match 98.0%; Score 676; DB 15; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 9.1e-206; Indels 0; Gaps 0;
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 15 CTTGAGAACAGGTTCTCCCTCCAGTCACAGTTGCTGAGTTAGATTGCTGCAGT 74
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QY 75 GCCGCCCTGCAGAAATCTGTAGCTCTTTCTTTATGGGAACTCCGACCAAGCTGCTC 134
DB 61 GCCGCCCTGCAGAAATCTGTAGCTCTTTCTTTATGGGAACTCCGACCAAGCTGCTC 120
QY 135 CTTCTCTGGCCCTCTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
DB 121 CTTCTCTGGCCCTCTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 195 CTTGACAAAGTCCCACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
DB 181 CTTGACAAAGTCCCACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 255 GAGGCTAGCTTGGCTGTATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314
DB 241 GAGGCTAGCTTGGCTGTATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 315 GAGTCAAGTATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
DB 301 GAGTCAAGTATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 375 GAGGCTAGCTTGGCTGTATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 434
DB 361 GAGGCTAGCTTGGCTGTATACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 435 CTTGCCAGGCTCAGCAACAGGCTTAAGCAGATGTCATATTGAAGGTATGACCTGCATATC 494
DB 421 CTTGCCAGGCTCAGCAACAGGCTTAAGCAGATGTCATATTGAAGGTATGACCTGCATATC 480
QY 495 CAGAGAAATGTGCAAAAAGCTGAAGAGACACAGTGAAGAAAGCTTGAGAGAGAGAGATC 554
DB 481 CAGAGAAATGTGCAAAAAGCTGAAGAGACACAGTGAAGAAAGCTTGAGAGAGAGATC 540
QY 555 AAAGCAATTGGAAGAACTGGAATTGCTGTATAGTCTGTGAGAAATCCGCAATTGACCA 614
DB 541 AAAGCAATTGGAAGAACTGGAATTGCTGTATAGTCTGTGAGAAATCCGCAATTGACCA 600
QY 615 GAGCAAAAGCTGAAGAAATGATACTAACCCCTTTCCCTGCTAGAATAACAATTAGATG 674
DB 601 GAGCAAAAGCTGAAGAAATGATACTAACCCCTTTCCCTGCTAGAATAACAATTAGATG 660
QY 675 CCCCAAAAGCGATTTTT 690
DB 661 CCCCAAAAGCGATTTTT 676

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RESULT 7
 US-10-063-616-153
 Sequence 153, Application US/10063616
 Publication No. US20030013855A1
 GENERAL INFORMATION:
 APPLICANT: Baton, Dan L.
 APPLICANT: Pilyarov, Ellen
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, Christopher J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3230R1C1
 CURRENT APPLICATION NUMBER: US/10/063,616
 CURRENT FILING DATE: 2002-05-03
 Prior Application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 170
 SEQ ID NO 153
 LENGTH: 1152
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-063-616-153

Query Match 98.0%; Score 676; DB 15; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 9.1e-206; Indels 0; Gaps 0;
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 15 CTTGAGAACAGGTTCTCCCTCCAGTCACAGTTGCTGAGTTAGATTGCTGCAGT 74
DB 1 CTTGAGAACAGGTTCTCCCTCCAGTCACAGTTGCTGAGTTAGATTGCTGCAGT 60
QY 75 GCCGCCCTGCAGAAATCTGTAGCTCTTTCTTTATGGGAACTCCGACCAAGCTGCTC 134
DB 61 GCCGCCCTGCAGAAATCTGTAGCTCTTTCTTTATGGGAACTCCGACCAAGCTGCTC 120
QY 135 CTTCTCTGGCCCTCTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
DB 121 CTTCTCTGGCCCTCTGTGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 195 CTTGACAAAGTCCCACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
DB 181 CTTGACAAAGTCCCACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
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QY 435 CTTGCCAGGCTCAGCAACAGGCTTAAGCAGATGTCATATTGAAGGTATGACCTGCATATC 494
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DB 481 CAGAGAAATGTGCAAAAAGCTGAAGAGACACAGTGAAGAAAGCTTGAGAGAGAGATC 540
QY 555 AAAGCAATTGGAAGAACTGGAATTGCTGTATAGTCTGTGAGAAATCCGCAATTGACCA 614
DB 541 AAAGCAATTGGAAGAACTGGAATTGCTGTATAGTCTGTGAGAAATCCGCAATTGACCA 600
QY 615 GAGCAAAAGCTGAAGAAATGATACTAACCCCTTTCCCTGCTAGAATAACAATTAGATG 674
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QY 675 CCCCAAAAGCGATTTTT 690
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RESULT 8
 US-10-063-502-153

Query Match	98.0%;	Score 676;	DB 15;	Length 1152;
Best Local Similarity	100.0%;	Pred. No. 9.1e-206;		
Matches 676;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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 PRIOR APPLICATION NUMBER: 60/169835

Query Match 98.0%; Score 676; DB 15; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 9.1e-206;
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGACAGGTTCTCTCCGACGACGAGTTGCTCGAGTAGAATTGTCGCAATG 74
 DB 1 CTTGAGACAGGTTCTCTCCGACGACGAGTTGCTCGAGTAGAATTGTCGCAATG 60
 QY 75 GCCGCCCTGCAGAAATGTGTAGGCTTTCTCTTAATGGAGACCTGGCCACGAGCTGCCTC 134
 DB 61 GCCGCCCTGCAGAAATGTGTAGGCTTTCTCTTAATGGAGACCTGGCCACGAGCTGCCTC 120

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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28301

Query Match 98.0%; Score 676; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 9,1e-206;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAAAGGTTCTTCCCTCCAGTCAACAGTCTGAGTAAATTTGTGGAAG 74
DB 1 CTTGAGAAAGGTTCTTCCCTCCAGTCAACAGTCTGAGTAAATTTGTGGAAG 60
QY 75 GCGGCGCTGAGAAATCTGAGAGTCTTCTTCTTATGAGGACCTGAGCAACAGTCTG 134
DB 61 GCGGCGCTGAGAAATCTGAGAGTCTTCTTCTTATGAGGACCTGAGCAACAGTCTG 120
QY 135 CTTCTCTTGGCCCTCTTGTGATGAGGAGAGAGAGAGTCTGAGTCTGAGTCTG 194
DB 121 CTTCTCTTGGCCCTCTTGTGATGAGGAGAGAGAGAGTCTGAGTCTGAGTCTG 180
QY 195 CTTGAGCAAGTCACTTCCAGCAGCCCTTATATCAACCAACGCACTTCAAGTCTG 254
DB 181 CTTGAGCAAGTCACTTCCAGCAGCCCTTATATCAACCAACGCACTTCAAGTCTG 240
QY 255 GAGGCTAGCTTGGCTGATTAACAACAGAGCTTCTCTCATTTGAGGAGAACTGTC 314
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QY 315 GAGTCAAGTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 374
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QY 495 CAGAGAGATGAG 554
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QY 615 GAGCAAGTGAAG 674
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OY 675 CCCCCAGGATTTT 690
Db 661 CCCCCAGGATTTT 676

RESULT 11

US-10-066-273-125

Sequence 125, Application US/10066273
Publication No. US20030032062A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerltsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kljavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3130R1C2
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
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Query Match 98.0%; Score 676; DB 15; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 9,1e-206; Indels 0; Gaps 0;

Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAAAGGTTCTCTTCCAGTCACCAAGTGTCTGAGTAGAATTGTCTGCAATG 74
 DB 1 CTTGAGAAAGGTTCTCTTCCAGTCACCAAGTGTCTGAGTAGAATTGTCTGCAATG 60
 QY 75 GCCGCCCTGCGAAGATCTGTGAGCTTTCTTATGGGACCCGCGCCAGCAGCTGCTC 134

DB 61 GCCGCCCTGCGAAGATCTGTGAGCTTTCTTATGGGACCCGCGCCAGCAGCTGCTC 120
 QY 135 CTTCTCTTGGCCCTCTTGTGTACAGGAGAGACGCTGCGCCATCAGCTTCCACTGCAAG 194
 DB 121 CTTCTCTTGGCCCTCTTGTGTACAGGAGAGACGCTGCGCCATCAGCTTCCACTGCAAG 180
 QY 195 CTTGAGAAAGGTTCTCTTCCAGTCACCAAGTGTCTGAGTAGAATTGTCTGCAATG 254
 DB 181 CTTGAGAAAGGTTCTCTTCCAGTCACCAAGTGTCTGAGTAGAATTGTCTGCAATG 240
 QY 255 GAGCTAGCTTGGCTGTATTAACAACAGACGCTTCTCTATTTGGGAGAACTGTTCCAC 314
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 QY 315 GAGCTAGCTTGGCTGTATTAACAACAGACGCTTCTCTATTTGGGAGAACTGTTCCAC 374
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 QY 375 GAGCTAGCTTGGCTGTATTAACAACAGACGCTTCTCTATTTGGGAGAACTGTTCCAC 434
 DB 361 GAGCTAGCTTGGCTGTATTAACAACAGACGCTTCTCTATTTGGGAGAACTGTTCCAC 420
 QY 435 CTTGAGAAAGGTTCTCTTCCAGTCACCAAGTGTCTGAGTAGAATTGTCTGCAATG 494
 DB 421 CTTGAGAAAGGTTCTCTTCCAGTCACCAAGTGTCTGAGTAGAATTGTCTGCAATG 480
 QY 495 CAGAGAAATGTGCAAAAGCTGAAAGACACAGTGAAGAAAGCTTGGAGAGTGAAGATC 554
 DB 481 CAGAGAAATGTGCAAAAGCTGAAAGACACAGTGAAGAAAGCTTGGAGAGTGAAGATC 540
 QY 555 AAGCAATTGGAACAACTGATTTGCTGTTATATCTCTGAGAAATGCTTGCATTTGACCA 614
 DB 541 AAGCAATTGGAACAACTGATTTGCTGTTATATCTCTGAGAAATGCTTGCATTTGACCA 600
 QY 615 GAGCAAGCTGAAAGAAATGAATACTAACCCCTTCCCTGCTGAATAAACAATTAGATG 674
 DB 601 GAGCAAGCTGAAAGAAATGAATACTAACCCCTTCCCTGCTGAATAAACAATTAGATG 660
 QY 675 CCCCAGGAGATTTT 690
 DB 661 CCCCAGGAGATTTT 676

RESULT 12

US-10-066-494-125
 Sequence 125, Application US/10066494

Publication No. US20030032063A1

GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi
 APPLICANT: Kevin P. Baker
 APPLICANT: David A. Bolstein
 APPLICANT: Luc Desnoyers
 APPLICANT: Dan L. Eaton
 APPLICANT: Napoleone Ferrara
 APPLICANT: Sherman Fong
 APPLICANT: Wei-Qiang Gao
 APPLICANT: Hanspeter Gerber
 APPLICANT: Mary E. Gerritsen
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 APPLICANT: Paul J. Godowski
 APPLICANT: Austin L. Gurney
 APPLICANT: Ivar J. Kljavin
 APPLICANT: Jennie P. Mather
 APPLICANT: Mary A. Napier
 APPLICANT: James Pan
 APPLICANT: Nicholas F. Paoni
 APPLICANT: Margaret Ann Roy
 APPLICANT: Timothy A. Stewart
 APPLICANT: Daniel Tumas
 APPLICANT: Colin K. Watanabe
 APPLICANT: P. Mickey Williams
 APPLICANT: William I. Wood
 APPLICANT: Zemin Zhang

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3130R1C9
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
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PRIOR FILING DATE: 1998-12-01
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PRIOR FILING DATE: 1998-11-25
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PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 98.0%; Score 676; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 9,1e-206;

Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAAAGGTTCTCTTCCAGTACAGGTTGCTGAGTGAATGTCTGCAATG 74
DB 1 CTTGAGAAAGGTTCTCTTCCAGTACAGGTTGCTGAGTGAATGTCTGCAATG 60
QY 75 GCGGCGCTGAGAAATCTGAGAGTCTTTCTTATGGGAGCCCTGGCCACCAAGTGTCTC 134
DB 61 GCGGCGCTGAGAAATCTGAGAGTCTTTCTTATGGGAGCCCTGGCCACCAAGTGTCTC 120
QY 135 CTTCTCTTGGCCCTCTTGTATACAGGAGAGACAGTGGCCCATCAGTCCCATCTGAGAG 194
DB 121 CTTCTCTTGGCCCTCTTGTATACAGGAGAGAGAGTGGCCCATCAGTCCCATCTGAGAG 180
QY 195 CTTGAGAAAGTCCAACTTCCAGAGCCCTATATCAACCAACGACCTTATGCTGGCTAG 254
DB 181 CTTGAGAAAGTCCAACTTCCAGAGCCCTATATCAACCAACGACCTTATGCTGGCTAG 240
QY 255 GAAGCTGCTTGGCTGATTAACAACAAGAGTGTCTCATTTGGGAGAACTGTTCAC 314
DB 241 GAAGCTGCTTGGCTGATTAACAACAAGAGTGTCTCATTTGGGAGAACTGTTCAC 300
QY 315 GAAGCTGATATGAGTGAAGCGCTATCTGATGAAGAGGCTGAACCTTCACTTGA 374
DB 301 GAAGCTGATATGAGTGAAGCGCTATCTGATGAAGAGGCTGAACCTTCACTTGA 360
QY 375 GAAGTGTGTTCCCTCAATCTGATAGGTTCCAGCCTTATATGAGAGAGTGTGCTTC 434
DB 361 GAAGTGTGTTCCCTCAATCTGATAGGTTCCAGCCTTATATGAGAGAGTGTGCTTC 420
QY 435 CTGGCCAGGCTCAGCAACAGGCTTAAGCAATGTATATTTGAAGTGAAGTGTGCTTC 494
DB 421 CTGGCCAGGCTCAGCAACAGGCTTAAGCAATGTATATTTGAAGTGAAGTGTGCTTC 480
QY 495 CAGAGGATGTGCAAAAGCTGAAGACAGTGAAGAAAGCTTGAAGAGAGTGAAGATC 554
DB 481 CAGAGGATGTGCAAAAGCTGAAGACAGTGAAGAAAGCTTGAAGAGAGTGAAGATC 540
QY 555 AAAGCAATGTGAGAACTGAGATTGCTGTTATGTCTCTGAGAAATGCTGCAATTGACA 614
DB 541 AAAGCAATGTGAGAACTGAGATTGCTGTTATGTCTCTGAGAAATGCTGCAATTGACA 600
QY 615 GAGCAAGCTGAAGAAATGAATTAACCCCTTCCCTGCTAATAAATAAATTAATGATG 674

DB 601 GAGCAAGCTGAAGAAATGAATTAACCCCTTCCCTGCTAATAAATAAATTAATGATG 660
QY 675 CCCCCAAGCATTTT 690
DB 661 CCCCCAAGCATTTT 676

RESULT 13

US-10-230-163-243

Sequence 243, Application US/10230163

Publication No. US2003003635A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Desnoyers, Luc

APPLICANT: Gerltsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.

APPLICANT: Watanabe, Colin L.

APPLICANT: Wood, William I.

TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3530P1C96

CURRENT FILING DATE: 2002-08-28

PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/062287

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 PRIOR APPLICATION NUMBER: 60/169835

Query Match 98.0%; Score 676; DB 15; Length 1152;
 Best Local Similarity 100.0%; Pred.No.9.1e-206;
 Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 15 CTTGAGACAGGTTCTCCCTCCAGTCCAGTTCGAGTTAGTAATGTGTGCATG 74
 Db 1 CTTGAGACAGGTTCTCCCTCCAGTCCAGTTCGAGTTAGTAATGTGTGCATG 60
 Oy 75 GCCGCCCTGAGAAATCTGTGAGCTCTTCTTATGAGGAGACCTGAGCCAGCTGCTC 134

Db 61 |CCCCCCTGCAAGAAATCTGTAGCTCTTTCTTTATGGGAGCCCTGGCCACAGCTGCTC 120
Qy 135 |CTTCTCTTGGCCCTCTTGGTACAGAGAGAGAGCTGGCCCTATAGCTCCACATGCAAG 194
Db 121 |CTTCTCTTGGCCCTCTTGGTACAGAGAGAGAGCTGGCCCTATAGCTCCACATGCAAG 180
Qy 195 |CTTACAGAGTCCACTTCCAGACAGCCCTATATACCAACCCGACCTTATAGCTGCTAG 254
Db 181 |CTTACAGAGTCCACTTCCAGACAGCCCTATATACCAACCCGACCTTATAGCTGCTAG 240
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Db 241 |GAGGCTAGCTTGGCTGATTAACAACAAGAGCTTGGCTATGAGGAGAACTGTTCCAC 300
Qy 315 |GAGCTAGTATAGTGAAGCGCTGTATCTGATGAAGAGAGTGTGAACCTTGAA 374
Db 301 |GAGCTAGTATAGTGAAGCGCTGTATCTGATGAAGAGAGTGTGAACCTTGAA 360
Qy 375 |GAGTGTCTTCTCTCAATCTGATAGTTCAGGCTTATATGACAGAGAGTGTGCTTC 434
Db 361 |GAGTGTCTTCTCTCAATCTGATAGTTCAGGCTTATATGACAGAGAGTGTGCTTC 420
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Db 421 |CTGGCCAGGCTCAGCAACAGGCTAAGCAATGTCAATATGAAGTGAAGCTGATATC 480
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Db 481 |CAGAGAAATGTGCAAAAGCTGAGAGACAGTGAAGAAAGCTTGGAGAGTGAAGATC 540
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Db 541 |AAAGCAATGTGAGAACTGATTTGTGTTATGTCTGAGAAATGCTGCAATTTGACCA 600
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Db 601 |GAGCAAGCTGAATAAATAAATAAATAAATACCCCTTCCCTGCTAGAGAAATAAATAATGATG 660
Qy 675 |CCCCAAGCGATTTT 690
Db 661 |CCCCAAGCGATTTT 676

RESULT 14

US-10-066-269-125

Sequence 125, Application US/10066269

Publication No. US20030040014A1

GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerritsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kjaerav
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood

APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3130R1C4
CURRENT APPLICATION NUMBER: US/10/066,269
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
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;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 98.0%; Score 676; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 9,1e-206;
Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTTGAGAACAGGTTCTCTCCAGTACAGCAGTTGCTGAGTAAGATTGTCGCAATG 60
QY 75 GCGCCCTGCGAATAATCTGTAGCTCTTTCTTATAGGGGACCTTGGCCACCGCTGCTTC 134
DB 61 GCGCCCTGCGAATAATCTGTAGCTCTTTCTTATAGGGGACCTTGGCCACCGCTGCTTC 120
QY 135 CTTCTCTTGGCCCTCTTGTATACAGGAGAGAGAGCTGGCCCATCAGCTCCCACTGCAGG 194
DB 121 CTTCTCTTGGCCCTCTTGTATACAGGAGAGAGAGCTGGCCCATCAGCTCCCACTGCAGG 180
QY 195 CTTGACAAATCCAACTTCCAGCAGCCTTATATACCAACCGACCTTATGCTGCTAAG 254
DB 181 CTTGACAAATCCAACTTCCAGCAGCCTTATATACCAACCGACCTTATGCTGCTAAG 240
QY 255 GAGGCTAGCTTGGCTGATTAACAACAACAGCTTGTCTCATTTGGGAGAAACTGTTCCAC 314
DB 241 GAGGCTAGCTTGGCTGATTAACAACAACAGCTTGTCTCATTTGGGAGAAACTGTTCCAC 300
QY 315 GGAGTCAGTATGAGAGAGAGAGAGAGCTGATGATGAAGAGAGTGTCAACTTCACTTGA 374
DB 301 GGAGTCAGTATGAGAGAGAGAGAGAGCTGATGATGAAGAGAGTGTCAACTTCACTTGA 360
QY 375 GAAGTGTCTTCCCTCAATCTGATGATGTTCCAGCTTATATGACAGAGGTGTGCTTC 434
DB 361 GAAGTGTCTTCCCTCAATCTGATGATGTTCCAGCTTATATGACAGAGGTGTGCTTC 420
QY 435 CTGGCCAGGCTCAGCAACAGGCTAAGCAATGTCATATTGAAGGTGATGACTGATATC 494
DB 421 CTGGCCAGGCTCAGCAACAGGCTAAGCAATGTCATATTGAAGGTGATGACTGATATC 480
QY 495 CAGAGGAATGCAAAAGCTGAAGAGACAGTGAAGAAAGCTTGGAGAGTGAAGATC 554
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QY 555 AAAGCAATTGGAAGAACTGATTTGCTTTATGTCCTGAGAAATGCTGCAATTGACCA 614
DB 541 AAAGCAATTGGAAGAACTGATTTGCTTTATGTCCTGAGAAATGCTGCAATTGACCA 600
QY 615 GAGCAAGCTGAAAAATGAAATTAAGTAAAGCCCTTCTGCTAGAAATTAACATTAGATG 674

Db 601 GAGCAAGCTGAAATGAACTAACCCCTTCCCTGCTGAAATTAACAATTAGATG 660
QY 675 CCCCCAAGCGATTTT 690
Db 661 CCCCCAAGCGATTTT 676

RESULT 15

US-10-066-211-125

Sequence 125, Application US/10066211

Publication No. US20030044844A1

GENERAL INFORMATION:

APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerltsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kljavin
APPLICANT: Jennie P. Mather
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni
APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P1130R1C8
CURRENT APPLICATION NUMBER: US/10/066,211
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547

Query Match 98.0%; Score 676; DB 15; Length 1152;

Best Local Similarity 100.0%; Pred. No. 9,1e-206; Mismatches 0; Indels 0; Gaps 0;

Matches 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTTGAGAACAGGTTCTCTTCCAGTCACAGTCAGTGTGCTGAGTAATGTCTGCAATG 74
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Qy 75 GCAGCCCTGAGAAATCTGTGAGCTCTTCTTATGGGAGCCCTGACCAAGCTGCTC 1134
Db 61 GCAGCCCTGAGAAATCTGTGAGCTCTTCTTATGGGAGCCCTGACCAAGCTGCTC 120
Qy 135 CTTCTCTGGCCCTCTTGTGTAAGGAGGAGAGAGCTGCGCCATCAGCTCCACTGAGG 194
Db 121 CTTCTCTGGCCCTCTTGTGTAAGGAGGAGAGCTGCGCCATCAGCTCCACTGAGG 180
Qy 195 CTTGACAACTCCAACTTCCAGCAGCCCTTATATCCAAACCGACCTTCAATGCTGCTAAG 254
Db 181 CTTGACAACTCCAACTTCCAGCAGCCCTTATATCCAAACCGACCTTCAATGCTGCTAAG 240
Qy 255 GAGGCTAGCTGGCTGATTAACAACAGAGCTTCTCATTTGGGAGAACTGTTCCAC 314
Db 241 GAGGCTAGCTGGCTGATTAACAACAGAGCTTCTCATTTGGGAGAACTGTTCCAC 300
Qy 315 GGAGTCAATGATGATGAGGCTGCTATCTGATGAAAGAGTGTGTAATTCACCTTGA 374
Db 301 GGAGTCAATGATGATGAGGCTGCTATCTGATGAAAGAGTGTGTAATTCACCTTGA 360
Qy 375 GAACTGCTGTTCCCTCAATCTGATGATGATGATGATGATGATGATGATGATGATG 434
Db 361 GAACTGCTGTTCCCTCAATCTGATGATGATGATGATGATGATGATGATGATGATG 420
Qy 435 CTGGCCAGGCTGACCAAGCTTAACCAATGCTCAATGAAAGTGTGATGATGATGATG 494
Db 421 CTGGCCAGGCTGACCAAGCTTAACCAATGCTCAATGAAAGTGTGATGATGATGATG 480
Qy 495 CAGAGAAATGTGAAAGCTGAAGGACACAGTGAAGCTTGAAGAGTGAAGATC 554
Db 481 CAGAGAAATGTGAAAGCTGAAGGACACAGTGAAGCTTGAAGAGTGAAGATC 540
Qy 555 AAAGCAATGGAAGCTGAATGTTCTGTTATGCTCTGAGAAATCCTGCAATTTGACA 614
Db 541 AAAGCAATGGAAGCTGAATGTTCTGTTATGCTCTGAGAAATCCTGCAATTTGACA 600
Qy 615 GAGCAAAAGCTGAAGAAATGAATTAATACCCCTTCTGCTGTAAGAAATCAATTTGATG 674
Db 601 GAGCAAAAGCTGAAGAAATGAATTAATACCCCTTCTGCTGTAAGAAATCAATTTGATG 660
Qy 675 CCCCAGGAGATTTT 690
Db 661 CCCCAGGAGATTTT 676

Search completed: July 20, 2003, 03:46:02
Job time: 99.6244 sec

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QY	421	AGTGGTGTCCTTCTCTGGCCAGGCTTCAGCAACAGGCTAAGCAATGTCATATATGAAGTG	480
Db	421	AGTGGTGTCCTTCTCTGGCCAGGCTTCAGCAACAGGCTAAGCAATGTCATATATGAAGTG	480
QY	481	ATGACCTGCATATCCAGAGGAATGTGCAAAACCTGAAGACACAGTGAAGAAAGCTTGGAG	540
Db	481	ATGACCTGCATATCCAGAGGAATGTGCAAAACCTGAAGACACAGTGAAGAAAGCTTGGAG	540
QY	541	AGAGTGGAGAGATCCAAAGCAATTGGAGAACTGAGATTGCTGTTATGTCTCTGAGAAATG	600
Db	541	AGAGTGGAGAGATCCAAAGCAATTGGAGAACTGAGATTGCTGTTATGTCTCTGAGAAATG	600
QY	601	CTGCGACTTTGACCCAGAGCAAACTGATAAATGAATTAACCCCTTTCCCTGCTAGAA	660
Db	601	CTGCGACTTTGACCCAGAGCAAACTGATAAATGAATTAACCAACCCCTTTCCCTGCTAGAA	660
QY	661	ATAACATTAGATGCCCCCAAAAGCGATTTTT	690
Db	661	ATAACATTAGATGCCCCCAAAAGCGATTTTT	690

RESULT 2
US-09-354-243B-24
; Sequence 24, Application US/09354243B
Date: 09/01/2012

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GENERAL INFORMATION:
APPLICANT: Dumontier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Peptides
TITLE OF INVENTION: (Tifs)
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIORITY APPLICATION NUMBER: US09/178,973
PRIORITY FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 28
LENGTH: 690
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
IS-09-354-243B-24

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Query Match	100.0%;	Score 690;	DB 4;	Length 690;
Best Local Similarity	100.0%;	Pred. No. 5.6e-197;		
Matches 690;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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QY	61 AATTGCTGCAATGAGCGCGCCCTGCGAAGATGTGAGCTCTTTCCTTATGAGGACCTTAG	120
Db	61 AATTGCTGCAATGAGCGCGCCCTGCGAAGATGTGAGCTCTTTCCTTATGAGGACCTTAG	120
QY	121 CCACCAAGCTGCTCTTCTCTTGGCCCTCTTGGTACAGGAGAGAGCAAGCTGCGCCATCA	180
Db	121 CCACCAAGCTGCTCTTCTCTTGGCCCTCTTGGTACAGGAGAGAGCAAGCTGCGCCATCA	180
QY	121 GCTCCCACTGACGAGCTTGACAAAGTCCAACTTCACGAGAGCCTTATACCAACCGGACT	240
Db	181 GCTCCCACTGACGAGCTTGACAAAGTCCAACTTCACGAGAGCCTTATACCAACCGGACT	240
QY	241 TATAGCTGAGCTAAGAGAGCTAGCTTGGCTGATTAACAACAGAGCTTGTGCTCATTTAGGGG	300

Db 241 TCATGCTGGCTAAGGAGGCTAGCTTGGCTGATMAACAACAACAGCGTTCCGTCATTGGGG 3000

Qy 301 AGAACTGTCACGAGAGTCAGTATGAGTGAAGACGGCTGATGATGAAAGCAAGTCTGA 360

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Qy 361 ACTTCACCCCTGGAAGAAGTGTCTTCCCTCAATCTGATAGTTCCAGCCTTATATCAG 420

Db 361 ACTTCACCCCTGGAAGAAGTGTCTTCCCTCAATCTGATAGTTCCAGCCTTATATCAG 420

Qy 421 AGGTGTGTCCTTCTGTGCGACGGCTCAGCAACAGCTAAGCAATGTCAATTGAAGTGTG 480

Db 421 AGGTGTGTCCTTCTGTGCGACGGCTCAGCAACAGCTAAGCAATGTCAATTGAAGTGTG 480

Qy 481 ATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAGAAAGCTTGGAG 540

Db 481 ATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAGAAAGCTTGGAG 540

Qy 541 AGAGTGAAGAGATCAAAAGCAATGTGAGAACTGTGCTGTTATGTCTCGAGAAATG 600

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Qy 601 CCTGCATTGACCCAGAGCAAAAGCTGAAATAATGAATTAACCCCTTCCCTGCTAGAA 660

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Qy 661 ATTAACAATTAGATGCCCAAAAGCAATTTT 690

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RESULT 3
US-09-178-973B-7
; Sequence 7, Application US/09178973B
Debate No. 007770

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: APPLICANT: Dumoutier, Laure
: APPLICANT: Louhed, Jamila
: APPLICANT: Renaud, Jean-Christophe
: TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
: TITLE OF INVENTION: (Tifs)
: TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
: FILE REFERENCE: LMD 5543
: CURRENT APPLICATION NUMBER: US/09/178,973B
: CURRENT FILING DATE: 1998-10-26
: NUMBER OF SEQ ID NOS: 17
: SEQ ID NO 7
: LENGTH: 1119
: TYPE: DNA
: ORGANISM: Mus musculus
: US-09-178-973B-7

```

Query Match	59.3%	Score 409.2;	DB 4;	Length 119;
Best Local Similarity	76.1%;	Pred. No. 7.5e-113;		
Matches 504;	Conservative 0;	Mismatches 158;	Indels 0;	Gaps 0;

QY	29	CTCTTCCCCAGTCACCACTGCTCGAGTTAGAAATTGTCTGCATATGGCCGCCCTGCAGAA	88
Db	9	CTCTCTCTCACTATCAACTGTTGACACTTGTGGAGATCTGTATGGCTGTCTGCAGAA	68
QY	89	ATCTGTGACTCTTTTCTTATATGGGAGACCTTGGCCACCAAGTGTCTCTTCTTTGGCCCT	148
Db	69	ATCTAAGATTTTTCCTTATATGGGACCTTTGGCCGACGCTGCTTCTCATTTGCCCT	128
QY	149	CTTGTATACGAGGAGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTATGACAGTCCAA	208
Db	129	GTGGGCGCCAGAGGCAATGCCCTCCCTCAACCCCGGTGCAGCTTATAGATGTCCAA	188
QY	209	CTTCCAGACGCCCTTATATACCAACCGCACTTATGCTGTAGCTATAGGAGGCTAGCTTGGC	268
Db	189	CTTCCAGACGCCGTCATCTGTCAACCGCACTTATATGTGGCCAAAGAGGCGACGCTTGC	248

QY 2,9 TGATACACACAGAGCTTCTCTCTATGGGAGAAAGCTTCCACGAGTCAATGAG 328
DB 249 AGATACACACAGAGCTTCTCTCTATGGGAGAAAGCTTCCACGAGTCAATGAG 308
QY 329 TGAGGCTGCTATCTGATGAGAGAGTGTGTAACCTTGAAGAGTGTCTCC 388
DB 309 AGATGAGTCTACCTGATGAGAGAGTGTGTAACCTTGAAGAGTGTCTCC 368
QY 389 TCAATCTGATGAGTGTGTAACCTTGAAGAGTGTGTAACCTTGAAGAGTGTCTCC 448
DB 369 CCAGTACAGAGTGTGTAACCTTGAAGAGTGTGTAACCTTGAAGAGTGTCTCC 428
QY 449 CAACGAGTACAGAGTGTGTAACCTTGAAGAGTGTGTAACCTTGAAGAGTGTCTCC 508
DB 429 CAATGAGTCTACCTGATGAGAGAGTGTGTAACCTTGAAGAGTGTCTCC 488
QY 509 AAAGCTGAGAGACAGAGTGTGTAACCTTGAAGAGTGTGTAACCTTGAAGAGTGTCTCC 568
DB 489 AAAGCTGAGAGACAGAGTGTGTAACCTTGAAGAGTGTGTAACCTTGAAGAGTGTCTCC 548
QY 569 ACTGATTTGCTGTTATGCTCTGAGAAATGCTGATTTGACAGAGCAAGCTGAA 628
DB 549 ACTGATTTGCTGTTATGCTCTGAGAAATGCTGATTTGACAGAGCAAGCTGAA 608
QY 629 AATGATTAACCTAACCCCTTCCCTGAGAAATTAATGATGCCCCCAAGGATTT 688
DB 609 AAGGAGAACTGCTCTTCTCTCTCTTAAAGAAATTAATGATGCCCCCAAGGATTT 668
QY 689 TT 690
DB 669 TT 670

RESULT 4
US-09-419-568F-7

Sequence 7, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-419-568F-7

Query Match 59.3%; Score 409.2; DB 4; Length 1119;
Best Local Similarity 76.1%; Pred. No. 7.5e-113;
Matches 504; Conservative 0; Mismatches 158; Indels 0; Gaps 0;
QY 29 CTCCTTCCCACTACAGAGTGTCTGAGATTGATGCAATGGAGCCGCTGAGAA 88
DB 9 CTCCTTCCCACTACAGAGTGTCTGAGATTGATGCAATGGAGCCGCTGAGAA 68
QY 89 ATCTGAGCTCTTTCTTATGGGAGCCCTGAGCAAGTGTCTCTTCTTGAGCCCT 148
DB 69 ATCTGAGCTCTTTCTTATGGGAGCCCTGAGCAAGTGTCTCTTCTTGAGCCCT 128
QY 149 CTGAGAGAGAGAGAGAGAGTGTGAGCAAGTGTCTCTTCTTGAGCCCT 208
DB 129 GTGGAGAGAGAGAGAGAGTGTGAGCAAGTGTCTCTTCTTGAGCCCT 188

QY 209 CTCAGAGAGCCCTATATACCAACGAGCTTCTATGCTGCTTAAGAGGCTAGCTTGC 268
DB 189 CTCAGAGAGCCCTATATACCAACGAGCTTCTATGCTGCTTAAGAGGCTAGCTTGC 248
QY 269 TGATACACACAGAGCTTCTCTCTATGGGAGAAAGCTTCCACGAGTCAATGAG 328
DB 249 AGATACACACAGAGCTTCTCTCTATGGGAGAAAGCTTCCACGAGTCAATGAG 308
QY 329 TGAGGCTGCTATCTGATGAGAGTGTGTAACCTTGAAGAGTGTCTCC 388
DB 309 AGATGAGTCTACCTGATGAGAGTGTGTAACCTTGAAGAGTGTCTCC 368
QY 389 TCAATCTGATGAGTGTGTAACCTTGAAGAGTGTGTAACCTTGAAGAGTGTCTCC 448
DB 369 CCAGTACAGAGTGTGTAACCTTGAAGAGTGTGTAACCTTGAAGAGTGTCTCC 428
QY 449 CAACGAGTACAGAGTGTGTAACCTTGAAGAGTGTGTAACCTTGAAGAGTGTCTCC 508
DB 429 CAATGAGTCTACCTGATGAGAGAGTGTGTAACCTTGAAGAGTGTCTCC 488
QY 509 AAAGCTGAGAGACAGAGTGTGTAACCTTGAAGAGTGTGTAACCTTGAAGAGTGTCTCC 568
DB 489 AAAGCTGAGAGACAGAGTGTGTAACCTTGAAGAGTGTGTAACCTTGAAGAGTGTCTCC 548
QY 569 ACTGATTTGCTGTTATGCTCTGAGAAATGCTGATTTGACAGAGCAAGCTGAA 628
DB 549 ACTGATTTGCTGTTATGCTCTGAGAAATGCTGATTTGACAGAGCAAGCTGAA 608
QY 629 AATGATTAACCTAACCCCTTCCCTGAGAAATTAATGATGCCCCCAAGGATTT 688
DB 609 AAGGAGAACTGCTCTTCTCTCTCTTAAAGAAATTAATGATGCCCCCAAGGATTT 668
QY 689 TT 690
DB 669 TT 670

RESULT 5
US-09-354-243B-7

Sequence 7, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-354-243B-7

Query Match 59.3%; Score 409.2; DB 4; Length 1119;
Best Local Similarity 76.1%; Pred. No. 7.5e-113;
Matches 504; Conservative 0; Mismatches 158; Indels 0; Gaps 0;
QY 29 CTCCTTCCCACTACAGAGTGTCTGAGATTGATGCAATGGAGCCGCTGAGAA 88
DB 9 CTCCTTCCCACTACAGAGTGTCTGAGATTGATGCAATGGAGCCGCTGAGAA 68
QY 89 ATCTGAGCTCTTTCTTATGGGAGCCCTGAGCAAGTGTCTCTTCTTGAGCCCT 148
DB 69 ATCTGAGCTCTTTCTTATGGGAGCCCTGAGCAAGTGTCTCTTCTTGAGCCCT 128

OY	149	CTTGGAACAGGGAGAGCAGCTGCGCCCAATCAGCTCCACTGAGGCTTGACAAAGTCCAA	208
Db	129	GTGGGCCAGAGGCGAAATGCGCTGCCCGCTCAACACCCGGGTGCAAGCTTGAGGTCCAA	188
OY	209	CTTCAGACAGCCCTTATATCACCAAACCGCACCTTCATGCTGGCTPAGAGGCTAGCTTGGC	268
Db	189	CTTCAGACAGCCGTCATGTCATCGCAACCGCACCTTTATGTGTGGCCAGAGAGCCAGCCTTGC	248
OY	269	TGATTAACAACACAGACGTTTCGTCTCATTTGGGGAGAAACTGTTCCACGAGTCAGTATGAG	328
Db	249	AGATTAACAACACAGACGTCGCGCTCATCGGGAGAAACTGTTCCAGAGATCAGTCTAA	308
OY	329	TGAGGCTGCTCATTCGATAGACAGGTCGTGAACCTCACCCCTGGAAGAGTGTGTTCCC	388
Db	309	AGATAGAGTCTACCTGATAGACAGGTGCTCAACTTCACCCCTGGAAGACCTTTGCTCCC	368
OY	389	TCAATCTGATAGAGTTCCAGCCTTATATGACAGAGGTGTGTGCCCTTCCTGGCCAGGCTCAG	448
Db	369	CCAGTCAGACAGGTTCCAGCCCTCAATGACAGAGGTGTGTACCTTCTTGACCAAACTCAG	428
OY	449	CACACGGCTAAGCACATGTCATATTGAAGGTGATGACTTGACATATCCAGAGATGTGCA	508
Db	429	CAATCAGTCAAGCTCCTTGACATATCAGCGGTGCGACAGAACATCCAGAGAAATGTGAC	488
OY	509	AAAGCTGAAGGACACAGTGAATAAAGCTTGAGAGAGTGAAGATCAAGACATTTGGAGA	568
Db	489	AAAGCTGAAGGACACAGTGAATAAAGCTTGAGAGAGTGAAGATCAAGCGATTTGGGA	548
OY	569	ACTGATTTGCTGTTATGTCTCTGGAATAGTGGCTGCATTTGACGAGCAAAAGCTGAAA	628
Db	549	ACTGACCTGCTGTTATGTCTCTGAGAAATGCTTGCTGTGAGCAGAAAGAACTAGAA	608
OY	629	AATGAATTAACTAACCCCTTTCCCTGCTAGAAATTAACAATTAGATGCCCAAGCAATTT	688
Db	609	AACGAAGAATCTCCTTCTCTCTCTTAATAAAGACATTAAGATCCCTGAATGACCTTT	668
OY	689	TT 690	
Db	669	TT 670	

```

RESULT 6
US-09-178-973B-9
: Sequence 9, Application US/09178973B
: Patent No. 6274710
: GENERAL INFORMATION:
: APPLICANT: Dumoutier, Laure
: APPLICANT: Louhed, Jamila
: APPLICANT: Renaud, Jean-Christophe
: TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
: TITLE OF INVENTION: (Tifs)
: FILE REFERENCE: LUD 5543
: CURRENT APPLICATION NUMBER: US/09/178, 973B
: CURRENT FILING DATE: 1998-10-26
: NUMBER OF SEQ ID NOS: 17
: SEQ ID NO 9
: LENGTH: 1111
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-178-973B-9

```

Query Match	59.1%	Score 407.6	DB 4:	Length 1111,
Best Local Similarity	76.0%	Pred. No. 2.2e-112		
Matches	503;	Conservative	0;	Mismatches 159; Indels 0; Gaps 0.

QY	CTCTTCCCAAGTCAACAGTTCTCTGAGTTAATTTGTGTCAATGGCCGCCCTGCACAA	88
DB	CTCTCTCTCAGTATCAACTTTTACACTTGTGGATGGATGGATGGCTGTCTTCAAAA	66
QY	ATGTGTAGCTTTTCTTATATGGGACCTTGGCCACCAAGTCTCTTCTTCTTGGCCTT	148

Db	67	TTATATAGTTTTCCTTATG369ACATTTGGCCCGCAGCTCCTGCTTCATTCAGCCCT	126
Oy	149	CTTGATACAGGAGAGAGACGCTGGGCCCATCAGCTCCACCTCAGAGCTTGACAAAGTCCAA	208
Db	127	GTTGGCCCGAGAGGGAATTCGCTGGCCCATCAACCCGGTGTCAAGCTTGAGGTGTCAA	186
Oy	209	CTTCAGCAGACCTTATATCACCACCCGACCTTCATGCTGCTGAAGAGAGCTAGTTGAC	268
Db	187	CTTCCAGAGACCGTACATGTCACACCGACCTTTATGCTGGCCAGAGAGCCAGCCTTGC	246
Oy	269	TGATPACACACAGACGTTGCTTCATTTGGGGGAAACTGTTCCACGAGTCAATATGAG	328
Db	247	AGATPACACACAGACGTCGGGCTCATCGGGGAAACCTGTCCGAGGAGTCAGTCTAA	306
Oy	329	TGAGGCGCTCATCTGATGAAAGCAGAGTGTGAACCTTCACCCCTGSAAGAAGTGCTTCCC	388
Db	307	GGATCAGTGTCTACCTGATGAAAGCAGAGTGTCACTTCACCTTGAGAAACATTTGCTCCC	366
Oy	389	TCAATCTGATAGTTCACGCTTATATGACAGAGGTGTGCTCCCTTCGGCCAGGCTCAG	448
Db	367	CCAGTCAGACAGGTTCCGGCCCTCATCAGAGAGGTGTGCTTCTCTACCAAACTCAG	426
Oy	449	CAACAGGCTAAGCACATGTCATATTGAAGTGTATCCTGCATATCCAGAGATGTGCA	508
Db	427	CAATCAGTCAAGCTCTCTCTCAATCAGTGTGTACCAACAGCAATCCACAAAGATGTGAG	486
Oy	509	AAAGCTGAAGACACAGTGAAGAAAGCTTGAGAGAGTGTGAGAGATCAAGCAATTGTGAG	568
Db	487	AAGCTGAAGAGACAGTGAAGAAAGCTTGAGAGAGCGAGAGATCAAAAGCATTCGGGA	546
Oy	569	ACTGGATTGTGTTTATGTCCTGAGAAATGCTGCATTTTGACAGAGCAAGCTGAAG	628
Db	547	ACTGGACCTGTGTTTATGTCCTGAGAAATGCTGCGCTGTGAGGAGAAAGAGCTAGAA	606
Oy	629	AATGATATACATAACCCCTTTCCCTGCTAGAAATACAAATTGATGCCCCAAGCATTT	688
Db	607	AACGAGAACTGCTCTCTCTGCTCTTCAAAAAGAAACAATAGATCCCTGAAATGACCTT	666
Oy	689	TT 690	
Db	667	TT 668	

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RESULT 7
US-09-419-568F-9
: Sequence 9, Application US/09419568F
: Patent No. 633613
: GENERAL INFORMATION:
: APPLICANT: Dumoutier, Laure
: APPLICANT: Louhed, Jamila
: APPLICANT: Renaud, Jean-Christophe
: TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
: TITLE OF INVENTION: (Tfirs) The Proteins Encoded, and Uses Thereof
: FILE REFERENCE: LDD 5543.2
: CURRENT APPLICATION NUMBER: US/09/419,568F
: CURRENT FILING DATE: 1999-10-18
: PRIOR APPLICATION NUMBER: US09/354,243
: PRIOR FILING DATE: 1999-07-16
: PRIOR APPLICATION NUMBER: US09/178,973
: PRIOR FILING DATE: 1998-10-26
: NUMBER OF SEQ ID NOS: 29
: SEQ ID NO 9
: LENGTH: 1111
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
US-09-419-568F-9

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Query Match	59.1%	Score 407.6	DB 4	Length 1111
Best Local Similarity	76.0%	Pred. 10, 2.2e-112		
Matches 503	Conservative 0	Mismatches 155	Indels 0	Gaps 0
29 CTCCTTCCCAAGTCAGATTCTGTGCAATGGCGCGCCCTGCAGA 88 GY				

Db 7 CTCCTCTCTCAAGTATCAACTTTTGACATTGTGGCATGGTGATGGCTGCTCTCGAGAA 66
Qy 89 ATCTGTAGCTCTTTCTTTATGGGAGCCCTGGCCACACAGCTGCTCTCTCTGGCCCT 148
Db 67 ATCTATGAGTTTTCCTTATGGGAGCTTTGGCCGACAGCTGCTCTCTCTCTGGCCCT 126
Qy 149 CTTGTGACAGGAGAGAGAGCTGCGCCATCAAGCTTCCACTGAGGCTTGACAAGTCCAA 208
Db 127 GTGGGCCCCAGAGGAGAAATGCGCTGCGCTCAACACCCGCTGCAACCTTGAAGTGTCCAA 186
Qy 209 CTTGAGAGAGCCCTTATATCAACACCGCCTTCAATGCTGGCTTAAGAGGCTAGTTGGC 268
Db 187 CTTGAGAGAGCCCTTATATCAACACCGCCTTCAATGCTGGCTTAAGAGGCTAGTTGGC 246
Qy 269 TGATTAACAACAACAAGAGCTGCTCTCAATTTGGGAGAAATCTTCCACGAGTCAATATGAG 328
Db 247 AGATTAACAACAACAAGAGCTGCTCTCAATTTGGGAGAAATCTTCCACGAGTCAATATGAG 306
Qy 329 TGAGGCGCTGCTATCTGATGAGAGAGGCTGTAATTTCACTTGAAGAGTGTCTTCCC 388
Db 307 GGATCAGTGTCTACCTGATGAGAGAGGCTGCTCAATTTCACTTGAAGAGTGTCTTCCC 366
Qy 389 TCAATCTGATGAGTTCAGAGCTTATATGAGAGAGGCTGCTTCCCTGGCCAGGCTCAG 448
Db 367 CCAGTACAGAGAGGCTTCCGCTTCAATGAGAGAGGCTGCTTCCCTGGCCAGGCTCAG 426
Qy 449 CAACAGGCTAAGACATGTCATATTTGAGAGTATGAGTATCTGATATCCAGAGAGTATGCA 508
Db 427 CAATCAGTGTCTACCTGATGAGAGAGGCTGCTCAATTTCACTTGAAGAGTGTCTTCCC 486
Qy 509 AAAGCTGAAGAGACAGAGTGAAGAAAGCTTGAAGAGAGTGAAGATCAAAAGCAATTGAGA 568
Db 487 AAGCTGAAGAGAGACAGTGAAGAAAGCTTGAAGAGAGTGAAGATCAAAAGCAATTGAGA 546
Qy 569 ACTGATTTGCTGTTATGCTCTGAGAAATGCTGCAATTTGACAGAGAGAAAGCTGAAA 628
Db 547 ACTGAGCTGCTGTTATGCTCTGAGAAATGCTGCTGAGAGAGAAAGCTGAAA 606
Qy 629 AATGAATACTAACCCTTTTCCCTGCTAGAAATAACAATTAGATCCCAAGGCAATT 688
Db 607 AACGAAGAAGCTGCTCTCTCTGCTCTTAAAGAAACAATAGATCCCTGAATGAGCTTT 666
Qy 689 TT 690
Db 667 TT 668
RESULT 8
US-09-354-243B-9
Sequence 9, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louned, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
TITLE OF INVENTION: (Tifs)
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-354-243B-9
Query Match 59.1%; Score 407.6; DB 4; Length 1111;

Best Local Similarity 76.0%; Pred. No. 2,2e-112;
Matches 503; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
Qy 29 CTCCTCCCACTGACAGAGTGTCTGAGTGAATTTGTGCAATGAGCCCTGACAGAA 88
Db 7 CTCCTCTCTCAAGTATCAACTTTTGACATTGTGGCATGGTGATGGCTGCTCTCGAGAA 66
Qy 89 ATCTGTAGCTCTTTCTTTATGGGAGCCCTGGCCACACAGCTGCTCTCTCTGGCCCT 148
Db 67 ATCTATGAGTTTTCCTTATGGGAGCTTTGGCCGACAGCTGCTCTCTCTCTGGCCCT 126
Qy 149 CTTGTGACAGGAGAGAGAGCTGCGCCATCAAGCTTCCACTGAGGCTTGACAAGTCCAA 208
Db 127 GTGGGCCCCAGAGGAGAAATGCGCTGCGCTCAACACCCGCTGCAACCTTGAAGTGTCCAA 186
Qy 209 CTTGAGAGAGCCCTTATATCAACACCGCCTTCAATGCTGGCTTAAGAGGCTAGTTGGC 268
Db 187 CTTGAGAGAGCCCTTATATCAACACCGCCTTCAATGCTGGCTTAAGAGGCTAGTTGGC 246
Qy 269 TGATTAACAACAACAAGAGCTGCTCTCAATTTGGGAGAAATCTTCCACGAGTCAATATGAG 328
Db 247 AGATTAACAACAACAAGAGCTGCTCTCAATTTGGGAGAAATCTTCCACGAGTCAATATGAG 306
Qy 329 TGAGGCGCTGCTATCTGATGAGAGAGGCTGTAATTTCACTTGAAGAGTGTCTTCCC 388
Db 307 GGATCAGTGTCTACCTGATGAGAGAGGCTGCTCAATTTCACTTGAAGAGTGTCTTCCC 366
Qy 389 TCAATCTGATGAGTTCAGAGCTTATATGAGAGAGGCTGCTTCCCTGGCCAGGCTCAG 448
Db 367 CCAGTACAGAGAGGCTTCCGCTTCAATGAGAGAGGCTGCTTCCCTGGCCAGGCTCAG 426
Qy 449 CAACAGGCTAAGACATGTCATATTTGAGAGTATGAGTATCTGATATCCAGAGAGTATGCA 508
Db 427 CAATCAGTGTCTACCTGATGAGAGAGGCTGCTCAATTTCACTTGAAGAGTGTCTTCCC 486
Qy 509 AAAGCTGAAGAGACAGAGTGAAGAAAGCTTGAAGAGAGTGAAGATCAAAAGCAATTGAGA 568
Db 487 AAGCTGAAGAGAGACAGTGAAGAAAGCTTGAAGAGAGTGAAGATCAAAAGCAATTGAGA 546
Qy 569 ACTGATTTGCTGTTATGCTCTGAGAAATGCTGCAATTTGACAGAGAGAAAGCTGAAA 628
Db 547 ACTGAGCTGCTGTTATGCTCTGAGAAATGCTGCTGAGAGAGAAAGCTGAAA 606
Qy 629 AATGAATACTAACCCTTTTCCCTGCTAGAAATAACAATTAGATCCCAAGGCAATT 688
Db 607 AACGAAGAAGCTGCTCTCTCTGCTCTTAAAGAAACAATAGATCCCTGAATGAGCTTT 666
Qy 689 TT 690
Db 667 TT 668
RESULT 9
US-09-419-568F-25
Sequence 25, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louned, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 25
LENGTH: 4797
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
US-09-419-568F-25

Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e-67;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

37.4%; Score 258; DB 4; Length 4797;
1 TGCACAGCAGAAATCTTCAGAACAGGTTCTCTCCAGTCACAGAGTTGCTGAGTTAG 60
1 TGCACAGCAGAAATCTTCAGAACAGGTTCTCTCCAGTCACAGAGTTGCTGAGTTAG 60
1 TGCACAGCAGAAATCTTCAGAACAGGTTCTCTCCAGTCACAGAGTTGCTGAGTTAG 60
61 AATTGCTGCATAGGCGCCCTGTCAGAAATCTGTAGCTCTTCCCTTATGAGGACCTTGG 120
61 AATTGCTGCATAGGCGCCCTGTCAGAAATCTGTAGCTCTTCCCTTATGAGGACCTTGG 120
121 CCACAGAGTGCCTCTCTCTTCTTGGCCCTCTTGTAGAGGAGAGAGAGAGAGAGAGAG 180
121 CCACAGAGTGCCTCTCTCTTCTTGGCCCTCTTGTAGAGGAGAGAGAGAGAGAGAGAG 180
181 GCTCCCACTGACAGGCTTGAACAAGTCCAGTCCAGAGAGCCCTATATCAACACCGACCT 240
181 GCTCCCACTGACAGGCTTGAACAAGTCCAGTCCAGAGAGCCCTATATCAACACCGACCT 240
241 TCATGCTGGCTAAGAGG 258
241 TCATGCTGGCTAAGAGG 258

RESULT 10
US-09-354-243B-25

Sequence 25, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
TITLE OF INVENTION: (Tifs)
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 25
LENGTH: 4797
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-354-243B-25

Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e-67;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

37.4%; Score 258; DB 4; Length 4797;
1 TGCACAGCAGAAATCTTCAGAACAGGTTCTCTCCAGTCACAGAGTTGCTGAGTTAG 60
1 TGCACAGCAGAAATCTTCAGAACAGGTTCTCTCCAGTCACAGAGTTGCTGAGTTAG 60
1 TGCACAGCAGAAATCTTCAGAACAGGTTCTCTCCAGTCACAGAGTTGCTGAGTTAG 60
61 AATTGCTGCATAGGCGCCCTGTCAGAAATCTGTAGCTCTTCCCTTATGAGGACCTTGG 120
61 AATTGCTGCATAGGCGCCCTGTCAGAAATCTGTAGCTCTTCCCTTATGAGGACCTTGG 120
121 CCACAGAGTGCCTCTCTCTTCTTGGCCCTCTTGTAGAGGAGAGAGAGAGAGAGAGAG 180
121 CCACAGAGTGCCTCTCTCTTCTTGGCCCTCTTGTAGAGGAGAGAGAGAGAGAGAGAG 180
181 GCTCCCACTGACAGGCTTGAACAAGTCCAGTCCAGAGAGCCCTATATCAACACCGACCT 240
181 GCTCCCACTGACAGGCTTGAACAAGTCCAGTCCAGAGAGCCCTATATCAACACCGACCT 240

QY 241 TCATGCTGGCTAAGAGG 258
DB 241 TCATGCTGGCTAAGAGG 258

RESULT 11
US-09-178-973B-17

Sequence 17, Application US/09178973B
Patent No. 6274710
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: (Tifs)
FILE REFERENCE: LUD 5543
CURRENT APPLICATION NUMBER: US/09/178,973B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 17
LENGTH: 5935
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-178-973B-17

Query Match
Best Local Similarity 72.2%; Pred. No. 3e-28;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

18.5%; Score 127.6; DB 4; Length 5935;
29 CTCCTTCCCACTACACAGTGTGCTGAGTTAGAAATGTCTGCATAGGCCCGCTGCAGAA 88
356 CTCCTTCCCACTACACAGTGTGCTGAGTTAGAAATGTCTGCATAGGCCCGCTGCAGAA 415
89 ATCTGTAGGCTTTCTTCTTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 148
416 ATCTGTAGGCTTTCTTCTTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 475
149 CTGTGTAGAGGAG 208
476 GTGGGCCAG 535
QY 209 CTTCAGAGAGCCCTTATATCAACAGCGACCTTATGCTGTGCTAAGAGG 258
DB 536 CTTCAGAGAGCCCTTATATCAACAGCGACCTTATGCTGTGCTAAGAGG 585

RESULT 12
US-09-419-568F-29

Sequence 29, Application US/09419568F
Patent No. 631613
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 29
LENGTH: 5935
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-419-568F-29

Query Match
Best Local Similarity 18.5%; Score 127.6; DB 4; Length 5935;

Best Local Similarity 72.2%; Pred. No. 3e-28;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 29 CTCCTTCCAGTACACAGTTGCTCGAGTTAGATTGTCTGCATATGGCCGCCCTGCAGAA 88
Db 356 CTCCTCTCTAGTTATACCTTTTGAACCTTGCATGCGTGTATGCTGTCTGCAGAA 415
QY 89 ATCTGTAGCTCTTCTTATAGGGGACCTGGCCACAGCTGCTCTCTCTTGGGCCCT 148
Db 416 ATCTATAGATTTCCTTATAGGGGACTTGGCCGCACTGCTCTCTCTCTATGGCCT 475
QY 149 CTGTGTACAGGAGAGACAGCTGCGCCCATCAGCTCCCATCTGCAGCTTGAACATCCAA 208
Db 476 GTGGGCCAGAGAGCAATGCGTCCCATCAACACCGGCGAGCTTGAAGTGTCCAA 535
QY 209 CTTCACAGAGCCCTATATCAACCAACCGACCTTCATCTGCTTAAGAGG 258
Db 536 CTTCACAGAGCCGTAATCGTCAACCGACCTTATGTGCGCAAGAGG 585

RESULT 13

US-09-354-243B-29
Sequence 29, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:

APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
TITLE OF INVENTION: (TIIFS)
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354, 243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178, 973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 29
LENGTH: 5935
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

US-09-354-243B-29

Query Match 18.5%; Score 127.6; DB 4; Length 5935;
Best Local Similarity 72.2%; Pred. No. 3e-28;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 29 CTCCTTCCAGTACACAGTTGCTCGAGTTAGATTGTCTGCATATGGCCGCCCTGCAGAA 88
Db 356 CTCCTCTCTAGTTATACCTTTTGAACCTTGCATGCGTGTATGCTGTCTGCAGAA 415
QY 89 ATCTGTAGCTCTTCTTATAGGGGACCTGGCCACAGCTGCTCTCTCTTGGGCCCT 148
Db 416 ATCTATAGATTTCCTTATAGGGGACTTGGCCGCACTGCTCTCTCTCTATGGCCT 475
QY 149 CTGTGTACAGGAGAGACAGCTGCGCCCATCAGCTCCCATCTGCAGCTTGAACATCCAA 208
Db 476 GTGGGCCAGAGAGCAATGCGTCCCATCAACACCGGCGAGCTTGAAGTGTCCAA 535
QY 209 CTTCACAGAGCCCTATATCAACCAACCGACCTTCATCTGCTTAAGAGG 258
Db 536 CTTCACAGAGCCGTAATCGTCAACCGACCTTATGTGCGCAAGAGG 585

RESULT 14

US-09-178-973B-8
Sequence 8, Application US/09178973B
Patent No. 6274710
GENERAL INFORMATION:

APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: (TIIFS)
FILE REFERENCE: LUD 5543
CURRENT APPLICATION NUMBER: US/09/178, 973B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 8
LENGTH: 7445
TYPE: DNA
ORGANISM: Mus musculus

US-09-178-973B-8

Query Match 18.3%; Score 126; DB 4; Length 7445;
Best Local Similarity 71.7%; Pred. No. 1e-27;
Matches 165; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 29 CTCCTTCCAGTACACAGTTGCTCGAGTTAGATTGTCTGCATATGGCCGCCCTGCAGAA 88
Db 2034 CTCCTCTCTACTTATACCTTGTGACACTTGTGCATCTCTGATGCTGTCTCTGCAGAA 2093
QY 89 ATCTGTAGCTCTTCTTATAGGGGACCTGGCCACAGCTGCTCTCTTGGGCCCT 148
Db 2094 ATCTATAGATTTCCTTATAGGGGACTTGGCCGCACTGCTCTCTCTATGGCCT 2153
QY 149 CTGTGTACAGGAGAGACAGCTGCGCCCATCAGCTCCCATCTGCAGCTTGAACATCCAA 208
Db 2154 GTGGGCCAGAGAGCAATGCGTCCCATCAACACCGGCGAGCTTGAAGTGTCCAA 2213
QY 209 CTTCACAGAGCCCTATATCAACCAACCGACCTTCATCTGCTTAAGAGG 258
Db 2214 CTTCACAGAGCCGTAATCGTCAACCGACCTTATGTGCGCAAGAGG 2263

RESULT 15

US-09-419-568F-8
Sequence 8, Application US/09419568F
Patent No. 6331613
GENERAL INFORMATION:

APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: (TIIFS) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419, 568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354, 243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178, 973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 8
LENGTH: 7445
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:

US-09-419-568F-8

Query Match 18.3%; Score 126; DB 4; Length 7445;
Best Local Similarity 71.7%; Pred. No. 1e-27;
Matches 165; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 29 CTCCTTCCAGTACACAGTTGCTCGAGTTAGATTGTCTGCATATGGCCGCCCTGCAGAA 88
Db 2034 CTCCTCTCTACTTATACCTTGTGACACTTGTGCATCTCTGATGCTGTCTCTGCAGAA 2093
QY 89 ATCTGTAGCTCTTCTTATAGGGGACCTGGCCACAGCTGCTCTCTTGGGCCCT 148
Db 2094 ATCTATAGATTTCCTTATAGGGGACTTGGCCGCACTGCTCTCTCTATGGCCT 2153
QY 149 CTGTGTACAGGAGAGACAGCTGCGCCCATCAGCTCCCATCTGCAGCTTGAACATCCAA 208

Db 2154 GTGGGCCAGAGGCAATGGCTGCCCGTCAACACCCGGTGCAGCTTGAGGTGTCCAA 2213
QY 209 CTTCCAGCAGCCCTTATATCAACCAACCGACCTTCATGCTGTGCTTAAGGAGG 258
Db 2214 CTTCCAGCAGCCGTACATCGTCAACCGCACCTTTATGCTGGCCCAAGGAGG 2263

Search completed: July 19, 2003, 19:48:03
Job time : 27.7543 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:03:00 ; Search time 8036.2 Seconds

(without alignments)
17372.171 Million cell updates/sec

Title: US-09-751-797-25

Sequence score: 1 tgcacacagcagaatcttcag.....gatgcacacagcagattttc 4797

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba:
2: gb_hcg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pac:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_scs:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
23: em_pac:
24: em_ph:
25: em_pl:
26: em_ro:
27: em_scs:
28: em_un:
29: em_vi:
30: em_hcg_hum:
31: em_hcg_inv:
32: em_hcg_other:
33: em_hcg_mus:
34: em_hcg_pin:
35: em_hcg_rtd:
36: em_hcg_man:
37: em_hcg_vrt:
38: em_sy:
39: em_hcgo_hum:
40: em_hcgo_mus:
41: em_hcgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4797	100.0	4797	AR201415	AR201415 Sequence
2	4797	100.0	4797	AX459972	AX459972 Sequence
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4	4740.2	98.8	8393	AF387519	AF387519 Homo sapi
5	4735.4	98.7	133350	AC022511	AC022511 Homo sapi
6	3353.2	69.9	135146	AC087562	AC087562 Pan trogl
7	3023.8	63.0	191111	AC007458	AC007458 Homo sapi
8	686	14.3	7445	AR165227	AR165227 Sequence
9	686	14.3	7445	AR201398	AR201398 Sequence
10	686	14.3	7445	AX459954	AX459954 Sequence
11	686	14.3	8970	MMU294727	AJ294727 Mus muscu
12	650	13.6	5935	AR165234	AR165234 Sequence
13	650	13.6	5935	AR201417	AR201417 Sequence
14	650	13.6	5935	AX459988	AX459988 Sequence
15	650	13.6	5935	MMU294728	AJ294728 Mus muscu
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17	258	5.4	690	AR201414	AR201414 Sequence
18	258	5.4	690	AX459971	AX459971 Sequence
19	258	5.4	690	HS4277247	AJ277247 Homo sapi
20	244	5.1	1152	AX092422	AX092422 Sequence
21	244	5.1	1152	AX358990	AX358990 Sequence
22	244	5.1	1152	AX362483	AX362483 Sequence
23	244	5.1	1152	AX392477	AX392477 Sequence
24	244	5.1	1152	AX403770	AX403770 Sequence
25	244	5.1	1152	AX454768	AX454768 Sequence
26	244	5.1	1152	AX491246	AX491246 Sequence
27	244	5.1	1167	AF279437	AF279437 Homo sapi
28	240	5.0	1139	AX054620	AX054620 Sequence
29	237	4.9	1132	AX048204	AX048204 Sequence
30	207	4.3	1116	AX151713	AX151713 Sequence
31	207	4.3	1116	AX179578	AX179578 Sequence
32	207	4.3	1116	AX468783	AX468783 Sequence
33	159.4	3.3	418	AX459964	AX459964 Sequence
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35	142.2	3.0	214042	AC023149	AC023149 Homo sapi
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43	136.6	2.8	153590	AC098970	AC098970 Homo sapi
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45	133.6	2.8	48994	AC109363	AC109363 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS AR201415
DEFINITION Sequence 25 from patent US 6359117.
ACCESSION AR201415
VERSION AR201415.1 GI:20252303
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4797)
AUTHORS Dumoutier,L., Louted,J. and Renaud,J.-C.
TITLE Isolated nucleic acid molecules which encode T cell inducible factors (TIFs), the proteins encoded, and uses therefor
JOURNAL Patent: US 6359117-A 25 19-MAR-2002;

FEATURES Location/Qualifiers
source 1..4797 /organism="unknown"
BASE COUNT 1339 a 910 c 1063 g 1485 t
ORIGIN
Query Match 100.0%; Score 4797; DB 6; Length 4797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TGACACAGAGATCTTCAGAACAGGTTCTCTCCAGTACACAGTTCGTGAGTTAG 60
QY 61 AATTGCTGCAATGCGCGCCCTTCAGAAATCTGTAGCTTTCTTATGGGACCTGG 120
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QY 181 GCTCCACCTGACAGCTTGAACAATCCACTTCAGAGCGCTATATCAACCAACGCACT 240
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QY 361 TTATCCCTGAGGATGATAAATTTCTGTTTTTTCAGAGCATCTTGGGAAATGGGCTT 420
Db 361 TTATCCCTGAGGATGATAAATTTCTGTTTTTTCAGAGCATCTTGGGAAATGGGCTT 420
QY 421 TTTTTTTCTTGAATCTTCTCTCAATTTGGCCTTTATGATACATATGATGATTTT 480
Db 421 TTTTTTTCTTGAATCTTCTCTCAATTTGGCCTTTATGATACATATGATGATTTT 480
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QY 781 CCGTGTGCGCTTCATGGGATCTTGGGATGATGATGATGATGATGATGATGATG 840
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QY 1201 TTGAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
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Db 1321 GCTTGGAAATGATTCATTGATCTAAGTTGTTGAGGAGGAGGATGATGAGAGAA 1380
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QY 1501 CATTGAAACATGAAAAAAGTTGATGAGTGGGCGCCAGTAAAGGCTTGAAGACT 1560
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QY 1561 ACTGAAGAGGCTTAATTTCAATGAGATGTTTATGATGATGATGATGATGATG 1620
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QY 1621 CAATTTCTGAGATACGATGAGTATTCTTACAGAAATTTGATGATGATGATG 1680
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Db 1741 AGGAAAGTACGATTTCTGGGCTCAAGGGAATTCAGAGTCAAGGTAATCTAGGTC 1800
QY 1801 TGTGAAATCTAGTCAATGTTGGGCAAAATTTCTAAGAGCTTTAAATTCAGGTAAT 1860
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QY 1861 ACTGTAACCTCATGGGTGTGAGGTTCAATAAAGTTTCAGACAACTTAAGATGATG 1920
Db 1861 ACTGTAACCTCATGGGTGTGAGGTTCAATAAAGTTTCAGACAACTTAAGATGATG 1920
QY 1921 CTGTGATTTGTTTATAGATATGAAAGTGTAGCTTCAGATCAGAGGAATGTGCA 1980
Db 1921 CTGTGATTTGTTTATAGATATGAAAGTGTAGCTTCAGATCAGAGGAATGTGCA 1980
QY 1981 AAGCTGAAGACACAGTGAAGAAAGTGAAGTGAATCTGTAATCTAGTCAATGCAAT 2040
Db 1981 AAGCTGAAGACACAGTGAAGAAAGTGAAGTGAATCTGTAATCTAGTCAATGCAAT 2040

OY	2041	AGGAGAGCAAAATGGTGTTTCTTTCTCCTTCCTTCCTCCATACACTTGGAATTTTCA	2100
Dp	2041	AGGAGAGCAAAATGGTGTTTCTTTCTCCTTCCTTCCTCCATACACTTGGAATTTTCA	2100
OY	2101	CTTAATTCCTCTACACAACGAGGCATTACTTTGGGTGTGTATGTATATATTATA	2160
Dp	2101	CTTAATTCCTCTACACAACGAGGCATTACTTTGGGTGTGTATGTATATATTATA	2160
OY	2161	TATCTAGAATGTCAGTTTTCCAATCTTGGCAATTGTAGAAATTTCTAGAACCTGGTTGGACT	2220
Dp	2161	TATCTAGAATGTCAGTTTTCCAATCTTGGCAATTGTAGAAATTTCTAGAACCTGGTTGGACT	2220
OY	2221	TAGCTTGTCTTAGTCACATACCTCAGATTTCTGGGGATGSGTCAGTGGCAGAGATAGGCGTA	2280
Dp	2221	TAGCTTGTCTTAGTCACATACCTCAGATTTCTGGGGATGSGTCAGTGGCAGAGATAGGCGTA	2280
OY	2281	GAAATGCAAGGTGCTCGAATCCCAGGCCAGCATTTTCCCGGTGGATACAGATTAGTTT	2340
Dp	2281	GAAATGCAAGGTGCTCGAATCCCAGGCCAGCATTTTCCCGGTGGATACAGATTAGTTT	2340
OY	2341	TGTATCACATTAAATCTTATAGGAAAATTTCCAGATTCCTATTGACTATGTAATCTGAAAG	2400
Dp	2341	TGTATCACATTAAATCTTATAGGAAAATTTCCAGATTCCTATTGACTATGTAATCTGAAAG	2400
OY	2401	TACTTGTTTAAAAACAGAAAAATGCTATGSGGCAATTTATTTGAAGTCATTTTGAAGT	2460
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OY	2461	CATTAAATGCAATGCTTTGAAAACCTTGGAAAGTAATACAGAAACAAATGAGAAABAAGCTGG	2520
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Dp	2521	ACTTGCAATATPAGGGCTAATTTCTGAGAGTAATAACACTTATTTGAAATATCATAAATATC	2580
OY	2581	TATCAGATATTTGAATTAATGTTTAAAAAGCAGAGACAGACACCCTGATCTTTTATACAG	2640
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Dp	2641	GTTCAAATNAGGTAAAAATATTACPAAGATTTATTAATTTAAATGGAAGTCTGAATT	2700
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Dp	3001	AACAAGCTTAACTTTAATTTCCCTTTTCCCTCTTGACTTTTAAAAAACGTTTCTTC	3060
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Dp	3121	TTAAATGTGAACCCAGTTCCTGTGTATGAACCTATTATCTAACAATGGAGGCTGAA	3180
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Dp	3181	TGTTAGCATGCCACACAGCAAGCATGCTTTACACATCTTGCTTTAAAAATTACTGATTC	3240
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Dp	3301	TGTCATTTTCAACACCTTTAATCCATTTTGAAGAAATCAATTCATTTTGCAATGGGCTT	3360
Oy	3361	GCCATGTGGAAGAGTATTATGCTTTTTTGTCTGTAGCTTCAGAAAGCACAGAGGGAGA	3420
Dp	3361	GCCATGTGGAAGAGTATTATGCTTTTTTGTCTGTAGCTTCAGAAAGCACAGAGGGAGA	3420
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Dp	3421	GCAAATGTTGTCAGAGAAAAGATCAACAGAGAGAGAACTGTCAAGCTGTCTGAATAAG	3480
Oy	3481	GTGTTTTGGGAGGCAATTAATCCCTCTGTGTGGGGGTAAAGCAGAAACGACGGTTGGTA	3540
Dp	3481	GTGTTTTGGGAGGCAATTAATCCCTCTGTGTGGGGGTAAAGCAGAAACGACGGTTGGTA	3540
Oy	3541	GTAAATGCAATGACAGACAGTAGGGAGCATTAACCTTTAAATTTCTTTATAGTCTTGAG	3600
Dp	3541	GTAAATGCAATGACAGACAGTAGGGAGCATTAACCTTTAAATTTCTTTATAGTCTTGAG	3600
Oy	3601	TCTTTGAGATGAAAAGAAATATCTTTTGGCCTTATGTCAAAAAGAGATGAGAAAGTGA	3660
Dp	3601	TCTTTGAGATGAAAAGAAATATCTTTTGGCCTTATGTCAAAAAGAGATGAGAAAGTGA	3660
Oy	3661	AAGGGCGGAAGAAAGCAGGAAAAAGAAACCATGTATTATATAGAGCAATGGTGACA	3720
Dp	3661	AAGGGCGGAAGAAAGCAGGAAAAAGAAACCATGTATTATATAGAGCAATGGTGACA	3720
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LOCUS Sequence 26 from Patent WO0210393.
DEFINITION AX459972
ACCESSION AX459972
VERSION AX459972.1 GI:21725708
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Dumoutier, L. and Renaud, V.C.
Isolated nucleic acid molecules which encode c cell inducible
factors, or interleukin-21, the proteins encoded, and uses thereof
Patent: WO 0210393-A 26-07-FEB-2002
JOURNAL LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 800 CAAGTCAACTTCAAG 859

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Db 6741 TCTGAGAAATGCTTCGATTTGACCGAGCAAGCTGAAATGAATTAACCTTCCCTTT 6800
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Db 6801 CCTGCTAGAAATTAACATTTGATGCTCCCAAGGCAATTTT 6841

RESULT 5
AC022511/c
LOCUS Homo sapiens 12 BAC RP11-71J4 (Roswell Park Cancer Institute Human
DEFINITION BAC Library) complete sequence.
ACCESSION AC022511
VERSION AC022511.22 GI:146659924
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133350)
Murny,D.M., Adams,C., Adio-Oduola,B., Ali-ouman,F.R., Allen,C.,
Albrooks,S.L., Amaratunga,H.C., Are,J.R., Banks,T., Barhara,J.,
Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Boyle,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chin,D., Crowder,I., Christopoulos,C., Cleveland,C.D.,
Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Emerling,S., Escotto,M., Falls,T., Ferraguto,D.,
Flegg,N., Ford,U., Foster,P., Frantz,P., Gabis,A., Gao,J.,
Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,U.H., Guvera,W.,
Gunnarane,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K.,
Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O.,
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Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudan,S.,
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Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtenberg,O., Lieu,C., Liu,J., Liu,W.,
Loulseged,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Magua,P., Marondel,I., Martin,R., Luna,R.,
Martindale,A., Martinez,E., Massey,E., Mawhney,E., McLeod,M.P.,
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Minter,Z., Mitchell,T., Mohabbat,K., Montgomery,K.T., Morgan,M.,
Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokweto,S.,
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Peety,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L.,
Quiles,M., Ren,Y., Rives,M., Rojals,A., Rojudoakan,I., Rolfe,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shm,C.,
Shooshari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A.,
Stanley,H., Stone,H., Tansey,J., Taylor,C., Taylor,T., Telford,B.,
Thomas,N., Thomas,S., Umami,K., Vasquez,L., Vera,V., Villalobon,D.,
Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R.,
Washington,C., Wallington,S., Williams,G., Williamson,A.,
Wlezlyk,R., Woodson,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J.,
Zorilla,S., Kuchelapati,R. and Gibbs,R.
TITLE Direct Submission
JOURNAL Unpublished

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REFERENCE
AUTHORS
2 (bases 1 to 133350)
Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 133350)
Worley,K.C.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (11-JUL-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2001 this sequence version replaced gi:12556660.
COMMENT
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu

```

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STS are identified using ePCR (genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3369-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

----- Summary Statistics -----

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Contig length: 150667
Phrap values in estimate: 149705
Average error rate (BCM-Phrap estimate): 1.52849e-05
Fraction of Phrap values less than 40 : 0.0165588
Number of consensus changing edits: 83
Number of N's in consensus : 0

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----- Consensus changing edits -----
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Db	5835	CCACACCTAACCCCTCCTTCCCTCCTTCCACAGAGACCCCTTACCCCAACTCCTCCTCCTT	5776
QY	1098	CCCCCTTACCCCTTAAGCTAGCAGAGAAAGTCTCTTGGCAGCAGGTATATCAGAGTCATT	1157
Db	5775	CCCCCTTACCCCTTAAGCTAGCAGAGAAAGTCTCTTGGCAGCAGGTATATCAGAGTCATT	5716
QY	1158	TGGATCATAGAGTATTTGGCTTTTGGCTTGACTGATCATCTTGAAGTTATATAGTGTG	1217
Db	5715	TGGATCATAGAGTATTTGGCTTTTGGCTTGACTGATCATCTTGAAGTTATATAGTGTG	5656
QY	1218	AATGGGCTCTGGAACTTAACTGATACAGAGCCGCAATTGTGTTCCTCCGAAAAAAGCA	1277
Db	5655	AATGGGCTCTGGAACTTAACTGATACAGAGCCGCAATTGTGTTCCTCCGAAAAAAGCA	5596
QY	1278	ACTCAGGTTGGCTTAAGATGAGAAAAGTGTGG-AAAACATCTAGCTGTGGAAATGATC	1336
Db	5595	ACTCAGGTTGGCTTAAGATGAGAAAAGTGTGGAAAACATCTGATGTGGAAATGATC	5536
QY	1337	CATTGAGCTTAAGTGTGTTGAGGGAGGGGATGCGATGGAGAAATTAAGAGAAAGTG	1396
Db	5535	CATTGAGCTTAAGTGTGTTGAGGGAGGGGATGCGATGGAGAAATTAAGAGAAAGTG	5476
QY	1397	GGAAATGGGAAAGGCTTAAAGTCGGTGTGGGTCCGACAGCTGTGCCCTGTGTGATCAT	1456
Db	5475	GGAAATGGGAAAGGCTTAAAGTCGGTGTGGGTCCGACAGCTGTGCCCTGTGTGATCAT	5416
QY	1457	GGGAAGCCACAAATCCGAGGCGGTGTAACCTGATGCGCGTGAACATTGAAATATAGA	1516
Db	5415	GGGAAGCCACAAATCCGAGGCGGTGTAACCTGATGCGCGTGAACATTGAAATATAGA	5356
QY	1517	AAAAAGTTTGGTGGAGTGGGCGCAGTAAAAAGCCCTAGAGACTACTAGAAAGGGCTTAA	1576
Db	5355	AAAAAGTTTGGTGGAGTGGGCGCAGTAAAAAGCCCTAGAGACTACTAGAAAGGGCTTAA	5296
QY	1577	TTTTCACTAGATGTTTTATATGTAACATTTCTGTTCTAAGATCAATTTTCTGGAGATA	1636
Db	5295	TTTTCACTAGATGTTTTATATGTAACATTTCTGTTCTAAGATCAATTTTCTGGAGATA	5236
QY	1637	CGATTGAGGTTTATATTCCTTACAAATTTGGATATACTACCGCGCTCTTCCCAAAATGC	1696
Db	5235	CGATTGAGGTTTATATTCCTTACAAATTTGGATATACTACCGCGCTCTTCCCAAAATGC	5176
QY	1697	AAACCTCAGTGAAGTATTTCCCAAAATGAGAAGAGTCTCTTGAAGGAAAGTGAAGTGAAT	1756
Db	5175	AAACCTCAGTGAAGTATTTCCCAAAATGAGAAGAGTCTCTTGAAGGAAAGTGAAGTGAAT	5116
QY	1757	TCTGGCGTCCAAAGGGAATTCAGAGCTCAGGAAATCTAAGTCACTGTTGAATCTAAGTC	1816
Db	5115	TCTGGCGTCCAAAGGGAATTCAGAGCTCAGGAAATCTAAGTCACTGTTGAATCTAAGTC	5056
QY	1817	ATTGTGGGCAAAATTACTAAGAGCTTTAATTTCCAGGTGAATTGTACTGTACTCATGGG	1876
Db	5055	ATTGTGGGCAAAATTACTAAGAGCTTTAATTTCCAGGTGAATTGTACTGTACTCATGGG	4996
QY	1877	TGTGAGGTTTATATAAGTTTCCAGACCAACATTAAGATAGTATGCTTATATTTTAT	1936
Db	4995	TGTGAGGTTTATATAAGTTTCCAGACCAACATTAAGATAGTATGCTTATATTTTAT	4936
QY	1937	AGCATATTTGAAGGTGATGACCTGCAATTCAGAGAAATGTCCAAAGCTGAAAGGACAAG	1996
Db	4935	AGCATATTTGAAGGTGATGACCTGCAATTCAGAGAAATGTCCAAAGCTGAAAGGACAAG	4876
QY	1997	TGAAAAAGGTAGGACTGATACTGTCAATGCTAAGTCAATGCAATAGAGAGCAAAATGTT	2056
Db	4875	TGAAAAAGGTAGGACTGATACTGTCAATGCTAAGTCAATGCAATAGAGAGCAAAATGTT	4816
QY	2057	GTTTTTCTTCTCCTTCTTCTTCCCATCACTTGTGATTTTTCATTGATCTCCTTACA	2116
Db	4815	GTTTTTCTTCTCCTTCTTCTTCCCATCACTTGTGATTTTTCATTGATCTCCTTACA	4756
QY	2117	CCAGGCGCATTAATTTGGTGTCTGTGTATGATATATATCTATATCTAGATGTCAGTT	2176

D	b		4755	CCAGGGGATTACTTGTGTGTGTGTATGTAGATATATCTATATCTAGATGTCACTT	4658
O	y		2177	TCCAAATCTTGCAAATTTGTAGAATTCAGAACCTGGTGGGATCTTAGCTTGAC	2238
D	b		4695	TCCAAATCTTGCAAATTTGTAGAATTTGAAGACTGGTGGGATCTTAGCTTGAC	4638
O	y		2237	ATAAATCTCAGATTTGGGGAGTGTCACTGGCAGAGATAGGGCTTGAATGCAGGTCCTG	2298
D	b		4635	ATAAATCTCACATTTCTGGGGAGTGTCACTGGCAGAGATAGGGCTGAATTCAGGTCCTG	4578
O	y		2297	AATCCAAAGCAGACCTTTCCCGGTGGTGTACAAGTAATGTTTTGGACCATTAATCT	2358
D	b		4575	AATCCAAAGCAGACCTTTCCCGGTGGTGTACAAGTAATGTTTTGGACCATTAATCT	4518
O	y		2357	TAGGGAATTTCAAGATTCCTATTAATCTCATGTAACTGAGAAATCTGTTAAAAACA	2418
D	b		4515	TAGGGAATTTCAAGATTCCTATTAATCTCATGTAACTGAGAAATCTGTTAAAAACA	4458
O	y		2417	GAAAAATGCTATGGGCAAAATTTATTTGAAGTCATTTTGAAGTCATTAATGCAATGCTT	2478
D	b		4455	GAAAAATGCTATGGGCAAAATTTATTTGAAGTCATTTTGAAGTCATTAATGCAATGCTT	4398
O	y		2477	TGAACCTTGGAGAAATTAATCTCAGAACATAGAGAAAAGCTGGACCTTGCAATAGGCT	2538
D	b		4395	TGAACCTTGGAGAAATTAATCTCAGAACATAGAGAAAAGCTGGACCTTGCAATAGGCT	4338
O	y		2537	AATTTCTGAGATTAATAACACTTTATTTGGAATTAATCAATATCTATCAGATTTGATTA	2598
D	b		4335	AATTTCTGAGATTAATAACACTTTATTTGGAATTAATCAATATCTATCAGATTTGATTA	4278
O	y		2597	TAGTTTAAAGCAAGACAGACAAACCCGATCTCTTTTATACAGATTCAATTAGATTA	2658
D	b		4275	TAGTTTAAAGCAAGACAGACAAACCCGATCTCTTTTATACAGATTCAATTAGATTA	4218
O	y		2657	AATTTTGTAGAAGATTTATATATGTAAATGGAAGTCGAATGTGTAGCTTTTTTTC	2718
D	b		4215	AATTTTGTAGAAGATTTATATATGTAAATGGAAGTCGAATGTGTAGCTTTTTTTC	4158
O	y		2717	TTCTCTCTCCCATCAAGACCTTCATTTCTAGTTCTTCTCTCACTCCCTCAACAAATCC	2778
D	b		4155	TTCTCTCTCTCCCATCAAGACCTTCATTTCTAGTTCTTCTCTCACTCCCTCAACAAATCC	4098
O	y		2777	CTAGGAGCATTTATCCATGGTGGGCTGTGTACATTTCTATAGTAGATATACATAT	2838
D	b		4095	CTAGGAGCATTTATCCATGGTGGGCTGTGTACATTTCTATAGTAGATATACATAT	4038
O	y		2837	GTGGCTATTTTGTGAAAAGAAACAACAATGGAAGCTTAGACTAACAATATGACTACC	2898
D	b		4035	GTGGCTATTTTGTGAAAAGAAACAACAATGGAAGCTTAGACTAACAATATGACTACC	3978
O	y		2897	CCAATACCGAGAGAAATATTAGAGGAGGTGAABATGACCGCTTGCAAGCAGATACAAT	2958
D	b		3975	CCAATACCGAGAGATATTAGAGGAGGTGAABATGACCGCTTGCAAGCAGATACAAT	3918
O	y		2957	AAATACTCAGAAACATGAAGGCTCAATGTATGAAATTTTCAGTAAACAGCTTAACCTTA	3018
D	b		3915	AAATACTCAGAAACATGAAGGCTCAATGTATGAAATTTTCAGTAAACAGCTTAACCTTA	3858
O	y		3017	ATTCCCCCTTTTCCCTCTTGACTTTTAAAAAAGCTTTCTCTGAGCATCATTTAT	3078
D	b		3855	ATTCCCCCTTTTCCCTCTTGACTTTTAAAAAAGCTTTCTCTGAGCATCATTTAT	3798
O	y		3077	GAGGTACAGCTTTCTCTCTTGATTAATTAAGAGCTTTGTATGTTTAAATTTGAAGGCC	3138
D	b		3795	GAGGTACAGCTTTCTCTCTTGATTAATTAAGAGCTTTGTATGTTTAAATTTGAAGGCC	3738
O	y		3137	AGTCTCTGTTTATAGAACTATTAATCAGACATGAGAGGCTGAATGTTAGCATCCACAG	3198
D	b		3735	AGTCTCTGTTTATAGAACTATTAATCAGACATGAGAGGCTGAATGTTAGCATCCACAG	3678
O	y		3197	ACAAGCATGCTTTACACATCTTGCTTAAAAAATTAAGTATTCATCTTGCTTGTTCT	3258

Db 3675 ACAGGATGCTTTACATCTTGTAAATAATTCATCTTCTGCTGCT 3616
 QY 3257 TTAGAAAAGTGAAGTGAAGAGAGAAATCTCATGATCTGTGTGATTTTCAAGACC 3316
 Db 3615 TTAGAAAAGTGAAGTGAAGAGAGAAATCTCATGATCTGTGTGATTTTCAAGACC 3556
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 KEYWORDS
 Pan troglodytes
 SOURCE
 ORGANISM
 Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
 1 (bases 1 to 135146)
 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
 Alsbrooks, S.L., Amaratunga, H.C., Are, J.R., Banks, T., Barbara, J.,
 Benton, J., Blinova, K., Blankenburg, K., Bonnin, D., Bouck, J.,
 Bowe, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bunay, C.,
 Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
 Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R.,
 Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
 Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
 Davy-Carroll, L., Dedeleich, D.A., Delaney, K.R., Delgado, O.,
 Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Drepper, H.,
 Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
 Elhaj, C., Escotto, M., Fales, T., Farraguto, D., Flagg, N., Ford, J.,
 Foster, P., Frintz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
 Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
 Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
 Hernandez, J., Hernandez, O., Hodgson, A., Hughes, M., Hollaway, C.,
 Hollins, B., Homs, F., Howard, S., Huber, J., Hui, S., Hume, J.,
 Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jollivet, S.,
 Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
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 Lewis, L., Li, J., Li, Z., Lichtenarge, O., Liu, C., Liu, J., Liu, W.,
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 Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
 Martinez, E., Massey, B., Mauniny, E., McLeod, M.P., Meador, M.,
 Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
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RESULT 8
ARI65227 7445 bp DNA linear PAT 17-OCT-2001
LOCUS ARI65227
DEFINITION Sequence 8 from patent US 6274710.
ACCESSION ARI65227
VERSION ARI65227.1 GI:16238720
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7445)
AUTHORS Dumoulier L., Lohued J. and Renaud J.-C.
TITLE Antibodies which specifically bind T cell inducible factors (Tifs)

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JOURNAL Patent: US 6274710-A 8 14-AUG-2001;
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BASE COUNT 2058 a 1570 c 1597 g 2220 t
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Query Match 14.3% Score 686; DB 6; Length 7445;
Best Local Similarity 53.8%; Pred. No. 8.1e-148;
Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

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 ACCESSION AR201398
 VERSION AR201398.1 GI:20252286
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 7445)
 AUTHORS Dumoutier,L., Louhed,J. and Renaud,J.-C.
 TITLE Isolated nucleic acid molecules which encode T cell inducible factors (TIFs), the proteins encoded, and uses therefor
 JOURNAL Patent: US 6359117-A 8 19-MAR-2002;
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 Best Local Similarity 53.8%; Pred. No. 8,1e-148;
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DEFINITION Sequence 8 from Patent WO0210393.
ACCESSION AX459954
VERSION AX459954.1 GI:21725690
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SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Dumoutier, L. and Renaud, J.C.
TITLE Isolated nucleic acid molecules which encode a cell inducible
JOURNAL Patent: WO 0210393-A 8-07-FEB-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
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Location/Qualifiers
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 AUTHORS Dumoutier, L., Van Roost, E., Ameys, G., Michaux, L. and Renauld, J.C.
 TITLE IL-TIF/IL-22: genomic organization and mapping of the human and
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 JOURNAL Genes Immun. 1 (8), 488-494 (2000)
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 AUTHORS Renauld, J.C.
 TITLE Direct Submission
 JOURNAL Submitted (18-SEP-2000) Renauld J.C., UCL 74.59, Ludwig Institute
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 DEFINITION Sequence 17 from patent US 6274710.
 ACCESSION ARI65234
 VERSION ARI65234.1 GI:16238731
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 5935)
 AUTHORS Dumoulier, L., Louhed, J. and Renaud, J.-C.
 TITLE Antibodies which specifically bind T cell inducible factors (TIFs)
 JOURNAL Patent: US 6274710-A 17 14-Aug-2001;
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Query Match 13.6%; Score 650; DB 6; Length 5935;
 Best Local Similarity 56.5%; Pred. No. 1.8e-139;
 Matches 1863; Conservative 0; Mismatches 1285; Indels 152; Gaps 29;

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LOCUS
DEFINITION Sequence 42 from Patent WO2010393.

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 VERSION AX459988.1 GI:21725722
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 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 Dumoutier, L. and Renaud, J. C.
 Isolated nucleic acid molecules which encode a cell inducible factor, or interleukin-21, the proteins encoded, and uses thereof
 Patent: WO 0210393-A 42 07-FEB-2002;
 LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
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 Best Local Similarity 56.5%; Pred. No. 1.8e-139;
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 QY 269 AATCTGTCTCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 328
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 DB 656 GCTTATCT 703
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 QY 449 TTTGAG 508
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 VERSION AJ294728.1 GI:11967894
 KEYWORDS IL-TIF beta protein; ILT1Fb gene.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 5935)
 Dumoutier L., Van Roost E., Ameys G., Michaux L. and Renauld J.C.
 IL-TIF/IL-22: genomic organization and mapping of the human and
 mouse genes
 JOURNAL Genes Immun. 1 (8), 488-494 (2000)
 MEDLINE 21069354
 PUBMED 11197690
 REFERENCE 2 (bases 1 to 5935)
 Renauld J.C.
 Direct Submission
 Submitted (18-SEP-2000) Renauld J.C., UCL 74.59, Ludwig Institute
 for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels,
 BELGIUM
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:06:30 ; Search time 4199.55 Seconds

(Without alignments)
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Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em_estin:*

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5: em_estov:*

6: em_estopl:*

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8: em_hlc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hlc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vit:*

22: em_gss_fun:*

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25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	373.8	7.8	377	17	AQ212781 HS_3118_B
3	267.4	5.6	389	17	AQ104025 HS_3108_B
4	140	2.9	1035	14	BQ436632 AGENCOURT
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6	132.8	2.8	426	17	AQ012598 CIT-HSP-2

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19	122	2.5	680	17	AO625928 CITBI-EI-
20	122	2.5	715	17	AO628187 CITBI-EI-
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AQ762065
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 534)
Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T.,
Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and
Hood L.

TITLE
JOURNAL
MEDLINE
COMMENT
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end web server: http://www.htsc.washington.edu

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 REFERENCE 1 (bases 1 to 377)
 AUTHORS Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T.,
 Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and
 Hood L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas G.G., Wallace J.C., Hood L.
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
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 DB 241 TGAAGTCAATTTGAGATGATTAATGATGATGATGATGATGATGATGATGATGAT 300
 QY 2503 CAATGAGAAAGAGCTGAGCTTCATATAGGGCTAATTTCTGGAGTAAATTAACACTTAT 2562
 DB 301 CAATGAGAAAGAGCTGAGCTTCATATAGGGCTAATTTCTGGAGTAAATTAACACTTAT 360
 QY 2563 TTGAATTATCATTAAT 2579
 DB 361 TTGAATTATCATTAAT 377

RESULT 3
 A0104025/c 389 bp DNA linear GSS 28-AUG-1998
 LOCUS
 DEFINITION HS_3108_B1_C01_T7 CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3108 Col=1 Row=F, DNA sequence.
 ACCESSION A0104025
 VERSION A0104025.1 GI:3478961
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 389)

AUTHOR	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,W.D. and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Plate: 3108 row: F column: 1 Class: BAC ends High quality sequence stop: 389.
FEATURES	Location/Qualifiers 1..389 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="plate=3108 Col=1 Row=F" /clone_1pb="CIR Approved Human Genomic Sperm Library D" /sex="male" /note="Organ: sperm; Vector: pBel0BAC11, BAC clones in E-Coli DH10B"
BASE COUNT	119 a 86 c 65 g 118 t 1 others
ORIGIN	
Query Match	5.6%; Score 267.4; DB 17; Length 389;
Best Local Similarity	92.8%; Pred. No. 1.6e-48;
Matches 347; Conservative	0; Mismatches 17; Indels 10; Gaps 6;
QY	1709 GATTTCCTCCCAAGATGAAGAGAGGTCTCTGTAAAGGAAGTACCTGATTCGGGCTCCA 1768
DB	364 GATTTCCCAAGATGAAGAGGTCTCTGT--AAGGAAGTACGATTCGGG--TCNA 311
QY	1769 GGAATTCAGAGCTCAGGAATCTAGTCACTGTGAAATCTGAGTCATTTGGGCAA 1828
DB	310 AGGATTCAGAGCTCA-GAATATAGTCTCTTT-AAATCTAGTCATTGT--GCCAA 254
QY	1829 ATTACTAAGAGCTTTAATTCAGAGTGAATTGTACTGTACCTCCATGGGTGAGGTTCA 1888
DB	253 ATTACTAAGAGCTTT-ATTCAGGTGAATTGTACTGTACCTCCATGGGTGAGGTTCA 195
QY	1889 TTAAGTTTCAGACACAACCTTAAGTATAGTATGCTGTATTGTTTATAGCATATTGAAG 1948
DB	194 TTAAGTTTCAGACACAACCTTAAGTATAGTATGCTGTATTGTTTATAGCATATTGAAG 135
QY	1949 GTGATGACCTGCATATCCAGAGAGATGTCACAAAGCTGAAAGACACAGTGAAGAGTGA 2008
DB	134 GTGATGACCTGCATATCCAGAGAGATGTCACAAAGCTGAAAGACACAGTGAAGAGTGA 75
QY	2009 GACTGATTAAGTCAATGCTTAAGTCATGATGCAATAGAGAGACAAATGTTGTTTCTTCC 2068
DB	74 GACTGATTAAGTCAATGCTTAAGTCATGATGCAATAGAGAGACAAATGTTGTTTCTTCC 15
QY	2069 TTTCTTTTCTTCCCA 2082
DB	14 TTTCTTTTCTTCCCA 1
RESULT 4	
LOCUS	BQ436632/c 1035 bp mRNA linear EST 24-MAY-2002
DEFINITION	BQ436632 7582829 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6045008
ACCESSION	BQ436632
VERSION	BQ436632.1 GI:21175708
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	unpublished (1999) Contact: Robert Strauberg, Ph.D. Email: rgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LRAM3288 row: 1 column: 09 High quality sequence stop: 473.
FEATURES	Location/Qualifiers
SOURCE	1..1035
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:6045008"
	/clone_lib="NIH MGC_92"
	/tissue_type="embryonal carcinoma, cell line"
	/lab_host="DH10B (phage-resistant)"
	/note="Organ: testis; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
BASE COUNT	285 a 246 c 189 g 314 t 1 others
ORIGIN	
Query Match	2.9% Score 140; DB 14; Length 1035;
Best Local Similarity	72.8%; Pred. No. 2.6e-20;
Matches 195; Conservative	0; Mismatches 70; Indels 3; Gaps 1;
Dy	4026 AGATGTTTAAATCAGAGTGTCCAATCATTTGGCTTCCTCGACCACTTGA--AAGA 4082
Dd	270 AAATCATTTAAACCAAGGTGTCCAATCTGTGCTCCGCGGCCACACTGAAAGA 211
Dy	4083 ATTGCTTGGTACACACATAAATACAAACAATAGCTGATGAGCTAAAAAAGTCATG 4142
Dd	210 ATTGTTTGGAACCAACATAAATACACTAACATAGCTGATGAACTAAAAAATGTAA 151
Dy	4143 CATTAATCTCACTGTTTTTAAGAAGTTATGTAATTCTGTAGGGTGATCAAAGCT 4202
Dd	150 AAAACAATCTAATATGTTTTAGGAAGTTTATGAAITTTGTTGGCTGCATCAAAGCT 91
Dy	4203 GTCCGTGGCCATGTGCGGCTGTGGGGCTGACAGTTGACCAAGCTCTTATAGTAATCTG 4262
Dd	90 GTCTGTGGCCACATGCGGCGCATGTGTCGTGGTGAACAACTGATTTAAACATTAA 31
Dy	4263 TCATAGATAGTTTGGAGCTGCAAAACA 4290
Dd	30 ACTTTTCTCAATTGACCAAGTAATA 3
RESULT 5	
A2449260	562 bp DNA linear GSS 04-OCT-2000
LOCUS	
DEFINITION	IM024J321F Mouse 10kb plasmid UUC1M library Mus musculus genomic
ACCESSION	clone UUC1M024J321 F, DNA sequence.
VERSION	A2449260
KEYWORDS	A2449260.1 GI:10602872
GSS	
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Scuriongnathi; Muridae; Murineae; Mus.
	(bases 1 to 562) Barber,M., Beacorn,T., Duval,B., Hamll,C., Dunn,D., Aoyagi,A., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,Istilah,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

TITLE
JOURNAL
COMMENT

'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0247 row: J column: 21
Seq primer: CGTTGTAAACGACGCGCAGCT
Class: plasmid ends
High quality sequence stop: 562.

FEATURES
source
1. 562
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MUGCIM024721"
/clone_1lb="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (G14732114[bp]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 119 a 155 c 116 g 172 t
ORIGIN

Query Match 2.8%; Score 133.4; DB 17; Length 562;
Best Local Similarity 61.1%; Pred. No. 7.5e-19;
Matches 367; Conservative 0; Mismatches 176; Indels 58; Gaps 7;

QY 374 TACATAAATTTCTGTTTTCAGAGACTTTGGGAATGCTTTTCTTGA 433
DB 8 TACCTATGTTTCTGCTCTTGAAGACTCTTTAAGACTGATCTTTTCAATTC 67
QY 434 -----ACTCTTCCTTCATTTTGGCTTTATGATCATATGATTTTC 481
DB 68 TTTCAGAGTCTAGGAACATTTCTATTTTGGCTTCAGATACATATGATTTAT 127
QY 482 CCAAGAGCGGCATTCAGTATTCATCTGATGATTTTCTTATGCTCTGTG 541
DB 128 CTACAGGCGGCATTAG--AAAGCACCACAGCATGCACTTCCATCTCTGTG 185
QY 542 ATGTTCTAATCAGCAGCAGCATCTGAATTCCTTTAGTCTTATGATGCTGTG 601
DB 186 TCTCTCTGAATCACTCTCTGCTACTC-----CTG 220
QY 602 GGGAGACGGAGGGGACATGCTATGATTAATTTTCTATTTGCTCAATGCC 661
DB 221 AGACCACTGTGACATACATCTCTTACAGGCTTTTCTCATCTCTCTCATCCA 280

QY 662 GACCCCTAGCTTTTCTCTCTTCCAGGCTAGCTGCTGATPAACACAGACCTTGT 721
DB 281 GGCACCTTAGGTTTTC-TCTCTTTCAGGCGACCTTGACATPAACACAGATGTCGG 339
QY 722 CTCATTGGGAGAACTGTTCCAGGAGTCAGTAACTAGCTAGTGTGACGAGGCG 781
DB 340 CTCATGCGGAGAACTGTTCCAGAGAGTCAGTAACTGCTGCTGATGACGAGGC 399
QY 782 CGTGTGCGCTCCATGAGGTCCTTGGGTGTGTGATGATGTTAGCTTATCCCTTAT 841
DB 400 -----TAGCTCGGAGAGCTGTGAGACCTCTGGGATAG----TCTGAGCTAT 442
QY 842 GACCCCTTGTGTTTCCCTTCCAGCTGACAGATGATGAGGCTGCTATCTGATGAGCAG 901
DB 443 GACCCCTGCTGCTTCTTCTCCAGCTGACAGCTAGAGATGATGATGATGAGCAG 502
QY 902 TGCTGAATTCACCCCTGAGAGAGCTGTTCCTCAATCATATGTTCCAGCCTTATA 961
DB 503 TGCTCAACTTC-CCCTGGAAGAGTTCCTGCTCCCGATCAAGATTCAGCCTTACA 561
QY 962 T 962
DB 562 T 562

RESULT 6
A0012598/c 426 bp DNA linear GSS 06-JUN-1998
LOCUS CIT-HSP-229915.TR CIT-HSP Homo sapiens genomic clone 229915, DNA
DEFINITION
ACCESSION A0012598
VERSION A0012598
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 426)
Adams, M.D., Rounlet, S.D., Zhao, S., Field, C.E., Baas, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M., and Venter, J.C. 1998.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
Other GSSes: CIT-HSP-229915.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
1. 426
/organism="Homo sapiens"
/db_xref="GDB:7154145"
/db_xref="taxon:9606"
/clone="229915"
/clone_1lb="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"

BASE COUNT 129 a 93 c 75 g 129 t
ORIGIN
Query Match 2.8%; Score 132.8; DB 17; Length 426;
Best Local Similarity 77.9%; Pred. No. 1e-18;

Matched	173;	Conservative	0;	Mismatches	47;	Indels	2;	Gaps	1;
QY	4027	GATGTTTAAATCAGAGTGTCCAAATCATTTGGCTTCCTGGACCACTTGAAGAATG	40868						
Db	226	GAATTTCACTAGACCGGGTGTCCATCTTTGGCTTCCTGGCCACCTGGAAGATTG	167						
QY	4087	TCTTGGTACACATAAATACAGAACATAGCTGATGAGTAAATAAG--TCCATGCA	41444						
Db	166	TCTTGGGCCAACGTAATAATCTCTACAAATAGCTATGAGCTTAAAGAAATGCTCA	107						
QY	4145	TAAATCTCATCTGTTTAAAGAAATTATGAATTTCTGTAAGGCTGATTCAAAGCTGT	42040						
Db	106	AAATCTCATATGTTTCAAGAAAGTTTACAAATTTGATAGTGTGCAATTAAGCTGT	47						
QY	4205	CCTGGGCATGTGCGGCTGTGGGTGTGAGGTTGACAAGCT	4246						
Db	46	CCTGGGACACATGTGGCCCAAGGCTGAGGTGGGACAAAGCT	5						
RESULT 7									
LOCUS	BH609959	617 bp	DNA	linear	GEN 18-DEC-2001				
DEFINITION	HIV25H1 Suprt1 HIV-1 in vitro integration lines Homo sapiens genomic clone HIV25H1, DNA sequence.								
ACCESSION	BH609959								
VERSION	BH609959.1	GI:17922568							
KEYWORDS	GSS.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
AUTHORS	1 (bases 1 to 617) Schroeder,A.R.W., Shinn,P., Chen,H., Berry, C., Ecker,J.R. and Bushman,F.								
TITLE	Unpublished Sites for HIV-1 Integration in the Human Genome								
JOURNAL	Contact: Frederic Bushman								
COMMENT	The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1630 Fax: 858 554 0341 Email: bushman@salk.edu Class: PCR with specific primers.								
FEATURES	Location/Qualifiers								
source	1..617 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="HIV25H1" /clone_1ib="Suprt1 HIV-1 in vitro integration lines" /note="Integration sites were generated in vitro using naked Suprt1 DNA as a target. HIV preintegration complexes (PICs) were used as a source of integration activity. DNA was cleaved with restriction enzymes, linkers were ligated onto the cleaved DNA and DNAs were amplified using one primer that bound to the linker DNA and one that bound to the HIV cDNA. Junctions between integrated HIV proviruses and cellular DNA were cloned and sequenced."								
BASE COUNT	217 a 93 c 110 g 197 t								
ORIGIN									
Query Match	2.7%; Score 131.8; DB 17; Length 617;								
Best Local Similarity	78.0%; Pred. No.1.7e-18;								
Matches 188; Conservative	0; Mismatches 42; Indels 11; Gaps 2;								
QY	4032	TTTAATCAGAGTGTCCAAATTTGGCTTCCTGGACCACTTGA---AAGATTGTC	40868						
Db	319	TGTAATCGGGGTGCCAATCTTTTGGTTCCCAAGGCCAATTTGGAAGAAATTTGCC	378						
QY	4089	TTGTATACACATTAATACAGAACATATGCTGATGAGCTAA-----AAAAGTCA	41440						
Db	379	TTGGGCCACACATTAAGATCTAATGATGCTGATGAGCTTAAAAAAGAAAGTCTCA	438						

Oy	4141	TGCATTAATCCATCAGCTGTTTAAAGAAAGTTTAAAGATTTCTGTAGGAGTCATTCAAG	4200
Db	439	TGCTATAACTCTATATGTTTCAAGAAAGTTATGATTTGTGTGGCTGCATTCAAG	498
Oy	4201	CTGTCTGTGGCCATGTGTGGGCTGTGGCTGTGACAGTTTGACAAAGCTCTTAATAGTAATC	4260
Db	499	CCGTCTGTGGGCTGCATGTGGCCCATGGGCGCCACAGATTAGACAGCTTGATTAATAGTT	558
Oy	4261	T	4261
Db	559	T	559
RESULT 8			
LOCUS	AG092864	650 bp	DNA linear GSS 03-NOV-2001
DEFINITION	Pan troglodytes DNA, clone: PTB-093C12.R, genomic survey sequence.		
ACCESSION	AG092864		
VERSION	AG092864.1	GI:16644666	
KEYWORDS	GSS.		
SOURCE	Pan troglodytes male lymphoblast DNA, clone_lib.PTB Chimpanzee Male		
ORGANISM	BAC Library clone:PTB-093C12.R.		
REFERENCE	Par troglodytes		
AUTHORS	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.		
TITLE	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,		
JOURNAL	Totoki, Y., Watanabe, H. and Sakaki, Y.		
REFERENCE	BAC end sequences of library PTB		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 650)		
JOURNAL	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,		
REFERENCE	Totoki, Y., Watanabe, H. and Sakaki, Y.		
AUTHORS	Direct Submission		
TITLE	Submitted (02-AUG-2001) Aseo Fujiyama, The Institute of Physical		
JOURNAL	and Chemical Research (RIKEN), Genomic Sciences Center (GSC);		
REFERENCE	1-7-22 Suenho-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
AUTHORS	(E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,		
TITLE	Tel:81-45-503-9111, Fax:81-45-503-9170)		
JOURNAL	Clones are derived from the chimpanzee BAC library PTB This BAC end		
REFERENCE	was generated during the R&D process and may have higher chance of		
AUTHORS	clone tracking errors.		
TITLE	PRIMERS		
JOURNAL	Sequencing: MJ3rev		
REFERENCE	LIBRARY		
AUTHORS	Vector : pKS145		
TITLE	R.Site 1 : SacI		
JOURNAL	R.Site 2 : SacI.		
REFERENCE	Location/Qualifiers		
AUTHORS	1. .650		
TITLE	/organism="Pan troglodytes"		
JOURNAL	/db_xref="taxon:9598"		
REFERENCE	/clone="PTB-093C12.R"		
AUTHORS	/sex="male"		
TITLE	/cell_type="lymphoblast"		
JOURNAL	/clone_lib="PTB Chimpanzee Male BAC Library"		
REFERENCE	BASE COUNT		
AUTHORS	173 a 136 c 137 g 204 t		
TITLE	ORIGIN		
JOURNAL	Query Match		
REFERENCE	Best Local Similarity		
AUTHORS	Matches		
TITLE	212; Conservative		
JOURNAL	0; Mismatches		
REFERENCE	80; Indels		
AUTHORS	13; Gaps		
TITLE	2		
JOURNAL	3967 TGGAAATGGAAGAAAGCCTTAATGATTTGGTGAATACATAGTTCAAAGTCATTGGAGTGA		4026
REFERENCE	212 TGGAAAGAAAGATGTTGTTGTTTAAAGTAAGTAAGTAAGTAAGCGTTAGGC		331
AUTHORS	4027 GATGTTTAAATCAGAGTGTCCATATCTTTGGCTTCCCTGACACCTTGA-----AA		4086
TITLE	332 TATGTGCCAAATCAGGGGTCTCCATATCTTTGGCTTCCCTTGGGCACACTGGAAGAGAA		391
JOURNAL	4081 GAATGCTTGTGTACACCATTAATATCAAGACATAGTGTGATGAGCTAAAAAGTCCA		4140

Db 392 GAATTCCTGGGCGCACATAAATACACCAACATAGCTGATGACCTTTAAAAAATC 451
 QY 4141 TGCATTAATCTCATCTACTGTTTAAAGAAAGTTTATGAATTTCTGTAGGCGCATTCAG 4200
 Db 452 GCAAAAAACCTCAATAGTTTCAATAAAGTTTACGAATTTGTGTGGTTGCATTCAG 511
 QY 4201 CTGTCCCTGGGCGCATG-----TCGCGCCCTGTGGCGTCGACGTTGACCAAGCTCCTATA 4253
 Db 512 CCATCTCGAGCCATGACCCACATGTGGCTGTGGCGCGAGGCTGCAAACTGTGTGTA 571
 QY 4254 AGTAA 4258
 Db 572 AATCA 576

RESULT 9
 AQL13016/c 423 bp DNA linear GSS 29-AUG-1998
 LOCUS CIT-HSP-2375K21.TR CIT-HSP Homo sapiens genomic clone 2375K21. DNA
 DEFINITION
 ACCESSION AQL13016 GI:3489137
 VERSION AQL13016
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 423)
 Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Libher,K., Golden,K.,
 Berry,K., Granger,D., Sub,E., Wible,C., Shizuya,H., Simon,M. and
 Venter,M.C.
 Use of a random human BAC End Sequence Database for Sequence-Ready
 Map Building
 Unpublished (1998)
 JOURNAL Other GSSs: CIT-HSP-2375K21.TF
 COMMENT Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@igf.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..423
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2375K21"
 /clone_lib="CIT-HSP"
 /sex="Male"
 /cell_type="Sperm"
 /notes="Vector: pbeIOBAC11; Site_1: HindIII; Site_2:
 HindIII"

BASE COUNT 115 a 82 c 73 g 153 t

ORIGIN
 Query Match 2.7%; Score 129.2; DB 17; Length 423;
 Best Local Similarity 74.4%; Pred. No. 6.3e-18;
 Matches 177; Conservative 0; Mismatches 58; Indels 3; Gaps 1;

QY 4012 AGTCATTGAGTAGAGATGTTTAAATCAGAGTGCATTCATTTGGCTTCCCTGGACC 4071
 Db 247 AATTAATCTGAATATGAAATCCCTGCGAGAGGTGTCATCTTTGGCTTCCCTGGACC 188
 QY 4072 ACCTGAAGAATTTGTTGGTGAACACATTAATAATACAGAACATAGCTGATGAGCT- 4129
 Db 187 AATTTGGAAGAATTTGTTGGGCGACACAAAATATACATTAATGATGCTGATGAGAGCTTT 128
 QY 4130 -AAAAAGTCATGCAATATCTCATCTGTTTAAAGAAAGTTTATGAATTTCTGTAGG 4188

Db 127 AAAAAAAAAATCACAAATATCATCTCATTAAGTTTAAAGAAAGTTTAAATTTGTGTGA 68
 QY 4189 GTGCATTCAGAGTGTCTGCGGCAGATGTCGGGCTGTGGCGTCGACGTTGACCAACT 4246
 Db 67 CCACATTCAGAGCATTCAGAGGCTGCAATGCGCCATGCGGCTGCGAGTTGACCAACT 10

RESULT 10
 AG093514/c 680 bp DNA linear GSS 03-NOV-2001
 LOCUS Pan troglodytes DNA, clone: PTB-094A01.R, genomic survey sequence.
 ACCESSION AG093514
 VERSION AG093514.1 GI:16645316
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
 BAC library clone:PTB-094A01.R.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 BAC end sequences of Library PTB
 Unpublished
 2 (bases 1 to 680)
 REFERENCE Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 JOURNAL Direct Submision
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimbese@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.
 PRIMERS
 Sequencing: M13rev
 LIBRARY
 Vector : PK5145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers
 1..680
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-094A01.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 158 a 151 c 163 g 201 t 7 others

ORIGIN
 Query Match 2.6%; Score 127; DB 17; Length 680;
 Best Local Similarity 76.8%; Pred. No. 1.9e-17;
 Matches 182; Conservative 0; Mismatches 50; Indels 5; Gaps 2;

QY 4023 TAGAGATGTTTAAATCAGAGTGCATTCATTTGGCTTCCCTGGACCACTTG--AA 4079
 Db 633 TATCGCTGTTTAAAGCAAACTGTCCATCTTTGGCTTCCCTGGACCGCACTGAAAA 574
 QY 4080 AGAATTTGTTGGTACACATATAAATACAGAACATAGCTGATGAGCTAAAAAAATGCC 4139
 Db 573 AGAATTTGTTGGGCGACACATTAATATGCGAGAGATGCTGATGAGCTTAAAAAANA 514
 QY 4140 ATGCA -TAAATCTCATCTGTTTAAAGAAAGTTTATGAATTTCTGTAGGCTGATTCA 4197
 Db 513 CTGCACAAAATTTCTATTAACGTTTAAAGAAATTTACGAATTTGTGTGGCCCACTTCA 454
 QY 4198 AAGCTGTCTGGGCGCATGCGGCGCTGTGGCGTGAAGTTGGAAGCTCTTATTA 4254
 Db 453 AAGCATCTGGGCGCATATGTGCGCTGCGGCGCTGTGATGGAAGAAAGCTTATTAA 397

RESULT 11
 LOCUS AQ01154/c 928 bp DNA linear GSS 10-NOV-1999
 DEFINITION HS 3171 A2 H08 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone plate=3171 Col=16 Row=O, DNA sequence.
 ACCESSION AQ01154
 VERSION AQ01154.1 GI:6357344
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 928)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,D., Zhao,S., Adams,M.D. and Hood,L.
 COMMENT Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 JOURNAL 99380589
 MEDLINE
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 3171 row: O column: 16
 Seq primer: M13 Reverse
 Class: BAC ends
 High quality sequence scop: 928.
 Location/Qualifiers
 source
 1. 928
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="plate=3171 Col=16 Row=O"
 /clone_11b="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"
 BASE COUNT 240 a 275 c 115 g 298 t
 ORIGIN

Query Match 2.6%; Score 126.4; DB 17; Length 928;
 Best Local Similarity 72.6%; Pred. No. 2,7e-17;
 Matches 193; Conservative 0; Mismatches 66; Indels 7; Gaps 2;

QY 4028 AGTTTAAATCGAGGTGCAATTCATTGGCTCCCTGGACCACTTGA-----AAG 4081
 DB 415 ATTCCTTAAGACAGGGGGTGTCACTTTTGCTCCCTGGCACTTGAAGAAAGAG 356
 QY 4082 AATTGCTTGTGACACATAAAATACAGAACATAGCTGATGAGCTAAAAAGTCAT 4141
 DB 355 AATTGCTTGTGACACATAAAATACATGACATGATGAGCTTAAAAAAT 296
 QY 4142 GCATAATCTCATCTGTTTAAAGAAAGTTTGAATTTCTGTTAGGCTGATCAAGC 4201
 DB 295 ACAAAAAAATAAATTTTAAAGAAAGTTTGAATTTGTTT-GGCTACATTTCAAGC 237
 QY 4202 TGTCCGGGGCATGTGGGCTGTGGGCTGAGGTTGGACAAGCTCTTAAGTAATCT 4261
 DB 236 TGTCCGGGGCATGTGGGCTGTGGGCTGAGGTTGGACAAGCTCTTAAGTAATCT 177
 QY 4262 GTCATAGATAGTTTGGAGCTGCAA 4287
 DB 176 GAAACATATTAATATCACACAGAAA 151
 RESULT 12

AM238510
 LOCUS xp27a05.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741552 3' similar to contigs MER30.D2 MER30 repetitive element ;, mRNA sequence.
 ACCESSION AM238510
 VERSION AM238510.1 GI:6570899
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 397)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 Email: cgephs-remail.nih.gov
 Tissue Procurement: Edward Shillito Ph.D., Silvio Gutkind Ph.D., Chichanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.
 CDNA Library Preparation: David B. Krizman, Ph.D.
 CDNA Library Arrayed by: Greg Lemmon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLNL at: www-bio.lnl.gov/btrp/image/image.html
 Possible reversed clone; polyT not found
 Seg primer: -40UP from Gibco
 High quality sequence scop: 370.
 Location/Qualifiers
 source
 1. 397
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2741552"
 /clone_11b="NCI_CGAP_HN10"
 /tissue_type="carcinoma in situ from retroviral trigone"
 /lab_host="DH10B"
 /note="Vector: PAMPI0; cDNA made by oligo-dT priming. Non-directionally cloned into the UDG sites of PAMPI0. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. CDNA Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
 BASE COUNT 128 a 70 c 82 g 117 t
 ORIGIN

Query Match 2.6%; Score 124; DB 10; Length 397;
 Best Local Similarity 77.4%; Pred. No. 9e-17;
 Matches 178; Conservative 0; Mismatches 45; Indels 7; Gaps 2;

QY 4034 TAAATCAGAGGTGCAATTCATTGGCTCCCTGGACCACTTGA---AAGATTGCTT 4090
 DB 25 TAAATCAGAGGTGCAATTCATTGGCTCCCTGGACCACTTGAAGAAAGATTGCTT 84
 QY 4091 GGTACACATATAAATACAGAAATAGCTGATGAGCT---AAAAAGTCATGACAT 4146
 DB 85 GGACACACATATAAATACAGAAATAGCTGATGAGCTTCAAAAAAATACACAAAAA 144
 QY 4147 AATTCATACGTGTTTAAAGAAAGTTTGAATTTCTGTTAGGCTGATCAAGCTGTC 4206
 DB 145 AGTCCTTAATGTTTAAAGTAAGTTTCAAAATTTGCTTGGGCCACATTGAAAGCATCC 204
 QY 4207 TGGGCGCATGTGGGCTGTGGGCTGAGGTTGGACAAGCTCTTAAGT 4256
 DB 205 TGGGCTCATGACGCCCATGGCCACAGGTTGGACAAGCTTGAAGTAAGT 254
 RESULT 13
 LOCUS AQ108812/c 461 bp DNA linear GSS 29-AUG-1998
 DEFINITION CIT-HSP-2373M12.TF CIT-HSP Homo sapiens genomic clone 2373M12, DNA

ACCESSION	sequence.
VERSION	AQI08812
KEYWORDS	AQI08812.1 GI:3485502 GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 461)
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Base,S., Linber,K., Golden,K., Berry,K., Granger,D., Suh,E., Wille,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other GSSs: CIT-HSP-2373M12.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: madams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13-21 Class: BAC ends.
FEATURES	Location/Qualifiers
SOURCE	1..461 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2373M12" /clone_id="CIT-HSP" /sex="Male" /cell_type="Sperm" /note=Vector: pBelobAC11, Site_1: HindIII, Site_2: HindIII"
BASE COUNT	127 a 97 c 101 g 136 t
ORIGIN	
Query Match	2.6%; Score 123.6; DB 17; Length 461;
Best Local Similarity	74.4%; Pred. NO.1.le-16;
Matches 186; Conservative	0; Mismatches 54; Indels 10; Gaps 2;
Cy	4007 TTCAAAGTCATTGATGATGAGATGTTTAAATCGAGAGTGCCAAATCTGGCTTCCT 4066
Dy	319 TTCATTGGCAACTTAATAAAGGAGAGCTTCCAAGCAGAATTGCAGAACTTTAGCTTCCT 260
Oy	4067 GGACCACCTTAAGAAGATTGTCTTGCTCACACATTAATAATCAAGAAC-----ATNGC 41220
Dy	259 GGGGCCACACTGGGGAATGTCTGGGGCCACACATTAATACAGTAGACCTAATGATGA 200
Oy	4121 TGATGAGCTAAAAAAGTCCATGC---ATAATCTCATACGTGTTTAAAGAAAGTTTANGA 41767
Dy	199 TGAAGAGCTAAAAAATAAATCTAAAAAATATCTCAGATGTTCCAGAAAAGTTTACA 140
Oy	4177 ATTTCGTGTAAGGGTGATTCATAAGCTGTCTCGGGCCATGTGGGGCTGTGGGCTGCAGCT 42368
Dy	139 ATTTGTGTTGGGCTGCATTCATAAGCTGTCTCGGGCCATGCGAGCTGTAGGCTGCGGGT 80
Oy	4237 TGGACAGAGCT 4246
Dy	79 TGGACAGAGCT 70
RESULT 14	
BG215075/c	BG215075 542 bp mRNA linear EST 21-APR-2001
LOCUS	R8334733 Athersys RAGE Library Homo sapiens cdna, mRNA sequence.
DEFINITION	BG215075
ACCESSION	BG215075.1 GI:33741096
VERSION	EST
KEYWORDS	

Source	Organism	Reference	Authors	Title	Journal	Medline	Comment
human.	Homo sapiens	Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 542)	Harrington, J., Sheff, B., Rundlett, S., Jackson, P. D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McIligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Kilkka, A., Hees, J., Cothren, K., Lo, K., Offenbacher, J., Dandig, J. and Ducar, M.	Creation of genome-wide protein expression libraries using random activation of gene expression	Nat. Biotechnol. 19 (5), 440-445 (2001)	21227151	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@athersys.com High quality sequence stop: 542. Location/Qualifiers
FEATURES	source	1..542	/organism="Homo sapiens"	/db_xref="taxon:9606"	/clone_lib="Athersys RAGE Library"	/cell_line="HT1080"	/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression'. Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
BASE COUNT	154 a	125 c	101 g	161 t	1 others		
ORIGIN							
Query Match	2.6%	Score 123.4	DB 12	Length 542			
Best Local Similarity	69.1%	Pred. No. 1.2e-16					
Matches 215	Conservative 0	Mismatches 86	Indels 10	Gaps 3			
Db	3952	TGTTTGCACAAAAGGTGGAATAGAAAAGCCTTAATGATTTGGTGAATACATGGTTCAA	40111				
Db	540	TTTTTTTTTTTAATGAGGAAAACCAAAATTCGATTTGGTATCCAGGATTAACAATTCAA	481				
Db	4012	AGTCATTTGAGTAGAGATGTTTAAATCAGAGGTGCCAATCATTTGGCTTCCCTGACC	40711				
Db	480	AGTAATAGACCT--TGGTGTTCTTAACATAGGGGTGTCCGATCTTCCGCTTCCCTGGGCC	423				
Db	4072	ACCTTGA-----AAGATTGCTTGGTATACACATAAATATCAAGA--ACAATAGCTGA	41223				
Db	422	ACATTGAGAGAGAGAAATGCTTGGGCCACACATAAATATCTTAACACAAATAGCTGA	363				
Db	4124	TGAGCTAAAAAAGTCATGATTAATCTCACTACTGTTTAAAGAAAGTTTGAATTTCTG	41833				
Db	362	TGAGCTTAATAAATAATCAAAAAAATCTCCAAAGTTTAAAGAAACCTTAACAAATTTGTG	303				
Db	4184	TTAGGGTGCATTCAAAGCTGCTCGGGCCATGTGCGGCTGTGGGCTGCAGGTTGGACAA	42433				
Db	302	TTGGGCGCGCATTCACAAAGCCGTCCTTAAGGCCACATGTGGCCCGTGGGCCATGGGTTGGACAA	243				
Db	4244	GCTCCTTATATA 4254					
Db	242	GTTTGTCTTAA 232					
RESULT 15	AO171322/c	383 bp	DNA	linear	GSF 17-OCT-1998		
LOCUS	HS-3071_B2_D10_MR_CIT	Approved Human Genomic Sperm Library D Homo					
DEFINITION	sapiens genomic clone Plate=3071 Col=20 Row=H, DNA sequence.						
ACCESSION	AO1713122						
VERSION	AO1713122.1	GI:3568689					
KEYWORDS	GSF.						

SOURCE	ORGANISM	TITLE
human.	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 383)	
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.	
JOURNAL MEDLINE COMMENT	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589	
CONTACT:	Mahairas GG, Wallace JC, Hood L	
High Throughput Sequencing Center	University of Washington	
401 Queen Anne Avenue North, Seattle, WA 98109, USA	Tel: (206) 616-3618	
Fax: (206) 616-3887	Email: jwallace@u.washington.edu	
Sequence Tagged Connector	Plate: 3071 row: H column: 20	
Class: BAC ends	High quality sequence stop: 383.	
FEATURES	Location/Qualifiers	
source	1..383	
/organism="Homo sapiens"	/db_xref="taxon:9606"	
/clone="Plate=3071 Col=20 Row=H"	/clone_lib="CIT Approved Human Genomic Sperm Library D"	
/sex="male"	/sex="Organ: sperm; Vector: pBelobAc11; BAC Clones in E-Coli DH10B"	
BASE COUNT	119 a 71 c 69 g 124 t	
ORIGIN		
Query Match	2.6% Score 122.6; DB 17; Length 383;	
Best Local Similarity	75.9%; Pred. No. 1.8e-16;	
Matches 180; Conservative 0; Mismatches 49; Indels 8; Gaps 2;		
Db	4035 AAATCAGGAGTGTCCAAATCATTTGGCTTCCTCGAACCACTTGA---AAGAATTGCTTG	4091
382 AAACTAGGGAATCCAATCTTTGGCTTCCTCGAACCGCAATTGGAGAAGATGTCTTG	323	
Db	4092 GTACACACATAAAAATACAGAACAATAGCTGATGACTAAAA----AGTCATGCATA	4146
322 GGCCATACACAAAAATACACTAACGATATCTGATGAGCTPAAAAAATTGAAAAAAAAA	263	
Db	4147 AATCTCAATCGTTTTTAAGAAAGTTTAGAATTTCTGTTAGGGGCATTCAAACCTGCC	4206
262 CCTCTCAATAAAGTTTTTAGGAAGTTTAGAATTGTGTGGGCTGCATTCAAACCTGCC	203	
Db	4207 TGGGCATGTGCGGCTGTGGGCGTGCAGAGTGTGACAAAGCTCCTTAATAAGTAATCTGT	4263
202 TGCGTCATGTGGGCCACGGGCTGCTCTTTGGACACAGCTGCTTTAATCATCTCT	146	

Search completed: July 19, 2003, 19:39:15
Job time : 4203.8 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2003, 09:02:25 ; Search time 657.876 Seconds

(without alignments)
16420.772 Million cell updates/sec

Title: US-09-751-797-25

Perfect score: 4797
Sequence: 1 tgcacaagaacgaattcttcag.....gatgccccaagcgattttc 4797

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: N_Geneseq_101002.*
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
25: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4797	100.0	4797	22	AA514876 Human partial geno
2	4797	100.0	4797	24	AA530646 Human TIF genomic
3	4797	100.0	4797	24	AA527151 Human T cell deriv
4	4781.8	99.7	4796	21	AA528840 Human T cell induc
5	686	14.3	7445	22	AA514859 Human partial geno
6	686	14.3	7445	24	AA530628 Mouse TIF alpha ge
7	686	14.3	7445	24	AA527134 Mouse T cell deriv
8	677.4	14.1	7444	21	AA528816 Murine T cell indu
9	650	13.6	5935	21	AA528818 Murine T cell indu

10	650	13.6	5935	22	AA514878 Mouse partial geno
11	650	13.6	5935	24	AA530650 Mouse TIF beta gen
12	650	13.6	5935	24	AA527153 Mouse T cell deriv
13	650	5.4	690	21	AA528839 Human T cell induc
14	650	5.4	690	22	AA514875 Human CDNA encodin
15	650	5.4	690	24	AA530645 Human TIF CDNA. H
16	650	5.4	690	24	AA527150 Human T cell deriv
17	650	5.1	1152	22	AA5292134 Human PRO10096 cdv
18	650	5.1	1152	22	AA5292134 Human PRO10096 cdv
19	650	5.1	1152	24	AA5292134 Human PRO10096 cdv
20	650	5.1	1152	24	AA5292134 Human PRO10096 cdv
21	650	5.1	1152	24	AA5292134 Human PRO10096 cdv
22	650	5.1	1152	24	AA5292134 Human PRO10096 cdv
23	650	5.0	1152	22	AA5292134 Human PRO10096 cdv
24	650	4.9	1152	22	AA5292134 Human PRO10096 cdv
25	650	4.9	1152	22	AA5292134 Human PRO10096 cdv
26	650	4.3	1116	22	AA5292134 Human PRO10096 cdv
27	650	4.3	1116	22	AA5292134 Human PRO10096 cdv
28	650	4.3	1116	24	AA5292134 Human PRO10096 cdv
29	650	4.3	1116	24	AA5292134 Human PRO10096 cdv
30	650	3.3	418	24	AA5292134 Human PRO10096 cdv
31	650	2.8	3727	22	AA5292134 Human PRO10096 cdv
32	650	2.7	537	22	AA5292134 Human PRO10096 cdv
33	650	2.7	74037	24	AA5292134 Human PRO10096 cdv
34	650	2.7	1111	21	AA5292134 Human PRO10096 cdv
35	650	2.7	1111	22	AA5292134 Human PRO10096 cdv
36	650	2.7	1111	24	AA5292134 Human PRO10096 cdv
37	650	2.7	1111	24	AA5292134 Human PRO10096 cdv
38	650	2.6	778	22	AA5292134 Human PRO10096 cdv
39	650	2.6	1119	21	AA5292134 Human PRO10096 cdv
40	650	2.6	1119	22	AA5292134 Human PRO10096 cdv
41	650	2.6	1119	24	AA5292134 Human PRO10096 cdv
42	650	2.6	1119	24	AA5292134 Human PRO10096 cdv
43	650	2.5	7680	21	AA5292134 Human PRO10096 cdv
44	650	2.5	5151	22	AA5292134 Human PRO10096 cdv
45	650	2.5	1448	22	AA5292134 Human PRO10096 cdv

ALIGNMENTS

RESULT 1	AA514876	AA514876 standard; DNA; 4797 BP.
ID	AA514876	AA514876 standard; DNA; 4797 BP.
AC	AA514876	AA514876 standard; DNA; 4797 BP.
XX	AA514876	AA514876 standard; DNA; 4797 BP.
DT	19-DEC-2001	(first entry)
XX	19-DEC-2001	(first entry)
DE	Human partial genomic DNA for T cell derived inducible factor, TIF.	
XX	Human; T cell derived inducible factor; TIF; ds; antiallergic;	
KW	antiallergic; cytokine; interleukin-9; IL-9; STAT transcription factor;	
KW	cancer; lymphoma; immune system disorder; allergy; asthma;	
KW	acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;	
KW	thyroiditis; melanoma; hepatoma.	
XX	thyroiditis; melanoma; hepatoma.	
OS	Homo sapiens.	
XX	Homo sapiens.	
EN	US2001024652-A1.	
XX	US2001024652-A1.	
PD	27-SEP-2001.	
XX	27-SEP-2001.	
PF	29-DEC-2000; 2000US-0751797.	
XX	29-DEC-2000; 2000US-0751797.	
XX	18-OCT-1999; 99US-0419568.	
PR	18-OCT-1999; 99US-0419568.	
PR	26-OCT-1998; 98US-0189773.	
XX	16-JUL-1999; 99US-0354243.	
XX	16-JUL-1999; 99US-0354243.	
PA	(DMMO/) DMMOUTIER L.	
PA	(LOUHA/) LOUHAED J.	
PA	(RENA/) RENAUD J.	
XX	(RENA/) RENAUD J.	

PI Dumoutier L, Louahed J, Renaud J;
XX WPI; 2001-638496/73.
XX New isolated nucleic acid molecules encoding T cell inducible factors,
PT useful as markers for expression or effect of interleukin (IL)-9 in a
PT subject and diagnosing susceptibility to asthma or allergy -
XX
PS Claim 1, Page 17-19, 26pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule, which encodes
CC a T cell derived inducible factor (TIF) which are upregulated by the
CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor
CC activation. The TIF proteins (or their mutants) may be used to test IL-9
CC antiagonists for their potency against lymphomas, immune system
CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
CC or inhibit differentiation of tissue types in which they are active and
CC therefore be used to develop treatments for melanomas and hepatomas.
CC The present sequence is a partial genomic sequence for Human TIF.
XX
XX Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;
SQ
Query Match 100.0%; Score 4797; DB 22; Length 4797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGCACAGAGAGATCTTTCAGAACAGGTTCTCTCCAGTCACAGTGTGAGTTAG 60
DB 1 TGCACAGAGAGATCTTTCAGAACAGGTTCTCTCCAGTCACAGTGTGAGTTAG 60
QY 61 AATTGTCTGCATGCGCCGCTGACAGAAATCTGTGAGCTTTTCTTATGGGAGCCCTG 120
DB 61 AATTGTCTGCATGCGCCGCTGACAGAAATCTGTGAGCTTTTCTTATGGGAGCCCTG 120
QY 121 CCACAGCTGCGCCCTCTCTCTCTGCGCTCTGTGTACAGGAGAGAGAGAGCCCATCA 180
DB 121 CCACAGCTGCGCCCTCTCTCTCTGCGCTCTGTGTACAGGAGAGAGAGCCCATCA 180
QY 181 GCTCCCACTGACAGGCTTGAACAATCCAGAGCCCTATATCAACAACCGACCT 240
DB 181 GCTCCCACTGACAGGCTTGAACAATCCAGAGCCCTATATCAACAACCGACCT 240
QY 241 TCATGCTGCTAAGAGGATATACATCTCAATCTGCTCTTCTCGTGGATCTTACTTGA 300
DB 241 TCATGCTGCTAAGAGGATATACATCTCAATCTGCTCTTCTCGTGGATCTTACTTGA 300
QY 301 ATCCAAATAGTCTTAACTTTCTTCAAGACATCTCTAAGAGCTTTAGAACCCACTGT 360
DB 301 ATCCAAATAGTCTTAACTTTCTTCAAGACATCTCTAAGAGCTTTAGAACCCACTGT 360
QY 361 TTATCCCTGAGGATATATTTTCTGTTTTTTCAGAGACTTTGGGAATCTGACTT 420
DB 361 TTATCCCTGAGGATATATTTTCTGTTTTTTCAGAGACTTTGGGAATCTGACTT 420
QY 421 TTTTCTTTTCTTGAATCTTCTCTCTCAATTTTGGCTTTATGATACATGATGAATTTT 480
DB 421 TTTTCTTTTCTTGAATCTTCTCTCTCAATTTTGGCTTTATGATACATGATGAATTTT 480
QY 481 CCCAAGAGGCGCATTCAGTAATCATGATGATTTTTTCTTATGCTCTGTG 540
DB 481 CCCAAGAGGCGCATTCAGTAATCATGATGATTTTTTCTTATGCTCTGTG 540
QY 541 CATTTGTTTAACTCATGACACATCTGAATCTGCTTTAGCTTTATGATGTTGCTCT 600
DB 541 CATTTGTTTAACTCATGACACATCTGAATCTGCTTTAGCTTTATGATGTTGCTCT 600
QY 601 GGGGAGAGGAGATGGGGACATGCTATGATTAATTTTTTTCTTATGCTCAATGCTC 660
DB 601 GGGGAGAGGAGATGGGGACATGCTATGATTAATTTTTTTCTTATGCTCAATGCTC 660
QY 661 AGACCTTAGTCTTTCTCTCTGAGGCTAGCTGGTGAATCAACAGAGAGCTTGG 720
DB 661 AGACCTTAGTCTTTCTCTCTGAGGCTAGCTGGTGAATCAACAGAGAGCTTGG 720

DB 661 AGACCTTAGTCTTTCTCTCTGAGGCTAGCTGGTGAATCAACAGAGAGCTTGG 720
QY 721 TCTCATTTGGGAGAAACCTGTTCCACGAGATCAGTGTAGCTAGTTGACAGAGG 780
DB 721 TCTCATTTGGGAGAAACCTGTTCCACGAGATCAGTGTAGCTAGTTGACAGAGG 780
QY 781 CCGTGTGCGGTCCATGAGTACTTGGGAGTGTGTATGATGTTAGTCTTATCCCTTA 840
DB 781 CCGTGTGCGGTCCATGAGTACTTGGGAGTGTGTATGATGTTAGTCTTATCCCTTA 840
QY 841 TGAACCTTTCTGTTTCCCTTCCACCTGACAGATGAGACCGCTCTATCTGATGAAC 900
DB 841 TGAACCTTTCTGTTTCCCTTCCACCTGACAGATGAGACCGCTCTATCTGAAGAC 900
QY 901 GGTCTGAATCTACCCCTTGAAGAGGCTTCCCTCAATGATAGTTGCTTCCAGCTTAT 960
DB 901 GGTCTGAATCTACCCCTTGAAGAGGCTTCCCTCAATGATAGTTGCTTCCAGCTTAT 960
QY 961 ATGACAGAGAGTGTGCTCTCTGAGGCTCAGCAACAGGCTAAGACATGTGTAGT 1020
DB 961 ATGACAGAGAGTGTGCTCTCTGAGGCTCAGCAACAGGCTAAGACATGTGTAGT 1020
QY 1021 TGAAGCTTCAAGCTTATGCTTACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTAC 1080
DB 1021 TGAAGCTTCAAGCTTATGCTTACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTAC 1080
QY 1081 CCCAATCTAC 1140
DB 1081 CCCAATCTAC 1140
QY 1141 TGTATTCAGAGATCATTTGGGATCATAGATATTTGCTTTCTTGTGATCTGATCAGTC 1200
DB 1141 TGTATTCAGAGATCATTTGGGATCATAGATATTTGCTTTCTTGTGATCTGATCAGTC 1200
QY 1201 TTGAGTTTATAGTGTGAATGGGGTCTGGAATTAAGTGTACAGAACCGCATTTGGTTTG 1260
DB 1201 TTGAGTTTATAGTGTGAATGGGGTCTGGAATTAAGTGTGTACAGAACCGCATTTGGTTTG 1260
QY 1261 TCTTGGGAAAAAAGCAACTCAGGTTGGTGAAGTGAAGAAAGTGTGGAAAAACATCTA 1320
DB 1261 TCTTGGGAAAAAAGCAACTCAGGTTGGTGAAGTGAAGAAAGTGTGGAAAAACATCTA 1320
QY 1321 GCTGTGAAATGATCATTTGAGTCTAAGTTTGTAGAGGAGGAGTGCATGAGAGAA 1380
DB 1321 GCTGTGAAATGATCATTTGAGTCTAAGTTTGTAGAGGAGGAGTGCATGAGAGAA 1380
QY 1381 ATTAGAAGAAAGTGGGAAATGGGAAGCTTAAAGTGGTGGTGGGAGACTGTT 1440
DB 1381 ATTAGAAGAAAGTGGGAAATGGGAAGCTTAAAGTGGTGGTGGGAGACTGTT 1440
QY 1441 GCCCTGTGATGTCTATGGGAAGCAAAATGGAGGGGTGTGAATCTGATCCGCTGAA 1500
DB 1441 GCCCTGTGATGTCTATGGGAAGCAAAATGGAGGGGTGTGAATCTGATCCGCTGAA 1500
QY 1501 CATTTGAACTATGAAAAAAGTTTGAAGTGTGGGCTCAATAAAGCCCTAGAGACTT 1560
DB 1501 CATTTGAACTATGAAAAAAGTTTGAAGTGTGGGCTCAATAAAGCCCTAGAGACTT 1560
QY 1561 ACTGAAGAGGCTTAAATTTTCAATGAGATGTTTATGTACATTTCTTGTCTAAGCATG 1620
DB 1561 ACTGAAGAGGCTTAAATTTTCAATGAGATGTTTATGTACATTTCTTGTCTAAGCATG 1620
QY 1621 CAATTTTCTGAGATAGAGTTTGAAGTTTATCTCTTACAGAAATTTGATTAACCTCTCG 1680
DB 1621 CAATTTTCTGAGATAGAGTTTGAAGTTTATCTCTTACAGAAATTTGATTAACCTCTCG 1680
QY 1681 CTCTTTTCAAAATGCAAACTCAGTAGATTTTCCAAAGATGAAGAGGCTCTCTGTA 1740
DB 1681 CTCTTTTCAAAATGCAAACTCAGTAGATTTTCCAAAGATGAAGAGGCTCTCTGTA 1740
QY 1741 AGGGAAGTACTGATTTCTGGGCTCAGAGGAATTCAGAGTCTCAGAAATCTAGTCA 1800
DB 1741 AGGGAAGTACTGATTTCTGGGCTCAGAGGAATTCAGAGTCTCAGAAATCTAGTCA 1800

QY	1801	TGTTGAAATCTAGGCTCATTTGGGGCAAAATTA	CTTAAGAGCTTTAATTCAGGTGAATTTGT	1860
Db	1801	TGTTGAAATCTAGGCTCATTTGGGGCAAAATTA	CTTAAGAGCTTTAATTCAGGTGAATTTGT	1860
QY	1861	ACTGTAACCTCATGGGTGTGGAGGTCA	TAAAGTTTCAGGCAACAATTAAATATGTTATG	1920
Db	1861	ACTGTAACCTCATGGGTGTGGAGGTCA	TAAAGTTTCAGGCAACAATTAAATATGTTATG	1920
QY	1921	CTTGTTATTGTTTTATATAGCATATTTGAAG	GTGATCACTGCAATATCCAGAGAAATGTGCAA	1980
Db	1921	CTTGTTATTGTTTTATATAGCATATTTGAAG	GTGATCACTGCAATATCCAGAGAAATGTGCAA	1980
QY	1981	AAGCTGAAGACACAGGTGAAAAAGTGAAG	CTGTAACTGTAAGTCAATGTAAGTCAATG	2040
Db	1981	AAGCTGAAGACACAGGTGAAAAAGTGAAG	CTGTAACTGTAAGTCAATGTAAGTCAATG	2040
QY	2041	AGGAGAGACAAATGTGTTTTCTTTCCTTCT	CTTCCCATGATCACTTTGGATTTTCA	2100
Db	2041	AGGAGAGACAAATGTGTTTTCTTTCCTTCT	CTTCCCATGATCACTTTGGATTTTCA	2100
QY	2101	CTTATATCTCCACCAACGAGGCGATTA	CTTTGGTGTCTGTATGTATAGATATATCTATA	2160
Db	2101	CTTATATCTCCACCAACGAGGCGATTA	CTTTGGTGTGTCTGTATGTATAGATATATCTATA	2160
QY	2161	TATCTAGATGTCAAGTTTCCAAATCTTG	CAAAATTTGTAATTTCTAAGACTGATGCAAT	2220
Db	2161	TATCTAGATGTCAAGTTTCCAAATCTTG	CAAAATTTGTAATTTCTAAGACTGATGCAAT	2220
QY	2221	TAGCTTGTCTTAGTCATTAACCTCAGAT	CTTGGGGATGTGTACATGTGCGAGAGATAGGCGTA	2280
Db	2221	TAGCTTGTCTTAGTCATTAACCTCAGAT	CTTGGGGATGTGTACATGTGCGAGAGATAGGCGTA	2280
QY	2281	GAATCGAGGTGCTCGTAATCCCAAGCC	ACGACTTTCCCGGTGGTGAATACAGATTAGTTT	2340
Db	2281	GAATCGAGGTGCTCGTAATCCCAAGCC	ACGACTTTCCCGGTGGTGAATACAGATTAGTTT	2340
QY	2341	TGTATACCATTAATCTTAAGGAAATTTT	CAGATTCCTATTTGATCATGTATATCTGAAGAAG	2400
Db	2341	TGTATACCATTAATCTTAAGGAAATTTT	CAGATTCCTATTTGATCATGTATATCTGAAGAAG	2400
QY	2401	TACTTGTTTAAAAACAGAAAAATGCC	CTATGCGCAAAATTTATTTGAAGTCAATTTTGAAGT	2460
Db	2401	TACTTGTTTAAAAACAGAAAAATGCC	CTATGCGCAAAATTTATTTGAAGTCAATTTTGAAGT	2460
QY	2461	CATTAATAGCATGTCTTTGGAACCTTG	GAAAGATAAATCTCAGAACATATGAAAAAAGACGTGG	2520
Db	2461	CATTAATAGCATGTCTTTGGAACCTTG	GAAAGATAAATCTCAGAACATATGAAAAAAGACGTGG	2520
QY	2521	ACTTGCAATATAGGGCTAATTTCTTG	AGATTAATTAACACTTAATTTGAAATTAATCAATATATC	2580
Db	2521	ACTTGCAATATAGGGCTAATTTCTTG	AGATTAATTAACACTTAATTTGAAATTAATCAATATATC	2580
QY	2581	TATCAGATATTTGATTAATAGTTTAA	AAAGCAGACAGACAACCCCGATCTCTTTTATACAG	2640
Db	2581	TATCAGATATTTGATTAATAGTTTAA	AAAGCAGACAGACAACCCCGATCTCTTTTATACAG	2640
QY	2641	GTTCAAAATAGAGTAAAAAATATTA	GTATAGTAAGATTTATATAGTTTAAATGGAAGTCTGAATT	2700
Db	2641	GTTCAAAATAGAGTAAAAAATATTA	GTATAGTAAGATTTATATAGTTTAAATGGAAGTCTGAATT	2700
QY	2701	GGTAAAGCTTTTTTTCTTCTCCCTC	CTCCCATCAAGACCTTCATATCTAGTTTCTCCCTCA	2760
Db	2701	GGTAAAGCTTTTTTTCTTCTCCCTC	CTCCCATCAAGACCTTCATATCTAGTTTCTCCCTCA	2760
QY	2761	CTCCCTCAACAAATCCCTAGGAGAC	ATTATCAATGTGGGCTGTGTACATTTCTATAG	2820
Db	2761	CTCCCTCAACAAATCCCTAGGAGAC	ATTATCAATGTGGGCTGTGTACATTTCTATAG	2820
QY	2821	TGAATGATACATCATGTGGCTAT	TTTGTGTAAAAAACAACAATATGGAAGCTTATAGCTA	2880
Db	2821	TGAATGATACATCATGTGGCTAT	TTTGTGTAAAAAACAACAATATGGAAGCTTATAGCTA	2880

QY	2881	ACAAATAGGATCTCAACCCAAAACCGGAGGAATGATTGGAGCACTGAAAGTGAAGCTTCTT	2940
Db	2881	ACAAATAGGATCTCAACCCAAAACCGGAGGAATGATTGGAGCACTGAAAGTGAAGCTTCTT	2940
QY	2941	GCAAGCAGGTGCACCTAAATGCTCAGAAACATGAAAGCTCCAGTGTGGAATTTTACGT	3000
Db	2941	GCAAGCAGGTGCACCTAAATGCTCAGAAACATGAAAGCTCCAGTGTGGAATTTTACGT	3000
QY	3001	AACAAGCTTAACTTAAATCCCCCTTTTCCCTCTTGACTTTTAAAAAAGCGTTTCTC	3060
Db	3001	AACAAGCTTAACTTAAATCCCCCTTTTCCCTCTTGACTTTTAAAAAAGCGTTTCTC	3060
QY	3061	CTGAGCATCATTTAATGAGTGTGACTGTTTCTTCCCTTGATTAATGGAAGCTTGTGACT	3120
Db	3061	CTGAGCATCATTTAATGAGTGTGACTGTTTCTTCCCTTGATTAATGGAAGCTTGTGACT	3120
QY	3121	TTAAATTTGTGAAGCCCAAGTTCTCTGTATATGAACATACTATCTGACATGGAGGCGTAA	3180
Db	3121	TTAAATTTGTGAAGCCCAAGTTCTCTGTATATGAACATACTATCTGACATGGAGGCGTAA	3180
QY	3181	TGTTAGCATGTCACAGACAAAGGCATGCTTTACACATCTTGCTTAAAAAATTAAGTATTC	3240
Db	3181	TGTTAGCATGTCACAGACAAAGGCATGCTTTACACATCTTGCTTAAAAAATTAAGTATTC	3240
QY	3241	ATCTTGCTTGTGTCTTTAGAAAAGTGAAGTGTGAGAGAGAGAATCTCATGTGTACTG	3300
Db	3241	ATCTTGCTTGTGTCTTTAGAAAAGTGAAGTGTGAGAGAGAGAATCTCATGTGTACTG	3300
QY	3301	TGTGATTTTCAAGACCTTTAATCCATTTTGAAGAATCAATTTATATTTGCAATGGGTT	3360
Db	3301	TGTGATTTTCAAGACCTTTAATCCATTTTGAAGAATCAATTTATATTTGCAATGGGTT	3360
QY	3361	GCCATGTGGAAGAGATTAATGCTTTTGTGTGTAGCTTACAGAAAGACACAGAGGGAGA	3420
Db	3361	GCCATGTGGAAGAGATTAATGCTTTTGTGTGTAGCTTACAGAAAGACACAGAGGGAGA	3420
QY	3421	GCAAATGTTGTTCAAGAAAAGATCAACAGAGAGAAAATGTCAGAGCTGTCTGAAATAGG	3480
Db	3421	GCAAATGTTGTTCAAGAAAAGATCAACAGAGAGAAAATGTCAGAGCTGTCTGAAATAGG	3480
QY	3481	GTCGTTTTGGGAGGCATTAATTCCTCTCGTTGGGGGTAAAGCAGAACCGAGTTGGTA	3540
Db	3481	GTCGTTTTGGGAGGCATTAATTCCTCTCGTTGGGGGTAAAGCAGAACCGAGTTGGTA	3540
QY	3541	GTTAAATGTCATGACAGACAGTGAAGGGAGCATTAACCTTAAATCTTTATATGCTCTGGAG	3600
Db	3541	GTTAAATGTCATGACAGACAGTGAAGGGAGCATTAACCTTAAATCTTTATATGCTCTGGAG	3600
QY	3601	TCTTTGAGATAGAAAAGATATCTTTTGTGCGCTTATGTCAAAAGAAAGATGGAAGGTGA	3660
Db	3601	TCTTTGAGATAGAAAAGATATCTTTTGTGCGCTTATGTCAAAAGAAAGATGGAAGGTGA	3660
QY	3661	AAGGCGGAGAGAAAGCAGGAAAAGAGAACCATGTATATATAGAGACATGTGTACA	3720
Db	3661	AAGGCGGAGAGAAAGCAGGAAAAGAGAACCATGTATATATAGAGACATGTGTACA	3720
QY	3721	AGGTTTTCTGGAATAATATGCAATATGATATGATTAGAGGAATTCAGTGGGAATGCTT	3780
Db	3721	AGGTTTTCTGGAATAATATGCAATATGATATGATTAGAGGAATTCAGTGGGAATGCTT	3780
QY	3781	TTCACTTGAATTTGGGTTTCTCTTCGATTAAGTTTGGATCCTCATCTGCATTGTGACTT	3840
Db	3781	TTCACTTGAATTTGGGTTTCTCTTCGATTAAGTTTGGATCCTCATCTGCATTGTGACTT	3840
QY	3841	GGAAGAGAGAAAGATGAAATGTTAGACCTATATCTGTTTTCTATTAACTAAGCAAGTG	3900
Db	3841	GGAAGAGAGAAAGATGAAATGTTAGACCTATATCTGTTTTCTATTAACTAAGCAAGTG	3900
QY	3901	GAAAAGCTTATTTTGGATTTTTCOCACAAAGGAAAACCTTCTTTTACCTGTTTGCA	3960
Db	3901	GAAAAGCTTATTTTGGATTTTTCOCACAAAGGAAAACCTTCTTTTACCTGTTTGCA	3960
QY	3961	AAAAAGTGAATAGAAAAGCCTTAAATGTATTTGTGTAATACATGCTTCAAGTCAATTTG	4020

Db 3961 AAAAGTGAATATGAAAAAGCCCTTAATGTAATGTGTAATACATGCTTCAAAAGTCATTG 4020
Qy 4021 AGTAGAGATGTTTTAAATCAGAGATGTCCTCAATCATTTGGCTTCCCTGGACCACTTGA 4080
Db 4021 AGTAGAGATGTTTTAAATCAGAGATGTCCTCAATCATTTGGCTTCCCTGGACCACTTGA 4080
Qy 4081 GAATGTTCTTGTACACATTAATAATACAGAACATAGCTGATAGCTTAATAAAGTCCA 4140
Db 4081 GAATGTTCTTGTACACATTAATAATACAGAACATAGCTGATAGCTTAATAAAGTCCA 4140
Qy 4141 TGCATTAATCTCATCTGTTTTAAGAAAGTTATGAATTTCTGTAGGGGTGATCAAG 4200
Db 4141 TGCATTAATCTCATCTGTTTTAAGAAAGTTATGAATTTCTGTAGGGGTGATCAAG 4200
Qy 4201 CTGTCTGGGCAATGTCGGGCTGTGGCTGACAGGTTGAGACAGCTCTTAATAAGTATC 4260
Db 4201 CTGTCTGGGCAATGTCGGGCTGTGGCTGACAGGTTGAGACAGCTCTTAATAAGTATC 4260
Qy 4261 TGTCAATAGTATGTTTGGAGCTGCAGAAACAGGCCAGCATATATGGTGGCACTGGGAT 4320
Db 4261 TGTCAATAGTATGTTTGGAGCTGCAGAAACAGGCCAGCATATATGGTGGCACTGGGAT 4320
Qy 4321 CCCCCAGATCCAGGCTCACTTCACTGCTCTGCTGCTGCTTAAGAAAGGGGTGTCACATC 4380
Db 4321 CCCCCAGATCCAGGCTCACTTCACTGCTCTGCTGCTGCTTAAGAAAGGGGTGTCACATC 4380
Qy 4381 TCTGCCAGCTTTTAAACAGCTTCAATAGTGTAGAGTGCACCTGAATTTGATGCTGCTG 4440
Db 4381 TCTGCCAGCTTTTAAACAGCTTCAATAGTGTAGAGTGCACCTGAATTTGATGCTGCTG 4440
Qy 4441 GTGGCTCTCAGTCCAGAGAGCCGTCATTTTAACTCTTTGGCAATATATCAATATCTAA 4500
Db 4441 GTGGCTCTCAGTCCAGAGAGCCGTCATTTTAACTCTTTGGCAATATATCAATATCTAA 4500
Qy 4501 AGGGATATTACATGATGTTTACAAATGCTTAAATCTGCTTCCATCAAC 4560
Db 4501 AGGGATATTACATGATGTTTACAAATGCTTAAATCTGCTTCCATCAAC 4560
Qy 4561 TAACTTGGCAATTTCTAAATTTGTCTCACTTAAAGAAATGCGATTAATGCTCAATACTT 4620
Db 4561 TAACTTGGCAATTTCTAAATTTGTCTCACTTAAAGAAATGCGATTAATGCTCAATACTT 4620
Qy 4621 TTGATTTCTTATTTTCAAGCTTGAAGAGATGAGAGATCAAGCAATTTGAGAACTGG 4680
Db 4621 TTGATTTCTTATTTTCAAGCTTGAAGAGATGAGAGATCAAGCAATTTGAGAACTGG 4680
Qy 4681 ATTGCTGTTTATGCTCTGAGAAATGCTGATTTGACAGAGCAAGCTGAATAATGA 4740
Db 4681 ATTGCTGTTTATGCTCTGAGAAATGCTGATTTGACAGAGCAAGCTGAATAATGA 4740
Qy 4741 ATAACTAAACCCCTTTCCCTGCTAGAAATTAACAATTAAGTACCCCAAGGCAATTTT 4797
Db 4741 ATAACTAAACCCCTTTCCCTGCTAGAAATTAACAATTAAGTACCCCAAGGCAATTTT 4797

RESULT 2
AAD30646
ID AAD30646 standard; DNA; 4797 BP.
XX
XX AAD30646:
XX
XX 21-MAY-2002 (first entry)
XX
XX Human TIF genomic DNA.
XX
XX T cell derived inducible factor; TIF; interleukin-21; IL-21; human;
XX STAT transcription factor; acute phase protein; inflammation;
XX chromosome 12; de.
XX Homo sapiens.
XX OS
XX
XX MO2002:0393-A2.

XX
PD 07-FEB-2002.
XX
XX 27-JUN-2001; 2001MO-US20485.
XX
XX 27-JUL-2000; 2000US-0626617.
XX
XX (LUDM-) LUDWIG INST CANCER RES.
XX
XX Dumoutier L, Renaud J;
XX
XX WPI; 2002-195964/25.
XX
XX Stimulating expression of STAT transcription factor and inducing
XX production of acute phase protein in a cell, involves contacting a cell
XX capable of expressing STAT with T cell derived inducible factors -
XX
XX Claim 6; Page 56-58; 64pp; English.
XX
XX The invention relates to nucleic acid molecules encoding T cell
XX derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
XX TIF polynucleotides are upregulated by the cytokine, IL-9, IL-TIF or
XX IL-21 molecules are implicated in activation of STAT transcription
XX factors, acute phase proteins and inflammation. The present sequence
XX is human TIF genomic DNA located on chromosome 12.
XX
SQ Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;
Query Match 100.0%; Score 4797; DB 24; Length 4797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGCACAGCAGAAATCTTCAAGAGGTTCTCTTCCCACTGACAGCTGCTGAGTTAG 60
Db 1 TGCACAGCAGAAATCTTCAAGAGGTTCTCTTCCCACTGACAGCTGCTGAGTTAG 60
Qy 61 AATGTTGCAATGCGCGCTGCAAGAAATCTGAGCTCTTCTTAAGGGGACCTGG 120
Db 61 AATGTTGCAATGCGCGCTGCAAGAAATCTGAGCTCTTCTTAAGGGGACCTGG 120
Qy 121 CCACAGCTGCTCTCTCTCTGAGCTCTTGTGACAGAGGAGAGAGAGCTGCGGCATCA 180
Db 121 CCACAGCTGCTCTCTCTCTGAGCTCTTGTGACAGAGGAGAGAGAGCTGCGGCATCA 180
Qy 181 GCTCCACTGAGAGCTTGAACAAGTCCAGTCCAGAGCCCTATATACCAACCGCACT 240
Db 181 GCTCCACTGAGAGCTTGAACAAGTCCAGTCCAGAGCCCTATATACCAACCGCACT 240
Qy 241 TCAATGCTGCTAAGAGAGTATCATCTCAATCTGCTCTTCTGCTGAGTCTTCTGGA 300
Db 241 TCAATGCTGCTAAGAGAGTATCATCTCAATCTGCTCTTCTGCTGAGTCTTCTGGA 300
Qy 301 ATCCAAATAGTCTTAACTTTTCTTCAAGAGCTCTTAAGAGCTTGAAGAACCACTGT 360
Db 301 ATCCAAATAGTCTTAACTTTTCTTCAAGAGCTCTTAAGAGCTTGAAGAACCACTGT 360
Qy 361 TTATCCCTGAGGAGTAAATTTCTGTTTTTCAAGAGCTCTTGGAAATGCGCTT 420
Db 361 TTATCCCTGAGGAGTAAATTTCTGTTTTTCAAGAGCTCTTGGAAATGCGCTT 420
Qy 421 TTTTCTTCTTGAATCT 480
Db 421 TTTTCTTCTTGAATCT 480
Qy 481 CCAAGAGGCGGCACTCAGTAATCATCTGATGATTTTCTCTTATGCTCTGTG 540
Db 481 CCAAGAGGCGGCACTCAGTAATCATCTGATGATTTTCTCTTATGCTCTGTG 540
Qy 541 CATGTTCTAACTGACACACATCTGAATTTCTGCTTTTATGATGTTGCTCT 600
Db 541 CATGTTCTAACTGACACACATCTGAATTTCTGCTTTTATGATGTTGCTCT 600
Qy 601 GGGAGAGCGGAGTGGGCAATGTCATGATAAATTTTCTATTTGCTCAATGCC 660

Db	601	GGGGAGACGGGATGGGGACATGCTCATGTAATAATTTTTTTTCTATTTCTCAAGTTC	660
Oy	661	AGACCCCTTAGTCCTTTCTTCTCTTCCAGAGCTAGCTTGAGTAAACAACAAGACGTTG	720
Db	661	AGACCCCTTAGTCCTTTCTTCTCTTCCAGAGCTAGCTTGAGTAAACAACAAGACGTTG	720
Oy	721	TCTCATTTGGGAGAAACTGTGTTCACGGAAGTCAGTGAAGCTACAGTTGTGACGACAGG	780
Db	721	TCTCATTTGGGAGAAACTGTGTTCACGGAAGTCAGTGAAGCTACAGTTGTGACGACAGG	780
Oy	781	CCGTGTGCGCTCCATGCGTACTTGGGGTGGGTGATGATGATGTTTAACTTATCCCTTA	840
Db	781	CCGTGTGCGCTCCATGCGTACTTGGGGTGGGTGATGATGATGTTTAACTTATCCCTTA	840
Oy	841	TGACCCCTTTCTGTTTCCCTTCCACTGTGAGTGAAGTGAAGGCTGTATCTGATGAACAG	900
Db	841	TGACCCCTTTCTGTTTCCCTTCCACTGTGAGTGAAGTGAAGGCTGTATCTGATGAACAG	900
Oy	901	GTGCTGAACCTCACCCCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGTTTCCAGCCTTAT	960
Db	901	GTGCTGAACCTCACCCCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGTTTCCAGCCTTAT	960
Oy	961	ATGCAAGAGGTGTGTCCTTCTTGCGCAAGCTCAGCAACAGGCTTAAGCAACATGTGTAAGT	1020
Db	961	ATGCAAGAGGTGTGTCCTTCTTGCGCAAGCTCAGCAACAGGCTTAAGCAACATGTGTAAGT	1020
Oy	1021	TCACCTCTCAGACCTATAGCCCACTAACCCCTCCTTCCCTTCCACAGAGACCCCTTAC	1080
Db	1021	TCACCTCTCAGACCTATAGCCCACTAACCCCTCCTTCCCTTCCACAGAGACCCCTTAC	1080
Oy	1081	CCCAACTCTCTCTCTTCCCTTACCCCTTACAGCTAGCAGGAAAGAGTCTTGCGACAG	1140
Db	1081	CCCAACTCTCTCTCTTCCCTTACCCCTTACAGCTAGCAGGAAAGAGTCTTGCGACAG	1140
Oy	1141	TGTTATCAGAGAGTCATTTGGGATCATAGAGTATTTGCTTTGCTTTGACTGACATC	1200
Db	1141	TGTTATCAGAGAGTCATTTGGGATCATAGAGTATTTGCTTTGCTTTGACTGACATC	1200
Oy	1201	TTGAGTTTATAGTGTGAATGGGGTCTTGAACTTAAGTATCAGAACCCGATTTGTTG	1260
Db	1201	TTGAGTTTATAGTGTGAATGGGGTCTTGAACTTAAGTATCAGAACCCGATTTGTTG	1260
Oy	1261	TCTTCGGAAGAAAGGCAACTCAGGTTGCGTATAGTAGAAGAGTGTGGGAAACATCTA	1320
Db	1261	TCTTCGGAAGAAAGGCAACTCAGGTTGCGTATAGTAGAAGAGTGTGGGAAACATCTA	1320
Oy	1321	GCTGTGGAATGATCCATTGAGTCTAAGTTGTTGAGGGGAGGGGATGCGATGAGAGAA	1380
Db	1321	GCTGTGGAATGATCCATTGAGTCTAAGTTGTTGAGGGGAGGGGATGCGATGAGAGAA	1380
Oy	1381	ATTGAGAGAGAAAGTGGGAAATGGGAAAGCTTTAAAGTGGTGTGGCTCGGACAGCTGT	1440
Db	1381	ATTGAGAGAGAAAGTGGGAAATGGGAAAGCTTTAAAGTGGTGTGGCTCGGACAGCTGT	1440
Oy	1441	GCCGCTGTGATGTCATGGAAGGCCACAAATTCGAAGCGTGTGAATTGATGCGGCTGAA	1500
Db	1441	GCCGCTGTGATGTCATGGAAGGCCACAAATTCGAAGCGTGTGAATTGATGCGGCTGAA	1500
Oy	1501	CATTTGAAACTATGAAAAAAGTTTGAATGAGTGCGCCAGTAAAGAGCCCTTAGACTT	1560
Db	1501	CATTTGAAACTATGAAAAAAGTTTGAATGAGTGCGCCAGTAAAGAGCCCTTAGACTT	1560
Oy	1561	ACTGAAGAGGCTTAATTTTCAATGAGATGTTTATATGTAATTTCTTGTCTTAAGCATG	1620
Db	1561	ACTGAAGAGGCTTAATTTTCAATGAGATGTTTATATGTAATTTCTTGTCTTAAGCATG	1620
Oy	1621	CAATTTTCTGAGATAGCATGAGGTTTATTTCTTCAAGAAATTTGCATTAACATCACTCG	1680
Db	1621	CAATTTTCTGAGATAGCATGAGGTTTATTTCTTCAAGAAATTTGCATTAACATCACTCG	1680
Oy	1681	CTCTTTCCAAATCAAACTCAGTAGAATTTCCCAAAGATGAAGAGGCTCTTGTGA	1740

Db	1681	CTCTTTCCAAATATGCAAACTCAGTAGGATTTCCCAAAATGAAGAGAGCTCTCTGTGA	1740
Qy	1741	AGGAGAGTGAACGTGATTTCTGGCGTCCAAAGGAAATTCAAAGCTCAGGAAATCTAGTCCAC	1800
Db	1741	AGGGAATGATCGAATTTCTGGCGTCCAAAGGAAATTCAAAGAGCTCAGGAAATCTAGTCCAC	1800
Qy	1801	TGTTGAAATCTAGGTCATTTGGGCAAAATTACTTAAGCTTTAAATTCGAGGTGAATTTGT	1860
Db	1801	TGTTGAAATCTAGGTCATTTGGGCAAAATTACTTAAGCTTTAAATTCGAGGTGAATTTGT	1860
Qy	1861	ACTGTAACCTCAATGGGTGTGGAGGTTCAATAAGTTTCAGACCAACATTAAGATGTTATG	1920
Db	1861	ACTGTAACCTCAATGGGTGTGGAGGTTCAATAAGTTTCAGACCAACATTAAGATGTTATG	1920
Qy	1921	CTTGATTAATGTTTATATAGCATATTTGAAGGTGATGACCTGCATATCCAGAGGAAATGTGCAA	1980
Db	1921	CTTGATTAATGTTTATATAGCATATTTGAAGGTGATGACCTGCATATCCAGAGGAAATGTGCAA	1980
Qy	1961	AAGCTGAAGACACAGTGAAGAAAGGTAGAGCTGAATACTGTCAATGCTTAAGTCAATGCAT	2040
Db	1961	AAGCTGAAGACACAGTGAAGAAAGGTAGAGCTGAATACTGTCAATGCTTAAGTCAATGCAT	2040
Qy	2041	AGGAGAGCAAAATGTTGTTTTCTTCTCTTCTTCTTCCATCAATCACTTTGGATTTTTTCA	2100
Db	2041	AGGAGAGCAAAATGTTGTTTTCTTCTCTTCTTCTTCCATCAATCACTTTGGATTTTTTCA	2100
Qy	2101	CTTGATTTCTCTACCAACGAGGCGATTACTTTGGGTCTGTGTATGTATATATCTATA	2160
Db	2101	CTTGATTTCTCTACCAACGAGGCGATTACTTTGGGTCTGTGTATGTATATATCTATA	2160
Qy	2161	TATCTAGATGTCAGTTTCCAAATCTTGCAATTTGAGAAATCTAGAACTGTGGAGTCT	2220
Db	2161	TATCTAGATGTCAGTTTCCAAATCTTGCAATTTGAGAAATCTAGAACTGTGGAGTCT	2220
Qy	2221	TAGCTTGTCTAGTCACTAATCCTCAGATCTTGSSGATGTCTAGTGGCAGAGATAGGCTA	2280
Db	2221	TAGCTTGTCTAGTCACTAATCCTCAGATCTTGSSGATGTCTAGTGGCAGAGATAGGCTA	2280
Qy	2281	GAAATGACAGTGTCCGGAATCCCAAGCCAGCACTTTCCCGGTGGGATAGACAGATAGTTT	2340
Db	2281	GAAATGACAGTGTCCGGAATCCCAAGCCAGCACTTTCCCGGTGGGATAGACAGATAGTTT	2340
Qy	2341	TGGTAACATTAATCTTAGGGAAATTTCCAGATTCCTATTTGACTCATGTAACTGGAAG	2400
Db	2341	TGGTAACATTAATCTTAGGGAAATTTCCAGATTCCTATTTGACTCATGTAACTGGAAG	2400
Qy	2401	TACTTGTTTAAAAACAGAAAAATGCCCTATGGGCAATTTATTTGAAGTCATTTTGAAGT	2460
Db	2401	TACTTGTTTAAAAACAGAAAAATGCCCTATGGGCAATTTATTTGAAGTCATTTTGAAGT	2460
Qy	2461	CATTAAATGCAATGCTTTGAAACCTTGGAAGAAATTAACCTCAGAAACATGGAAGAGCTGG	2520
Db	2461	CATTAAATGCAATGCTTTGAAACCTTGGAAGAAATTAACCTCAGAAACATGGAAGAGCTGG	2520
Qy	2521	ACTTGCAATATAGGGCTAAATTTCTGAGATTAATAACACTTAATTTGAATTAATCAATAATC	2580
Db	2521	ACTTGCAATATAGGGCTAAATTTCTGAGATTAATAACACTTAATTTGAATTAATCAATAATC	2580
Qy	2581	TATCAGATTAATGATTAATGTTTAAAAAGCAAGACAGACACCCGATCTCTTTTATACG	2640
Db	2581	TATCAGATTAATGATTAATGTTTAAAAAGCAAGACAGACACCCGATCTCTTTTATACG	2640
Qy	2641	GTTCAAAATAGAGTAATAAATATTTAGTAAGATTTATTTAGTTTAAATGGAAGTCTGAAT	2700
Db	2641	GTTCAAAATAGAGTAATAAATATTTAGTAAGATTTATTTAGTTTAAATGGAAGTCTGAAT	2700
Qy	2701	GGTAAGCTTTTTTTCTTCTCTCTCTCCATCAAGACCTTCAATCTAGTTTCTTCTTCA	2760
Db	2701	GGTAAGCTTTTTTTCTTCTCTCTCTCCATCAAGACCTTCAATCTAGTTTCTTCTTCA	2760
Qy	2761	CTTCCCTCAACAAATCCCTTAGGGAGATTTATTCATGTGTGGGCTGTGTATCTTATAG	2820
Db	2761	CTTCCCTCAACAAATCCCTTAGGGAGATTTATTCATGTGTGGGCTGTGTATCTTATAG	2820

2821 TGAATGATACCATCATGTGGCCTATTTGGTGAAGAAACAACATGAGAGGCTTGGACTA 2880
2821 TGAATGATACCATCATGTGGCCTATTTGGTGAAGAAACAACATGAGAGGCTTGGACTA 2880
2881 ACAATATGACTCACCCCAAAACCGAGAGATGATTTAGAGAGCGTAAAGTACGCTCTT 2940
2881 ACAATATGACTCACCCCAAAACCGAGAGATGATTTAGAGAGCGTAAAGTACGCTCTT 2940
2941 GCAGCAGGTACAACTAAATCTCAGAAACATGAAAGGCTCCAGTTGATGGAATTTTCAGT 3000
2941 GCAGCAGGTACAACTAAATCTCAGAAACATGAAAGGCTCCAGTTGATGGAATTTTCAGT 3000
3001 AACAGCTTAACCTTAATTTCCCTTTTCCCTCTGACTTTTAAAGGCTTCTTC 3060
3001 AACAGCTTAACCTTAATTTCCCTTTTCCCTCTGACTTTTAAAGGCTTCTTC 3060
3061 CTGAGCATCATTTAATGAGTGTGACTGTTCTTCTTGATTAATGAAAGGCTTGTAGTT 3120
3061 CTGAGCATCATTTAATGAGTGTGACTGTTCTTCTTGATTAATGAAAGGCTTGTAGTT 3120
3121 TTAATTTGTGAAGCCCACTTCTTGTATAGAACTATATATAGACATGAGAGGCTGAA 3180
3121 TTAATTTGTGAAGCCCACTTCTTGTATAGAACTATATATAGACATGAGAGGCTGAA 3180
3181 TGTAGCATGCCACAGACAGGAGCATGCTTACACATCTTGCTTAAATAATTAATGATTC 3240
3181 TGTAGCATGCCACAGACAGGAGCATGCTTACACATCTTGCTTAAATAATTAATGATTC 3240
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3241 ATCTTGCTTGTGTCTTTAGAAAGTGAAGTGTGAGAGAGAGAACTCATGATGATCTG 3300
3301 TGTGATTTTCAAGACCTTTAATCATTTTGAAGAACTCAATTTCAATTTGCAATGGTT 3360
3301 TGTGATTTTCAAGACCTTTAATCATTTTGAAGAACTCAATTTCAATTTGCAATGGTT 3360
3361 GCCATGTGAGAGAGTATGCTTTTGTGCTGAGTCTGAGAAAGCAGAGAGAGAGA 3420
3361 GCCATGTGAGAGAGTATGCTTTTGTGCTGAGTCTGAGAAAGCAGAGAGAGAGA 3420
3421 GCATGTTGTTTCAGAGAAAGATCAACAGAGAGAGAACTGTGAGAGCTGTCTGAATAGG 3480
3421 GCATGTTGTTTCAGAGAAAGATCAACAGAGAGAGAACTGTGAGAGCTGTCTGAATAGG 3480
3481 GTGCTTTTGGAGGAGATTAATTTCCCTCTCTGTTGGGGGTAAAGCAAGCAGGTTGGTA 3540
3481 GTGCTTTTGGAGGAGATTAATTTCCCTCTCTGTTGGGGGTAAAGCAAGCAGGTTGGTA 3540
3541 GTAAATGATGATGACAGACAGTGGGAGAGATTAATTTTAAATTTCTTTATAGTCTTGGAG 3600
3541 GTAAATGATGATGACAGACAGTGGGAGAGATTAATTTTAAATTTCTTTATAGTCTTGGAG 3600
3601 TCTTTGAGATGAGAAAGAAATCTTTTGGCCTTAATGTCAAAAAGAGATGAGAAAGTGA 3660
3601 TCTTTGAGATGAGAAAGAAATCTTTTGGCCTTAATGTCAAAAAGAGATGAGAAAGTGA 3660
3661 AAGGCGGAGAAAG 3720
3661 AAGGCGGAGAAAG 3720
3721 AGGTTTTCTTGAATTAATGCAAAATATGATATAGAGAGAAATTCAGTAGGAGATGCTT 3780
3721 AGGTTTTCTTGAATTAATGCAAAATATGATATAGAGAGAAATTCAGTAGGAGATGCTT 3780
3781 TTCACCTGAATTTGGGTTTCTCTTGATTAAGTTGGAGTCTCATCTGCAATTTGACTT 3840
3781 TTCACCTGAATTTGGGTTTCTCTTGATTAAGTTGGAGTCTCATCTGCAATTTGACTT 3840
3841 GGAGAGAGAAAGAAATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900
3841 GGAGAGAGAAAGAAATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900

3901 GAAAGACTATTTGGTATTTTCCACAAAAGTGAAGAACTTTCTTTACTGTTTGTCA 3960
3901 GAAAGACTATTTGGTATTTTCCACAAAAGTGAAGAACTTTCTTTACTGTTTGTCA 3960
3961 AAAAGTGAAGTGAAGAAAGGCTTAAATGATTTGGTGAATTCATGTTCAAAAGTCAATTG 4020
3961 AAAAGTGAAGTGAAGAAAGGCTTAAATGATTTGGTGAATTCATGTTCAAAAGTCAATTG 4020
4021 AGTAGAGATGTTTAAATTCAGAGAGTGCATCAATTTGGCTTCCCTGGACACCTTGAAA 4080
4021 AGTAGAGATGTTTAAATTCAGAGAGTGCATCAATTTGGCTTCCCTGGACACCTTGAAA 4080
4081 GAATTTCTTGGTACACATTAATAACAAGAAATAGCTGATGAGCTTAAAGTCA 4140
4081 GAATTTCTTGGTACACATTAATAACAAGAAATAGCTGATGAGCTTAAAGTCA 4140
4141 TGCATTAATCTCATCTGTTTAAAGAAATTTGATGAATTTCTTTAGGTCATTTCAAG 4200
4141 TGCATTAATCTCATCTGTTTAAAGAAATTTGATGAATTTCTTTAGGTCATTTCAAG 4200
4201 CTGTCTGGGCGCATGCGGCGCTGGGCTGGAGTGGAGCAAGCTCTTAATGATATC 4260
4201 CTGTCTGGGCGCATGCGGCGCTGGGCTGGAGTGGAGCAAGCTCTTAATGATATC 4260
4261 TGTATATGATGATTTTGGAGCTGCAGAAACAGGCCAATTAATGAGTGCATCGGAT 4320
4261 TGTATATGATGATTTTGGAGCTGCAGAAACAGGCCAATTAATGAGTGCATCGGAT 4320
4321 CCCCAGATCCAGCTCACTTCACTTCACTTCTCTGCTTGTGTTAAGAGGGTGTCACTC 4380
4321 CCCCAGATCCAGCTCACTTCACTTCACTTCTCTGCTTGTGTTAAGAGGGTGTCACTC 4380
4381 TCTGCCAGCTTTAAACAGCTTATAGTGTGAGTGCACCTGAATTTGATGCTGCTG 4440
4381 TCTGCCAGCTTTAAACAGCTTATAGTGTGAGTGCACCTGAATTTGATGCTGCTG 4440
4441 GTGCTCTCTCAGTCCAGAGAGCCGTCAATTTTAACTCTTGGCAATCATCAATACTAA 4500
4441 GTGCTCTCTCAGTCCAGAGAGCCGTCAATTTTAACTCTTGGCAATCATCAATACTAA 4500
4501 AGGATATTAATGATGATTTTAAACAGTCTTAAACTCGGTTTCTGTCTCATCAACC 4560
4501 AGGATATTAATGATGATTTTAAACAGTCTTAAACTCGGTTTCTGTCTCATCAACC 4560
4561 TTAATCTGCAATTTCTAATTTGTCACCTTAAAGAAACATGAGCAATTAATGCTCAATACT 4620
4561 TTAATCTGCAATTTCTAATTTGTCACCTTAAAGAAACATGAGCAATTAATGCTCAATACT 4620
4621 TTGCATTTCTAATTTTCAAGCTTGGAGAGAGTGGAGAGATCAAGCAATTTGGAGAACTGG 4680
4621 TTGCATTTCTAATTTTCAAGCTTGGAGAGAGTGGAGAGATCAAGCAATTTGGAGAACTGG 4680
4681 ATTTGCTGTTTATGCTCTGAGAAATGCTGCAATTTTCAAGCAATTTGGAGAAATGAG 4740
4681 ATTTGCTGTTTATGCTCTGAGAAATGCTGCAATTTTCAAGCAATTTGGAGAAATGAG 4740
4741 ATTAATAACCCCTTCCCTGCTGTAAGAAATTAATTAATGATGATGATGATGATGATGAT 4797
4741 ATTAATAACCCCTTCCCTGCTGTAAGAAATTAATTAATGATGATGATGATGATGATGAT 4797

RESULT 3
AAD27151
ID AAD27151 standard; DNA; 4797 BP.
AC AAD27151;
XX 09-APR-2002 (first entry)
XX
DE Human T cell derived inducible factor (TIF) beta genomic DNA.
XX T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;
KW protein therapy; STAT activation; differentiation; human; ds.

XX Homo sapiens.
 OS
 XX US6331613-B1.
 PN
 XX 18-DEC-2001.
 PD
 XX 18-OCT-1999; 99US-0419568.
 PF
 XX 26-OCT-1998; 98US-0178973.
 PR 16-JUL-1999; 99US-0354243.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Dumoutier L, Louhed J, Renaud J;
 P1 WPI, 2002-105277/14.
 DR
 XX Nucleic acids encoding T cell derived inducible factors useful for
 PT inducing STAT activation in cells -
 PS Claim 1; Column 31-36; 24pp; English.
 XX
 CC The present invention relates to an isolated nucleic acid molecule, which
 CC encodes a T cell derived inducible factor comprising an amino acid
 CC sequence encoded by 6 defined nucleotide sequences. The nucleic acid
 CC molecules are shown to be up regulated by the cytokine interleukin-9
 CC (IL-9) and are described as T Cell Derived Inducible Factors (TIFs). The
 CC invention is used in protein therapy. The nucleic acid molecules encode
 CC proteins which induce STAT activation in cells. They can be used, for
 CC example, in the stimulation of regeneration of targeted tissues.
 CC Further, their inhibitors or antagonists can be used to retard, prevent
 CC or inhibit differentiation of other tissues. The present sequence is
 CC human TIF beta genomic DNA.
 CC
 SQ Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;

Query Match 100.0%; Score 4797; DB 24; Length 4797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACAGCAGATCTTTCAGAACAGATTCCTTCCCAAGTCACAGATTGCTCGAGTTG 60
 DB 1 TGCACAGCAGATCTTTCAGAACAGATTCCTTCCCAAGTCACAGATTGCTCGAGTTG 60
 QY 61 AATTGTCTGCATGGCCGCCCTGCAAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGG 120
 DB 61 AATTGTCTGCATGGCCGCCCTGCAAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGG 120
 QY 121 CCACAGCTGCTCTCTTCTTGGCCCTTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 DB 121 CCACAGCTGCTCTCTTCTTGGCCCTTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 181 GCTCCAGCTGAGGCTTTCAGAAAGTCCAACTTCCAGAGCCCTATATCACCACCGCACT 240
 DB 181 GCTCCAGCTGAGGCTTTCAGAAAGTCCAACTTCCAGAGCCCTATATCACCACCGCACT 240
 QY 241 TCATCTGCTGCTAAGAGAGATCAATCTCAATCTGCTCTTCTTCTTCTTCTTCTTCTTCT 300
 DB 241 TCATCTGCTGCTAAGAGAGATCAATCTCAATCTGCTCTTCTTCTTCTTCTTCTTCTTCT 300
 QY 301 ATCCAAATAGTCTTAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 360
 DB 301 ATCCAAATAGTCTTAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 360
 QY 361 TTATCCCTGAGGAGATTAATTTCTGTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420
 DB 361 TTATCCCTGAGGAGATTAATTTCTGTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420
 QY 421 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 480
 DB 421 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 480

QY 481 CCCAAGAGGGCGCATTCAGTAATCCATCTGATGATTTTCTTCTTCTTCTTCTTCTTCTG 540
 DB 481 CCCAAGAGGGCGCATTCAGTAATCCATCTGATGATTTTCTTCTTCTTCTTCTTCTTCTG 540
 QY 541 CATTTGCTTAAATCAGATCAGACATCTGAATTCGCTTTTATGCTTTTATGATGCTCTCT 600
 DB 541 CATTTGCTTAAATCAGATCAGACATCTGAATTCGCTTTTATGCTTTTATGATGCTCTCT 600
 QY 601 GGGGAGAGCGGATGGGSCATGCTATGATTAATTTTCTTCTTCTTCTTCTTCTTCTTCT 660
 DB 601 GGGGAGAGCGGATGGGSCATGCTATGATTAATTTTCTTCTTCTTCTTCTTCTTCTTCT 660
 QY 661 AGACCCCTAAGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 720
 DB 661 AGACCCCTAAGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 720
 QY 721 TCTCATTTGGGAGAAATCTTCCACGAGTCAAGTATGATCAATGTTGATGACAGG 780
 DB 721 TCTCATTTGGGAGAAATCTTCCACGAGTCAAGTATGATCAATGTTGATGACAGG 780
 QY 781 CCGTGTCCGTCATGAGGATCTTGGGATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 781 CCGTGTCCGTCATGAGGATCTTGGGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 841 TGACCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
 DB 841 TGACCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
 QY 901 GTGCTGAATCTTCAACCTTGAAGAAAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
 DB 901 GTGCTGAATCTTCAACCTTGAAGAAAGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
 QY 961 ATGCAGAGAGTGTGTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
 DB 961 ATGCAGAGAGTGTGTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1020
 QY 1021 TCACTCTCAAGCTTATGCTTCACTTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
 DB 1021 TCACTCTCAAGCTTATGCTTCACTTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
 QY 1081 CCCAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
 DB 1081 CCCAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
 QY 1141 TGTATCAGAGATCAATTTGGATCATAGATATTTGCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
 DB 1141 TGTATCAGAGATCAATTTGGATCATAGATATTTGCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
 QY 1201 TTGATTTATAGTGTGATGAGGATCTTGAATTAAGTATCAGAAAGCCGCAATGGTTG 1260
 DB 1201 TTGATTTATAGTGTGATGAGGATCTTGAATTAAGTATCAGAAAGCCGCAATGGTTG 1260
 QY 1261 TCTTGGAAAAAAGCACTCAGGTTGCTTAAGATGAGAAAGGTTTGGGAAAAATCTTA 1320
 DB 1261 TCTTGGAAAAAAGCACTCAGGTTGCTTAAGATGAGAAAGGTTTGGGAAAAATCTTA 1320
 QY 1321 TCTTGGAAAAAAGCACTCAGGTTGCTTAAGATGAGAAAGGTTTGGGAAAAATCTTA 1380
 DB 1321 TCTTGGAAAAAAGCACTCAGGTTGCTTAAGATGAGAAAGGTTTGGGAAAAATCTTA 1380
 QY 1381 GCTGTGAAATGATATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 DB 1381 GCTGTGAAATGATATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 QY 1441 ATTAAGAGAAAGTGGGAAATGGGAAAGCTTAAAGTGGTGGTGGGAGAGACTGTT 1500
 DB 1441 ATTAAGAGAAAGTGGGAAATGGGAAAGCTTAAAGTGGTGGTGGGAGAGACTGTT 1500
 QY 1501 GGCCTGTGATGATCATGGGAAAGCCCAAAATCGGAGGCTTGAATGCTTGAATGCTTGA 1560
 DB 1501 GGCCTGTGATGATCATGGGAAAGCCCAAAATCGGAGGCTTGAATGCTTGAATGCTTGA 1560
 QY 1561 CATTTGAAACTATGAAAAAAGTTTGAAGGAGTGGGCTTGAATGAAAGGCTTGAAGCTT 1620
 DB 1561 ACTGAAGAGGCTTAATTTTCAATGAGATGTTTATGATCAATTTCTTGTCTTAAGATG 1620

Db	2661	GTTCAAATGAGTATAAAAATATTAGTAAGATTTATTAATAGTTAAATGGAAGCTGCAATT	2700
Qy	2701	GGTAAGCTTTTTTTTCTCTCTCTCCCATCAGACCTTCCATCTAGTTTCTTCTCTCA	2760
Db	2701	GGTAAGCTTTTTTTTCTCTCTCTCCCATCAGACCTTCCATCTAGTTTCTTCTCTCA	2760
Qy	2761	CTCCCTCACAAAATCCCTAGGGAGCATTTATCCATGCTGGGCTGCTGACATTTCTATAG	2820
Db	2761	CTCCCTCACAAAATCCCTAGGGAGCATTTATCCATGCTGGGCTGCTGACATTTCTATAG	2820
Qy	2821	TGAATGATACCATCATGTGGGCTATTGGTATMAAAGAAACAATAGGAAGCTTAGACTA	2880
Db	2821	TGAATGATACCATCATGTGGGCTATTGGTATMAAAGAAACAATAGGAAGCTTAGACTA	2880
Qy	2881	ACAAATAGTGCATCACCCCAAAACCGAGGAATGATTAGAGCAGTGAAGTGAAGCTCTT	2940
Db	2881	ACAAATAGTGCATCACCCCAAAACCGAGGAATGATTAGAGCAGTGAAGTGAAGCTCTT	2940
Qy	2941	GCAAGCAGGTCAACTAAATACTCAGAAACATGAAGGCTCCAGTTGATGAAATTTTCAGT	3000
Db	2941	GCAAGCAGGTCAACTAAATACTCAGAAACATGAAGGCTCCAGTTGATGAAATTTTCAGT	3000
Qy	3001	AACAAGCTTAACCTTAATCCGCCCTTTTCCCTCTGACCTTTTAAAAAACGGTTCTTC	3060
Db	3001	AACAAGCTTAACCTTAATCCGCCCTTTTCCCTCTGACCTTTTAAAAAACGGTTCTTC	3060
Qy	3061	CTGAGCATCATTTATATGATGATGATCTGTTCTTCTCTTGATTAATGGAAGCTTTGATTT	3120
Db	3061	CTGAGCATCATTTATATGATGATGATCTGTTCTTCTCTTGATTAATGGAAGCTTTGATTT	3120
Qy	3121	TTAAATGTGAAGCCAGTCTCTTGTATAGAACTATATCTAGACATGGAGGCTGAA	3180
Db	3121	TTAAATGTGAAGCCAGTCTCTTGTATAGAACTATATCTAGACATGGAGGCTGAA	3180
Qy	3181	TGTTAGCATGCCACAGACAGGACATGCTTTACATCTGCTTTAAAAAATTAAGTATTC	3240
Db	3181	TGTTAGCATGCCACAGACAGGACATGCTTTACATCTGCTTTAAAAAATTAAGTATTC	3240
Qy	3241	ATCTTGCTGTTGTCTTTAGAAAAGTGAAGTGAAGAGAGAGATCTCATGTGCATCTG	3300
Db	3241	ATCTTGCTGTTGTCTTTAGAAAAGTGAAGTGAAGAGAGATCTCATGTGCATCTG	3300
Qy	3301	TGTGATTTTCAAGACCTTTATTCATTTGAAAACATTAATTCATATTTCGCAATGGGTT	3360
Db	3301	TGTGATTTTCAAGACCTTTATTCATTTGAAAACATTAATTCATATTTCGCAATGGGTT	3360
Qy	3361	GCCATGTGGAAGATGATTAATGCTTTTGTGTAGCTTCAGAAAGCACAGGAGGAGGA	3420
Db	3361	GCCATGTGGAAGATGATTAATGCTTTTGTGTAGCTTCAGAAAGCACAGGAGGAGGA	3420
Qy	3421	GCAATGTTGTCACAGAAAGATCAACAGAGAGAAACCTGTCAGAGCTGTCTGAAATGG	3480
Db	3421	GCAATGTTGTCACAGAAAGATCAACAGAGAGAAACCTGTCAGAGCTGTCTGAAATGG	3480
Qy	3481	GTGGTTTTGGAGGACATTAATCCCTCTCGTTGGGGGTAAAGACGAAACGAGGTTGGTA	3540
Db	3481	GTGGTTTTGGAGGACATTAATCCCTCTCGTTGGGGGTAAAGACGAAACGAGGTTGGTA	3540
Qy	3541	GTAATAATGATGACAGACAGTAGGGGACGATTAACCTTAAATCTTTATATGCTTGGAG	3600
Db	3541	GTAATAATGATGACAGACAGTAGGGGACGATTAACCTTAAATCTTTATATGCTTGGAG	3600
Qy	3601	TCTTTGAGATAGAAAAGAAATCTTTTTTGGCTTATGTCAAAABAAGTATGGAAGAAGTGA	3660
Db	3601	TCTTTGAGATAGAAAAGAAATCTTTTTTGGCTTATGTCAAAABAAGTATGGAAGAAGTGA	3660
Qy	3661	AAGGCGGAAGAAAGCAGAAAGAGAAACATGATATTAATAGAGACATATGCTGACA	3720
Db	3661	AAGGCGGAAGAAAGCAGAAAGAGAAACATGATATTAATAGAGACATATGCTGACA	3720
Qy	3721	AGGTTTTTCTTGAATAATATGCAAAATATGATATGATTAGAGAAATTCAGTAGGAATGCTT	3780
Db	3721	AGGTTTTTCTTGAATAATATGCAAAATATGATATGATTAGAGAAATTCAGTAGGAATGCTT	3780


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QY 3781 TTCACTGAAATTTGGGTTTCTTCGATTAAGTTGGAGTCTCATCTGCATTTGACTT 3840
DB 3781 TTCACTGAAATTTGGGTTTCTTCGATTAAGTTGGAGTCTCATCTGCATTTGACTT 3840
QY 3841 GGAAGAGAAAGAAATGAAATGTTAGGACTATATCTGTTTCTATTAATAAGCAAGTGG 3900
DB 3841 GGAAGAGAAAGAAATGAAATGTTAGGACTATATCTGTTTCTATTAATAAGCAAGTGG 3900
QY 3901 GAAAAGACTTATTTGGTATTTTCCACAAAAGTGAAGAACTTTCTTTTACCTGTTTGTCA 3960
DB 3901 GAAAAGACTTATTTGGTATTTTCCACAAAAGTGAAGAACTTTCTTTTACCTGTTTGTCA 3960
QY 3961 AAAAGGTGGAATTAAGAAAAGCCTTAATGTAATGGTAATACATGTTCAAGTCATTTG 4020
DB 3961 AAAAGGTGGAATTAAGAAAAGCCTTAATGTAATGGTAATACATGTTCAAGTCATTTG 4020
QY 4021 AGTAGAGATGTTTAAATCAGAGAGTCCATCATTTGGCTTCCCTGAGCACTTGA 4080
DB 4021 AGTAGAGATGTTTAAATCAGAGAGTCCATCATTTGGCTTCCCTGAGCACTTGA 4080
QY 4081 GAATGCTTGGTACACATATAAATACAGACATATGCTGATGAGCTAAAAAGTCCA 4140
DB 4081 GAATGCTTGGTACACATATAAATACAGACATATGCTGATGAGCTAAAAAGTCCA 4140
QY 4141 TGCAATAAATCTCATCTGTTTAAAGAAATTTATGTAATTTCTGTTAGGGTGCATTAAG 4200
DB 4141 TGCAATAAATCTCATCTGTTTAAAGAAATTTATGTAATTTCTGTTAGGGTGCATTAAG 4200
QY 4201 CTGTCCTGGGCAATGTCGGGCTGTGGCTGCAGGTTGACAGCTCCTTATAGTAATC 4260
DB 4201 CTGTCCTGGGCAATGTCGGGCTGTGGCTGCAGGTTGACAGCTCCTTATAGTAATC 4260
QY 4261 TGTCAATAATGTTTGGAGCTGCAAAACAGGCCAAGCATATGAGTGGGCACTGGGAT 4320
DB 4261 TGTCAATAATGTTTGGAGCTGCAAAACAGGCCAAGCATATGAGTGGGCACTGGGAT 4320
QY 4321 CCCCAGATCCAGGCTCATCTGCTCTGCTCTGCTTAAAGAGGGGTGTCACTC 4380
DB 4321 CCCCAGATCCAGGCTCATCTGCTCTGCTCTGCTTAAAGAGGGGTGTCACTC 4380
QY 4381 TCTGCCAGCTTTTAAACAGCTTCATTAAGTGTAGGTGACCTGAATTTGATGCTGCTG 4440
DB 4381 TCTGCCAGCTTTTAAACAGCTTCATTAAGTGTAGGTGACCTGAATTTGATGCTGCTG 4440
QY 4441 GTGGCTCTCAGTCCAGAGAGCCGTCATTTAAGCTCTTTGGCAATCATCAATACTTA 4500
DB 4441 GTGGCTCTCAGTCCAGAGAGCCGTCATTTAAGCTCTTTGGCAATCATCAATACTTA 4500
QY 4501 AGGATATTACTATGAATGTTTAAAGTCTTAAGCTCGGTTCTGCTCATCAACC 4560
DB 4501 AGGATATTACTATGAATGTTTAAAGTCTTAAGCTCGGTTCTGCTCATCAACC 4560
QY 4561 TAATCTGCAATTTCTAAATTTGTTGCTTAAAGAAACATGGCATTAATGCTCAAACTCT 4620
DB 4561 TAATCTGCAATTTCTAAATTTGTTGCTTAAAGAAACATGGCATTAATGCTCAAACTCT 4620
QY 4621 TTGCATTTCTTATTTTCAAGCTTGAAGAGTGAAGATCAAGCAATTTGAGAACTGG 4680
DB 4621 TTGCATTTCTTATTTTCAAGCTTGAAGAGTGAAGATCAAGCAATTTGAGAACTGG 4680
QY 4681 ATTGCTGTTTATGCTGCAAGAAATGCTGCAATTTGACCAAGCAAGCTGAATAATA 4740
DB 4681 ATTGCTGTTTATGCTGCAAGAAATGCTGCAATTTGACCAAGCAAGCTGAATAATA 4740
QY 4741 AATACTAAACCCCTTTCCCTGCTAGAAATTAACATTTAGATGCCCCCAAGCGATTTT 4797
DB 4741 AATACTAAACCCCTTTCCCTGCTAGAAATTAACATTTAGATGCCCCCAAGCGATTTT 4797

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RESULT 4
AAA28840
ID AAA28840 standard; DNA; 4796 BP.

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XX AC AAA28840;
XX DT 04-SEP-2000 (first entry)
XX DE Human T cell inducible factor genomic DNA.
XX KW TIF; T cell derived inducible factor; interleukin 9; STAT; IL-9;
XX KW Anti-asthmatic; anti-allergic; cyostatic; inhibitor; antagonist;
XX KW probe; chromosome 12q15; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 108..4717
XX FT FT /tag= a
XX FT exon 1..257
XX FT FT /tag= b
XX FT intron 258..688
XX FT FT /tag= c
XX FT exon 689..754
XX FT intron 755..870
XX FT FT /tag= d
XX FT exon 871..1014
XX FT FT /tag= e
XX FT intron 1015..1938
XX FT FT /tag= f
XX FT exon 1939..2004
XX FT FT /tag= g
XX FT intron 2005..3837
XX FT FT /tag= h
XX FT exon 3838..4796
XX FT FT /tag= i
XX FT exon /tag= j
XX PN WO200024758-A1.
XX PD 04-MAY-2000.
XX PF 18-OCT-1999; 99WO-US24424.
XX PR 26-OCT-1998; 98US-0178973.
XX PR 16-JUL-1999; 99US-0354243.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Dumoutier L, Louhed J, Renaud J;
XX DR WPI; 2000-422495/36.
XX DR P-PSDB; AAY92879.
XX PT New nucleic acid molecule encoding a T cell derived inducible factor
XX PS for treating asthma, an allergy or lymphoma
XX PS Claim 1; Page 39-40; 46pp; English.
XX PS
XX CC This DNA encodes a human T cell derived inducible factor (TIF). The gene
XX CC was mapped to chromosome 12q15. The human TIF was identified based on
XX CC homology to a murine TIF, which was identified by subtraction cloning
XX CC from a murine lymphoma cell line BWS147 in the presence or absence of
XX CC interleukin 9 (IL-9). BWS147, can be grown in vitro, without the need to
XX CC add any cytokines to its culture medium. Many IL-9 activities are
XX CC mediated by activation of STAT transcription factors. The novel TIFs were
XX CC expressed in the presence of IL-9, but not in its absence. TIFs induce
XX CC STAT activation in cells. They can be used, e.g. in the stimulation of
XX CC regeneration of targeted tissues. Their inhibitors or antagonists can be
XX CC used to retard, prevent or inhibit differentiation of other tissues. The
XX CC TIFs and their coding sequences are useful in the treatment of asthma,
XX CC allergies and lymphoma (claimed). They are also useful for identifying
XX CC compounds that inhibit or activate T cell induced factor activity in a
XX CC cell (claimed).
XX SQ Sequence 4796 BP; 1339 A; 912 C; 1063 G; 1482 T; 0 other;

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Db 2101 CTTGATCTCTACCAACGAGGCGATTACTTTGGTGTCTGTGTATGTATATATCTAATA 2160
Qy 2161 TATCTAGATGTCAAGTTTCCAAATCTTGCAAAATTTAGAAATTTCTAGAACTGTTGGGATCT 2220
Db 2161 TATCTAGATGTCAAGTTTCCAAATCTTGCAAAATTTAGAAATTTCTAGAACTGTTGGGATCT 2220
Qy 2221 TAGCTTGTCTAGTCACTAATCTCAATCTCTGGGATGTGTCACTGGCAGAGATAGGGCTA 2280
Db 2221 TAGCTTGTCTAGTCACTAATCTCAATCTCTGGGATGTGTCACTGGCAGAGATAGGGCTA 2280
Qy 2281 GAATGAGGCTCCGGAATCCCAAGCAGACCTTTCCGGGTGGATACAGATTAGTTT 2340
Db 2281 GAATGAGGCTCCGGAATCCCAAGCAGACCTTTCCGGGTGGATACAGATTAGTTT 2340
Qy 2341 TGGTACCATTAATTTCTTAGGAAATTTCAATTTCTATTGACTCATGTAATCTGAAGAAG 2400
Db 2341 TGGTACCATTAATTTCTTAGGAAATTTCAATTTCTATTGACTCATGTAATCTGAAGAAG 2400
Qy 2401 TACTTGTAAAAACAGAAAAATGCTATGGCAAAATTTATTTGAAGTCATTTTGAAGT 2460
Db 2401 TACTTGTAAAAACAGAAAAATGCTATGGCAAAATTTATTTGAAGTCATTTTGAAGT 2460
Qy 2461 CATTAATGATGCTTTGAAACTTGGAGAAATTAATCTCAGAACAAATGAGAAAAAGACTGG 2520
Db 2461 CATTAATGATGCTTTGAAACTTGGAGAAATTAATCTCAGAACAAATGAGAAAAAGACTGG 2520
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Db 2521 ACTTCATATAGAGGCTAATTTCTGAGTATATAACCTATTTTGAATATCATATATATC 2580
Qy 2581 TATCAGATATTTGATTAATAGTTTAAAAAGCAAGAGCAGACAAACCCGATCTCTTTTATACAG 2640
Db 2581 TATCAGATATTTGATTAATAGTTTAAAAAGCAAGAGCAGACAAACCCGATCTCTTTTATACAG 2640
Qy 2641 GTTCAAAATAGATTAATAATTTAGTAAGATTTATTAATAGTTAAATGGAAGCTGAAT 2700
Db 2641 GTTCAAAATAGATTAATAATTTAGTAAGATTTATTAATAGTTAAATGGAAGCTGAAT 2700
Qy 2701 GGTAAAGCTTTTCTTCTCTCTCCATCAAGACCTTCATTTAGTTTCTTCTCTCA 2760
Db 2701 GGTAAAGCTTTTCTTCTCTCTCTCCATCAAGACCTTCATTTAGTTTCTTCTCTCA 2760
Qy 2761 CTCCTCAACAAATCCCTAGGAGCATTTATCCATGSGGCTGTGTCATTTCTAATAG 2820
Db 2761 CTCCTCAACAAATCCCTAGGAGCATTTATCCATGSGGCTGTGTCATTTCTAATAG 2820
Qy 2821 TGAATGATACCATCATGTGCGCTATTTGGTGAAGAAACAAACAATGGAAGGCTTAACAT 2880
Db 2821 TGAATGATACCATCATGTGCGCTATTTGGTGAAGAAACAAACAATGGAAGGCTTAACAT 2880
Qy 2881 ACAATAGTACACCCCAAAACCGAGAGATGATTAGAGCAGTGAAGAGTACGCTCTT 2940
Db 2881 ACAATAGTACACCCCAAAACCGAGAGATGATTAGAGCAGTGAAGAGTACGCTCTT 2940
Qy 2941 GGAAGAGGTACAACTAAATACTCAGAAAATGAGAGCTCCAGTTGAGAAATTTTCAAGT 3000
Db 2941 GGAAGAGGTACAACTAAATACTCAGAAAATGAGAGCTCCAGTTGAGAAATTTTCAAGT 3000
Qy 3001 AACCAAGCTTAACCTTAATTTCCCTTTTCCCTCTGACTTTTAAAAAAGCTTTCTTC 3060
Db 3001 AACCAAGCTTAACCTTAATTTCCCTTTTCCCTCTGACTTTTAAAAAAGCTTTCTTC 3060
Qy 3061 CTGAGCATCATTTAATAGAGTGAAGTGTCTTCTCTTGAATTAATGAGGCTTTGATGTT 3120
Db 3061 CTGAGCATCATTTAATAGAGTGAAGTGTCTTCTCTTGAATTAATGAGGCTTTGATGTT 3120
Qy 3121 TTAATTTGAGAGCCAGTCTCTGTTATAGAACTATATCTAGACATGAGAGGCTGAA 3180
Db 3121 TTAATTTGAGAGCCAGTCTCTGTTATAGAACTATATCTAGACATGAGAGGCTGAA 3180
Qy 3181 TGTATAGTCCACAGACAAAGGATGCTTATACATCTTGTCTTAAAAAATTAATGATTC 3240
Db 3181 TGTATAGTCCACAGACAAAGGATGCTTATACATCTTGTCTTAAAAAATTAATGATTC 3240

Db 3181 TGTATAGTCCACAGACAAAGGATGCTTATACATCTTGTCTTAAAAAATTAATGATTC 3240
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Db 3241 ATCTTGCTTTGTTCTTTAGAAAAAGTGAAGTGTGAGAGAGAAATCTCATGTGATCTG 3300
Qy 3301 TGTGATTTTCAAGACCTTAATCCATTTTGAAGAAATGAATTTCAATTTTGAATGGGTT 3360
Db 3301 TGTGATTTTCAAGACCTTAATCCATTTTGAAGAAATGAATTTCAATTTTGAATGGGTT 3360
Qy 3361 GCCATGTGGAAGAGATTAATGCTTTTGTGCTGAGCTTCAGAAAGCAGAGAGGAGA 3420
Db 3361 GCCATGTGGAAGAGATTAATGCTTTTGTGCTGAGCTTCAGAAAGCAGAGAGGAGA 3420
Qy 3421 GCAATGTTGTTCAAGAAAAGATCAACAGAGAGAACTGTCAAGCTGTCTGAATAGG 3480
Db 3421 GCAATGTTGTTCAAGAAAAGATCAACAGAGAGAACTGTCAAGCTGTCTGAATAGG 3480
Qy 3481 GTGTTTTGGAGGCAATTAATTTCCCTCTGTTGGGGGTAAAAAGCAAGCGAGTTGGTA 3540
Db 3481 GTGTTTTGGAGGCAATTAATTTCCCTCTGTTGGGGGTAAAAAGCAAGCGAGTTGGTA 3540
Qy 3541 GTAAATGATGACAGACAGTAGGAGCAATPAACTTTAAATCTTTATAGTCTTGGAG 3600
Db 3541 GTAAATGATGACAGACAGTAGGAGCAATPAACTTTAAATCTTTATAGTCTTGGAG 3600
Qy 3601 TCTTTGAGATAGAAAAAGATATCTTTTGGCCTTATGTCAAAAAGAGATAGAAAAGTGA 3660
Db 3601 TCTTTGAGATAGAAAAAGATATCTTTTGGCCTTATGTCAAAAAGAGATAGAAAAGTGA 3660
Qy 3661 AAGGCGGAGAAAGCAGAGAAAGAGAAACATGTATTTATTAAGAGCAATGTTGACA 3720
Db 3661 AAGGCGGAGAAAGCAGAGAAAGAGAAACATGTATTTATTAAGAGCAATGTTGACA 3720
Qy 3721 AGTTTTCTTGAATTAATGCAATATGATGATAGAGAAATTCAGAGGGAATGCTT 3780
Db 3721 AGTTTTCTTGAATTAATGCAATATGATGATAGAGAAATTCAGAGGGAATGCTT 3780
Qy 3781 TTCACTTGAATTTGGGTTTCTCTTCAATTAATGATTTGGGATCTCATCTGACTTTGACTT 3840
Db 3781 TTCACTTGAATTTGGGTTTCTCTTCAATTAATGATTTGGGATCTCATCTGACTTTGACTT 3840
Qy 3841 GAGAGAGAAAGATGATTTAGAGCTTATCTGCTTTTATTAATTAACAAAGCAAGTG 3900
Db 3841 GAGAGAGAAAGATGATTTAGAGCTTATCTGCTTTTATTAATTAACAAAGCAAGTG 3900
Qy 3901 GAAAAGACTTATTTGATTTTCCCAAAAAGTGAAGAACTTTCTTTACTGTTGTCA 3960
Db 3901 GAAAAGACTTATTTGATTTTCCCAAAAAGTGAAGAACTTTCTTTACTGTTGTCA 3960
Qy 3961 AAAAGGTGAAATTAAGAAAAAGCTTATGATTTGGTGAATACATGTTCAAAATCTTG 4020
Db 3961 AAAAGGTGAAATTAAGAAAAAGCTTATGATTTGGTGAATACATGTTCAAAATCTTG 4020
Qy 4021 AGTAGATGTTTAAATCAGAGTGTCCAATCTTTGGCTTCCCTGACCACTTTGAAA 4080
Db 4021 AGTAGATGTTTAAATCAGAGTGTCCAATCTTTGGCTTCCCTGACCACTTTGAAA 4080
Qy 4081 GAATGTCTTGTACACATTAATTAACAAGAAATAGCTAGTAGGCTTAAAAAGTCCA 4140
Db 4081 GAATGTCTTGTACACATTAATTAACAAGAAATAGCTAGTAGGCTTAAAAAGTCCA 4140
Qy 4081 GAATGTCTTGTACACATTAATTAACAAGAAATAGCTAGTAGGCTTAAAAAGTCCA 4140
Db 4081 GAATGTCTTGTACACATTAATTAACAAGAAATAGCTAGTAGGCTTAAAAAGTCCA 4140
Qy 4141 TGCATTAATCTCATCTGTTTAAAGAAATTTAAGAAATTTCTGTAAGGCTGATCAAG 4200
Db 4141 TGCATTAATCTCATCTGTTTAAAGAAATTTAAGAAATTTCTGTAAGGCTGATCAAG 4200
Qy 4201 CTGTCTGGGCAATGTGCGGCTGTGGGCTGCAAGTTGAGCAAGCTCTTAAATAGTAATC 4260
Db 4201 CTGTCTGGGCAATGTGCGGCTGTGGGCTGCAAGTTGAGCAAGCTCTTAAATAGTAATC 4260
Qy 4261 TGTCAATAGTATTTTGAAGCTGCAAAACAGGCAAGGATATAGTGGTGGCACTGGGAT 4320
Db 4261 TGTCAATAGTATTTTGAAGCTGCAAAACAGGCAAGGATATAGTGGTGGCACTGGGAT 4320

QY 2946 CAGTACACTAATACTAGAAACAGTAAAGCTCCAGTTGATGGAATTTTCAGTACAA 3005
 DB 4993 TGGGGTGGCTTAAGTAATAGAAAGAGGCTCCGGTTGATGGAATATCAGTAAGAT 4992
 QY 3006 GCTTAACCTTAATCCCTCTTTTCCCTCTTGAATTTTAAAGGCTTTCTCTAG 3065
 DB 4993 ATCTACCTTATCTCTCTTATGACAC-----TAAATCGTCTTTTCTTGG 5042
 QY 3066 CATCTTTAATAGTGTGATCTGTTCTTCTTGAATTAATGAAGCTTTGATTTTAA 3125
 DB 5043 TGTAGCTGATTAACACACTGT--TTCTTTGAGTGTATGCTTTGATGATTTTAA 5100
 QY 3126 TTGTAAAGCCAGTCTCTGTTATAGAACTTTATCTAGACATGAGGCTGAAATGTTA 3185
 DB 5101 GTGCTTGGCACTTTTGTAGAG--GGTTGTACTTTCAGACCTGGGCTTGAATGTTA 5158
 QY 3186 GCATCCACAGACAGGCACTGTTACATCTTCTTAAATAATTAATGATTTGATCTT 3245
 DB 5159 GCATGCCAAGGCAACACTTTGAAATGCTGTGTAAAGGTTATTTATCTTACT-- 5215
 QY 3246 GCTTGTCTTTAGAAAAGTGAAGTGTAGAGAGAGAAATCTCATGTGA----- 3296
 DB 5216 ----TGTCTTTGAAAAGTGAAGCTGTGTGAAGAAAGAACTCAGAGATGTGTTCT 5270
 QY 3297 -----TCTGTGATTTTCAAGACCTTTAATCCATTTGAAAATCAATT 3342
 DB 5271 CTGTAGAAAACCTTTTTCCTTAAATGCCATATCTCATCTTCACTCAAC--TT 5327
 QY 3343 TCATTTTGCATGGGTGTCATGTGGAAGAGTATATGCTTTTCTGTGATCTTCA 3402
 DB 5328 TGACTTTATACATGCTGTCAATGAAGAGTGTAAAGGCTTCTCATGCTGTGG 5387
 QY 3403 GAAAGCA-CAGAGAGAGAGCAATGTTGTTCAAGAAAGATCAACAGAGAGAAACTGT 3461
 DB 5388 AAAAGCACCAATAGAGGAGAGAAATGTTATGCTGAAGAACTGACCGGAGAGAAATGCT 5447
 QY 3462 CAGAGCTCTGAAATAGAGGTGTTTGGAGGCAATTAATCTCTGCTTGGGGTAA 3521
 DB 5448 CAGAGCTCCCCGAGAGCA-----CCACAGGTGTAAATGAG 5485
 QY 3522 AGCAGAACGCAAGTGTGATTAAT--GCATGACAGACAGTAAAGGAGAGATTAATCTTAA 3580
 DB 5486 AACAGTCCAGAGTGGCTCATGTAATTAAGAAATGAACAGAGAGAGAAATTAATCTTAA 5545
 QY 3581 AATCTTATAGTCTTGGAGTCTTGAATGAAAGAAATATCTTTTGGCTTATGCA 3640
 DB 5546 AGTTCAATAGGCTC-CGAGCTTAAGATACAAATATGCTGC--TTGGCTTATTAACA 5602
 QY 3641 AAAAGATATGAAAG-----TAAAGGCGGAGAAAGAGAGAGAAAGAGAG 3688
 DB 5603 AAGAGAGCTGGGAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGAG 5662
 QY 3689 AACCATGATTAATTAAGAGCAATGTAAGCAAGTCTTCTGAAATTAATGCAATATG 3748
 DB 5663 AGGACTGAAACAGCTACAAATCTCTTACAGACAGATTTTCTGAAACAACTTGAAGGT 5722
 QY 3749 ATAGATTAGAGAAATTCAGTAGGAATGCTTTTCACTGTAATTTGGGTTCTCT--T 3805
 DB 5723 AGTGAATAGTGAATGAGGGGAGCTTGGCTTGCATTTGAATCTGGGTTTGTCTCT 5782
 QY 3806 CGATTAAGTTGGGATCTCTATCTGCAATTTGACT--TGAGAGAGAGAAAGATGAATGT 3861
 DB 5783 CCATTAAGTTGAAAGGCTACCTTTTACCTCGAATGAGAGAGAGAGAGAGAGGAGT 5842
 QY 3862 TAGACCTATATCTGTTTCTATTAATAAGCAAGTGAAGAAAGACTTATTTGTAATTT 3921
 DB 5843 TATGATCTTACCTGAGATTTACTAGTTTACGAAAGAGAGAGAGAGAGAGAGAGAGAG 5902
 QY 3922 TTCCCAAGAAAGTGAAGAACTTTCTTTTACTGTTTGCMAAAGAGTGAAGATGAAGAAAG 3981
 DB 5903 CTGACAAAAGAAATGAGAACTGTGTTGTCTTGTGTTCTTTTGTAAAGAGAGAG 5962

QY 3982 CTTAATGATATGATGTAATACATGTTTCAAGTCAATTTGAGTAAAGATGTTTAAATCAG 4041
 DB 5963 AGGCAAGGCCGAGACACATGGGTTGAATGTTGGGCTTTGATCAAGGCTTTTGAATGAG 6022
 QY 4042 GAGTGTCCATCATTTTGGCTTCCCTGAGACACTTGAAGAAATGTCTTGTATACACAT 4101
 DB 6023 CACTATCAATATGAT-----GATCATGGTCAGGTGAGAGGC 6058
 QY 4102 AAAATACAGAAACATAGCTGATGAGCTTAAATAAGTCCATCATTAATCTACTGTTT 4161
 DB 6059 TACCTGTACAGGCCAGCCCTGCTGCTTCCGACTTAACATCTCCAGGCTTCAATATCACT 6118
 QY 4162 TAAAGAGTTTATGAATTTCTGTTAGGCTGATTCAGAGCTGCTGGGCCATGTGCGGC 4221
 DB 6119 TCTGTACTATTAGACAGATTGAGAGTTGAGAGAAACCTTTTTC----- 6163
 QY 4222 CTGTGGGCTGAGAGTTGAGCAAGCTCTTATATGTAATCTGTCAATGATGTTTGGAGC 4281
 DB 6164 -----AACCCCACTTAAATTTAATTTGACAAAGAGCTGTATATTTG 6205
 QY 4282 TGCAAAACAGGCCAAGGCATTAATGGGTGGACCTGGGATCCCAAGATCCAGGCTCACT 4341
 DB 6206 TGGATATACAGTGTATATTA----- 6227
 QY 4342 TCAGTCTCTTCTCTGTTAAGAGGGGTGTCACCTCTGCCCAGCTTTTAAAGC 4401
 DB 6228 ----TATATGTGATGTCATGTCAGAGGTTCAATATAGATTAATAGGCCATCAACAGC 6283
 QY 4402 TTCAATATGTTGAGGTGACCTGAATTAATGCTGCTGTGGCT--CTAGTCCAGAGA 4460
 DB 6284 TTATATGGTGTGAATTAATCAATATATAGTATGATGCTGTGGTGTCTTATAGTCAAGAA 6343
 QY 4461 GCGCTCATTTTAAAGCTTTGGGCAATCATATCAATTAATTAAGGAT-----T 4508
 DB 6344 GGCATGATTTTAAAGCTTTGGGCAATCATATTAATCTATGCTTAAATAATATATATGTT 6403
 QY 4509 TACTATGAATGTTTACAAATGCTTAAATCTGGTCTCTGCTCCATCAACCTAATCTTG 4568
 DB 6404 GATATTAATCTTTTAAAGAGGCTGATATCTGTTTGTGGTCTGACAGCAAGCAATATGCA 6463
 QY 4569 CAATTTCT--AATTTGTACTTTAGAAACATGCAATTAATGCTCAATATCTTTGCA 4625
 DB 6464 CCAAGCTTTTCTAATCTGTACACTTTAGAAATGCTAATCTGTGCTCAAAATGGTGTGTA 6523
 QY 4626 TTCTTATTTTCAAGCTTTGAGAGAGTGAAGATCAAGCAATTTGAGAACTGGATTTG 4685
 DB 6524 TTCTTATTTTCAATGCTTTGAGAGAGTGAAGATCAAGGAGATTTGGGAACTGGACCTG 6583
 QY 4686 CTGTTATGCTCTGAGAAATGCTGCTGATTTGACAGAGCAAGAGCTGAATAATGATTAAC 4745
 DB 6584 CTGTTATGCTCTGAGAAATGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6643
 QY 4746 TAAACCCCTTCCCTGTGTAATTAATTAATTAATGATGAGAGAGAGAGAGAGAGAGAG 4797
 DB 6644 TGTCTCTTCTGCTGCTTTTAAAGAAACAAATTAATGATCCCTGAATGAGACTTTT 6695

RESULT 6
 AAD30628
 ID AAD30628 standard; DNA; 7445 BP.
 XX AAD30628;
 XX 21-MAY-2002 (first entry)
 DE Mouse T1F alpha genomic DNA.
 XX T cell derived inducible factor; T1F; interleukin-21; IL-21; mouse;
 KW STAT transcription factor; acute phase protein; inflammation; ds.
 OS Mus musculus.
 XX
 PN W0200210393-A2.

XX 07-FEB-2002.
 PD 27-JUN-2001; 2001WO-US20485.
 XX 27-JUL-2000; 2000US-0626617.
 XX (LUDM-) LUDWIG INST CANCER RES.
 XX Dumoutier L, Renaud J;
 PI MPI; 2002-195964/25.
 DR Stimulating expression of STAT transcription factor and inducing
 XX production of acute phase protein in a cell, involves contacting a cell
 PT capable of expressing STAT with T cell derived inducible factors -
 XX
 XX Example 7; Page 49-53; 64pp; English.
 XX The invention relates to nucleic acid molecules encoding T cell
 CC derived inducible factors (TIFs) also known as Interleukin-21 (IL-21).
 CC TIF polynucleotides are upregulated by the cytokine, IL-9. IL-TIF or
 CC IL-21 molecules are implicated in activation of STAT transcription
 CC factors, acute phase proteins and inflammation. The present sequence
 CC is mouse TIF alpha genomic DNA.
 XX
 SO Sequence 7445 BP; 2059 A; 1568 C; 1597 G; 2221 T; 0 other;
 Query Match 14.3%; Score 686; DB 24; Length 7445;
 Best Local Similarity 53.8%; Pred. No. 6.3e-170;
 Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;
 QY 29 CTCCTTCCCGCAGCAGCAGTGTGCTGAGTAAATGTCGCAATGAGCGCCCTGAGAA 88
 DB 2034 CTCCTCTCACTTACCACTGTGACACTGTGCGATCTTGATGAGCTGCTTGCAGAA 2093
 QY 89 ATCTGTGAGCTCTTTCCTTATGAGGAGCCCTGGCCACAGCTGCTCTTCTTGGCCCT 148
 DB 2094 ATCTATGAGTTTTCCTTATGAGGAGCTTGGCCGCGCAGCTGCTCTTCTATGCCCC 2153
 QY 149 CTTGTGACGAGGAGGAGCAGCTGCGCCCATCAGCTCCCATGAGGCTGACAGTCCAA 208
 DB 2154 GTGGGGCCGAGGAGGAGGAGCTGCGCCGCTGCAACCCGGTGCMACTTGAAGGTGCCAA 2213
 QY 209 CTTCCAGCAGCCCTATATCAACCAACCGCCTCATGCTGGCTGAAGAGGTATACATTC 268
 DB 2214 CTTCCAGCAGCCGTAATGCTCAACCGCCTTATGCTGGCCAGAGGTATACAGCTGCA 2273
 QY 269 AATCTGCTCTTCTGCTGATCTAATTGGAATCCAAATAGTTCTTAAACCTTCTTCA 328
 DB 2274 TCTCTTCTCTCATACCGCTGCGCTTGCATTTCTCTAAGCATTTGCAACTCTTTAGGGG 2333
 QY 329 GAGCATCTCTAAGAGCTTTAGAACCCACTGTTTATCCCTGAGGGTATGAATTTCTG 388
 DB 2334 CGCTTATCTCCGAGAGCTCTCACTACCTATGTTT-----TCTGTCTTTAGAG 2382
 QY 389 TTTTTCAGAGACTCTTGGGAATCTGGCTTTTCTTGAATCTTCTTCCAT 448
 DB 2383 ACTCTTAAAGAGCTGGCTCTTTTCTATTTCTATTTCAAGCTCTCAGACATTTCTAT 2442
 QY 449 TTTGGCTTTATGATCATATGATGATTTTCCAAAGAGCGGCATTCAGATATCAT 508
 DB 2443 CTTGGCTTCAGAGACATATATGATTTATCTAAGAGGCGCATTT--AAGAGGCCA 2500
 QY 509 CTGATATTTTCTTCTTATGCTCTGTGATTTCTTAACTGATGACATCTG 568
 DB 2501 CCCACACATGCAATATTTCTATTTCTGTGCTCTTCTGAACATCACTCTGCGC 2560
 QY 569 AATTCTGCTTTAGTCTTATGATGATGCTCTGGGGAGACGGAGTGGGACATGCTAT 628
 DB 2561 TACTC-----CTGAGACCCACCTGGGACATATATCTCTAC 2595
 QY 629 GATAAATTTTTTCTATTTGCTCAATGTCAGACCCCTTATGCTTTCTCTTCCAG 688

DB 2596 TTACAGGCTTTCTTCCATCTCTTGTACACCCAGCCTTAGAGTTTCTCTCTTACG 2654
 QY 689 GCTAGCTTGGCTGATTAACAACAAGACGCTTGTCTCATTTGGGAGAACTGTTCCAGCA 748
 DB 2655 GCCAGCCTTGGAGATTAACAACAAGACGCTTGTCTCATTTGGGAGAACTGTTCCAGCA 2714
 QY 749 GTCAGTGAAGCTTACAGTTGAGCAACAAGGCGGTGCGCTCATGGGTACTTGGGT 808
 DB 2715 GTCACTGAATAGCTCTCACTGTGATGACAGGCG-----TAGCTGCGGAGCT 2761
 QY 809 GGTGATGATGATGTTTGGTCTTATCCCTTATGACCCCTTGTCTTCCCTCCACTGCG 868
 DB 2762 GGTGACCCCTCTGGGATAG--TCTGACGTATGACCCCTGCTGCTTGTGTCTTCTGCG 2817
 QY 869 AGATGATGAGCGCTGCTATGATGAGAGAGCTGCACTTCACTTGAAGAAGTGC 928
 DB 2818 AGCTTAAGATAGTCTCACTGATGAAGAGCTCTCACTTCACTTGAAGAAGTTC 2877
 QY 929 TGTCTCTCAATCTGATAGTTTCCAGCCTTATATGACAGAGGTGCTTCTTGGCCA 988
 DB 2878 TGTCTCTCTCAATCTGATAGTTTCCAGCCTTATATGACAGAGGTGCTTCTTGGCCA 2937
 QY 989 GGTGATGAGCGCTGCTATGATGAGAGAGCTGCACTTCACTTGAAGAAGTGC 1048
 DB 2938 AACTGAGCAATAGCTCACTGCTCTGATGAGTGTGCTGCTGCTCACTATGCTCTCT 2997
 QY 1049 CTCCTTCCCTCTTCCAGAGAGCCCTTACCCCACTCTCTCTCTTCCCTTCCCTTACCC 1108
 DB 2998 CTCCTCTCTTATTTCACTGATGAACCCAGAGCTCTGCTCTCTCTTCCAGAGAGTGA 3057
 QY 1109 TAAGCTAGCAGAGAGAGAGTGTCTTGGCAGAGTGTATACAGAGTCA-----TTTGGG 1161
 DB 3058 GGAAGGCGCTCAGACACACACACATCATAGGCCACTGAAATAGTCAACAAAGCTTGGC 3117
 QY 1162 ATCATAGATATTTGCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATG 1221
 DB 3118 TTCAATGATGATATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 3177
 QY 1222 GGTCTGGAATTAAGTGAAGAGAGCGCATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1281
 DB 3178 AAAAAATCACTCAAAATTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 3237
 QY 1282 A-----GGTGGTGAAGTGAAGAGTGTGG 1309
 DB 3238 AAGAGAAAGATCTGCTAGTATAGTATCTATGAGGAGGAGAGGAGGATATCCACTGA 3297
 QY 1310 GAAAAATCTAGCTGTGAAATGATCCATGATGATGATGATGATGATGATGATGATGATG 1369
 DB 3298 GTACAAGTACTTGTGGGAGAGAAATCCACTAGTACAAATGTTGTTGGCATGAGATC 3357
 QY 1370 CATGAGAGAAATTAAGAGAGAAAGTGGAAATGGAAGGCTTAA----- 1415
 DB 3358 CACTGATGACAAATCTTGTGGGAGAGAGAAATGACAGACAAAGTTGAAGGAGAG 3417
 QY 1416 -----GTGCTGTGCTGCGAGACTGTTGCCCTGTTGATGATGATGATGATGATGATG 1460
 DB 3418 AAGATGAGAGAGGCTCAGTGTGGGAGTGAAGTCACTCTTTCCATGATGATGAG 3477
 QY 1461 AGCCACAAATGAGAGGCTGTAATGATGATGATGATGATGATGATGATGATGATGATG 1520
 DB 3478 AGTTAAGAAACCAAGT--GTGATGATGATGATGATGATGATGATGATGATGATGATG 3536
 QY 1521 AGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1580
 DB 3537 ATTCAGAGAGAGGAGAGAGCTGAGAGAGCTGAGATTTAGAG--AGGCGGCTTTT 3594
 QY 1581 CACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1640
 DB 3595 CACAGAGAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3654
 QY 1641 TAGGTTTATCTTACAGAAATTTGATTAATCTGCTCTTCTTCCAAATGCAATC 1700


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QY 389 TTTTTCAGAGACTCTTTGGAACTCGCTTTTCTTTTCTTGAATCTTCTTCAT 448
Db 2383 ACTCTTAAAGACTGGGCTTTTCTTATTTCTATTTCAAGGTCTCAGACCATTTCTCAT 2442
QY 449 TTTGGCTTTATGATCATATGATGAAATTTTCCCAAGAGGGCCATTCACTAATCAT 508
Db 2443 CTGGGCTTCAGAGACATATCTGAAATTTTATCTACAGAGGGCCATT--AGAAAGCA 2500
QY 509 CTGATGATTTTCTTTTCTTTATGCTCTGTGCATTTTCTAATCATGACACATCTG 568
Db 2501 CCCAGAGCTGCAATCTTCTCATTTCTGTGCTCTCTCTGAATCATATCTCTGTGC 2560
QY 569 AATTGCTTTTATGCTTTATGATGTTGCTCTGGGAGACGGGATGGGCAATGCTAT 628
Db 2561 TACTC-----CTGAGCCCATCTGCGACATACATCTCTAC 2595
QY 629 GTATAAATTTTCTTATTTGCTCAATGTCAGACCCCTTAGCTTTTCTCTTCCAG 688
Db 2596 TTACAGGCTTTCTTCTCATCTCTGTCTACCCAGGACATTAGGGTTTC-TCTTTTCAG 2654
QY 669 GCTAGCTTGCTGATTAACAACAACAAGCTTCTCATTTGGGAGAACTGTTCCACGA 748
Db 2655 GCGAGCTTGCAGATTAACAACAACAAGCTTCTCATTTGGGAGAACTGTTCCAGGA 2714
QY 749 GTCACTGTAGCTACAGTTGTGACGAACAGGGCCGTGCGCTCATGGGATCTTGGGT 808
Db 2715 GTCACTGTAGCTACAGTTGTGACGAACAGGGCCGTGCGCTCATGGGATCTTGGGT 808
QY 809 GGTGTGATGATGTTTAAAGCTTATCCCTTATGACCCCTTCTGTTTCCCTTCCACCTCC 868
Db 2762 GGTGTGATGATGTTTAAAGCTTATCCCTTATGACCCCTTCTGTTTCCCTTCCACCTCC 868
QY 869 AGATGATGAGCGCTGCTATCTGATGAAGCAGTGTGATCTCACTTCACTTGAAGAAGTC 928
Db 2818 AGGCTAAAGATCAGTGTGATCTGATGAAGCAGTGTGATCTCACTTCACTTGAAGAAGTC 928
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QY 1162 ATCATAGAGTATTTGCTTTTCTGTTGATGATGATCACTTGAAGTTATAGTGTGAATG 1221
Db 3118 TTCAATTAATGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3177
QY 1222 GGGTCTGGAATTAAGTGTACAGAGCGCATTTGTTGTCTTCCGAAAGAGGACATCTC 1281
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 QY 4686 CTGTTATGCTCTGAGAAATGCTGCAATTTGACAGAGCAAGCTGAAATGAATAC 4745
 DB 6584 CTGTTATGCTCTGAGAAATGCTGCAATTTGACAGAGCAAGCTGAAATGAATAC 6643
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 DB 6644 TGCTCTTCCCTGCTTCTAAGAAAGCAATAGATCCCTGAATGATTTT 6695

RESULT 8
 ID AAA28816 standard; DNA; 7444 BP.
 AC AAA28816;
 XX
 DT 04-SEP-2000 (first entry)
 XX
 DE Murine T cell inducible factor alpha genomic DNA.
 XX
 XX TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;
 KM Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist; ss.
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT exon 1908..1932
 FT /tag= a
 FT /number= 1a
 FT CDS 2080..6615
 FT /tag= b
 FT /product= TIF-alpha
 FT intron 1933..2032
 FT /tag= c
 FT exon 2033..2262
 FT /tag= d
 FT /number= 1b
 FT intron 2263..2654
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 FT /number= 2
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 FT exon 2820..2963
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 FT intron 2964..3930
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 FT /tag= i
 FT exon 3931..3996
 FT /tag= j
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 FT intron 3997..6538
 FT /tag= k
 FT exon 6539..7137
 FT /tag= l
 FT /number= 5
 XX
 PN WO200024758-A1.
 XX
 PD 04-MAY-2000.
 PF 18-OCT-1999; 99WO-US24424.
 XX
 PR 26-OCT-1998; 98US-0178973.
 XX 16-JUL-1999; 99US-0354243.
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX Dumoutier L, Louhed J, Renaud J;
 PI

XX WPI: 2000-422495/36.
 DR P-PSDB; AAY92877.
 XX
 PT New nucleic acid molecule encoding a T cell derived inducible factor
 PT for treating asthma, an allergy or lymphoma
 XX
 PS Claim 1: Page 34-37; 46pp; English.

CC This DNA encodes T cell derived inducible factor (TIF) alpha identified
 CC by subtraction cloning from a murine lymphoma cell line BMS147 in the
 CC presence or absence of interleukin 9 (IL-9). BMS147, can be grown in
 CC vitro, without the need to add any cytokines to its culture medium. Many
 CC IL-9 activities are mediated by activation of STAT transcription
 CC factors. The novel TIFs were expressed in the presence of IL-9, but not
 CC in its absence. TIFs induce STAT activation in cells. They can be used,
 CC e.g. in the stimulation of regeneration of targeted tissues. Their
 CC inhibitors or antagonists can be used to retard, prevent or inhibit
 CC differentiation of other tissues. The TIFs and their coding sequences are
 CC useful in the treatment of asthma, allergies and lymphoma (claimed). They
 CC are also useful for identifying compounds that inhibit or activate T cell
 CC induced factor activity in a cell (claimed).

Sequence 7444 BP; 2058 A; 1570 C; 1596 G; 2220 T; 0 other;

Query Match 14.1%; Score 677.4; DB 21; Length 7444;
 Best Local Similarity 53.6%; Pred. No. 1.2e-167;
 Matches 2630; Conservative 0; Mismatches 1891; Indels 388; Gaps 43;

QY 29 CTCCTTCCCACTACCACTGCTGAGTATGAAATGCTGCAATGCGCCCTGCAAGA 88
 DB 2034 CTCCTTCCCACTATACCACTGCTGAGTATGAAATGCTGCAATGCGCCCTGCAAGA 2093
 QY 89 ATCTGAGAGCTCTTCTGATAGGAGACCTGGCCACAGCTGCTCTTCTGAGCCT 148
 DB 2094 ATCTGAGAGCTCTTCTGATAGGAGACCTGGCCACAGCTGCTCTTCTGAGCCT 2153
 QY 149 CTGATGAG 208
 DB 2154 GTGGGCCAG 2213
 QY 209 CTTCAG 268
 DB 2214 CTTCAG 2273
 QY 269 AATCTGCTCTTCTGATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 328
 DB 2274 TCTCTTCTCTCCATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2333
 QY 329 GAGCATCTCTAAG 388
 DB 2334 CGCTTATCTCCGAG 2382
 QY 389 TTTTTCAG 448
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 DB 2443 CTGGCCCTTACAG 2500
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 DB 2596 TTACAGAGCTTTCTCTTATGCTCTGATATGCTCTGATATGCTCTGATATGCTCTGAT 2654

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QY 2772 AATCCTTAGAGACATTTATCATGTGTGGGTGTGATCATTTCTATGTGAATGATACC 2831
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Db 4755 AGCCATGATAGACCACTATCTGCTGATGACATATTATATGACTTTACACAAACACACTT 4814
Qy 2832 ATCATGTGGCTTATTTGGTGAAGAAACA--ACAATGGAAGCTTAGACTTAACAATAGTGT 2889
Db 4815 GCTGTGTGGCTCTTTGGGGAAGGGAACAGATACAGAGAGCTCAGGCTAGCAAGTCTG 4874
Qy 2890 ACTCACCCCAAAACCGSAGSAAATGATTTAGAGCAGTGAAGAGGCTCTT--GCAGCAG 2948
Db 4875 ACTTCCCTTAAGCCAGAGGCAATGGTGTATAGCAAGAAAGTGAAGCTCTTTCGCAAGTGG 4934
Qy 2949 GTACACTAAATACTCAGAAACATGAAGGCTCCAGTTGATGGAATTTTCAGTAACAAGCT 3008
Db 4935 GTGTCTTAATAGTAATCAGAAACAGAGAGCTCCGTTGATGSAATTAACAGTAACATATTC 4994
Qy 3009 TAACCTTAATTCCTCCCTTTTCCCTCTGACCTTTTAAAAAAGCCTTTCTTCGAGCAT 3068
Db 4995 TACCTTAATCTCTCTATTCGAAAC-----TAAATCGTCTCTTTTCTTGTGTGT 5044
Qy 3069 CATTAAATGAGTGTGACTGTTTCTCCCTTGTATATGAAAGCTTTGATTTAAATG 3128
Db 5045 AGGCTGATTAACACACTTGT--TTCCTTTGAGTGTGATGCTTTGTATGATTTTATGTG 5102
Qy 3129 TGAAGCCAGTCTCTGTTATAGAACTATTATCAGACATGAGAGGCTGAATGTTAGCA 3188
Db 5103 CTCTGCAAGTCTCTGTTAGAG--GGTTGTATCTTGACACCTGGGCTTGATGTTAGCA 5160
Qy 3189 TGCCACAGACAAAGCATCTTTACACATCTTGTCTTAAAAAATTACTGATTTTCACTTGTCT 3248
Db 5161 TGCCAAAGGACACACTCTGTAATGCTGTGTAAAGTATTTATCTATTTACT----- 5214
Qy 3249 TGTGTCTTTGAAAGTGAAGTGTGAGAGAGAAATCTCATGTGTG----- 3296
Db 5215 --TGTCTTTGAAAGTGAAGCGTGTGTGAAAGAACTCAGAGAGATGTGTCTGTG 5272
Qy 3297 -----TCTGTGATTTTCAAGACCTTTATCCATTTTGAAGAAATCAATTCA 3345
Db 5273 TAGAAACTTTTTCCTTCCCTTAATGCTATATCACTTTTACGTAAC--TTTGA 5329
Qy 3346 TATTTGCAATGGTGGCCATGTGAAGATGATTAATGCTTTTGTGCTGATGCTTACAA 3405
Db 5330 CTTTATATCAATGCTGTCACTGAAGAAAGTGTGAGCCGCTCATGAGCTGTGGAA 5389
Qy 3406 AGCA--CAGAGGGAGAGCAATGTTGTTCAGAGAAAGATCAACAGAGAGAACTGTAG 3464
Db 5390 AGCACCAATAGGGAGAGAAATGTATGTGAGAAATCGACCGAGGAAACTGTGTAG 5449
Qy 3465 AGCTGTCTGAATAGGGTGTGTTGGAGGCACTTAATCCCTCTGTTGGGGGTAAAGC 3524
Db 5450 AGCTCCCCGAAAGCA-----CCACAGTGTTAAGTAGAAC 5487
Qy 3525 AGAACGAGGTGTGATTAAT--GCATGACAGACAGTAGGAGCATTAATTTAAAT 3583
Db 5488 AGTCACAGGTGGGCTCATGTATATGAAATGAAACAGAGGAGGAAATGATCTACAAAGT 5547
Qy 3584 TCTTATATGCTGTGAGCTTTGATGATGAAAGAAATATCTTTTGGCTTATGTCAAA 3643
Db 5548 TTCAATAGGCTC--CGAGTCTTAAAGATACAAATATGCTGC--TTGGGCTTATACAAAG 5604
Qy 3644 GAAATATGAAAG-----TGAAGGGCGGAAGAAAGCAGAGAAAGAAAGCAAC 3691
Db 5605 GAAGTCTGGGAAGGAGACAGTAGAGAGGAAATGAAAGGAGAAACAGATGTAGAG 5664
Qy 3692 CATGTATATATAGAGCAATGTGACAGAGTTTCTTGAAATATGCAATATATGATA 3751
Db 5665 ACTTGAAACAGCTACAAATCTCTACAGACATTTTCTTGAAACATCTAGAGAGTGT 5724
Qy 3752 GATTAGAGGAATTTAGTAGGAATGCTTTTCACTGTAATTTGGTTCTCT--TGA 3808
Db 5725 GGAATAGTATGATGAGGGGAGCTGTCTTGCAATTTGAATCTGGGTTTTGTCTCTCA 5784
Qy 3809 TTAAGTTTGGATCTCATCTGCATTTGACT--TGAGAGAGAAAGAAATGATTTAG 3864
Db 5785 TTGAGTTTGAAGGCTACCTTTTACCTTGAAATGAGAGGAAAGAGGGGTGTAT 5844

Qy 3865 GACCTATATCTGTTTCTTATTAACTAAGCAAGTGAAGAAAGACTTATTTGGTATTTTTC 3924
Db 5845 GACTCTTACCTCGAGGTTTACTAGTTACGAAATGGAACAGACACTCGGAGCTCTCTT 5904
Qy 3925 CCACAAAGTGAAGAACTTTCTTCTTACTGTTGTGCAAAAGGTGGAATATAGAAAGCCT 3984
Db 5905 GACAAAAAATGGAACCTGTTGTGTCTTGTGTTTCTTTTGTTTTAAAGACACAGG 5964
Qy 3985 TAAATGTTGGTGAATACATGTTCAAAAGTCATTTGATGAGATGTTTAAATCAGAG 4044
Db 5965 CAAGCCCGACACATAGGTTGAATGTGGGCTTTGATGACAGCTTTTGTGATGAGAC 6024
Qy 4045 TGTCAATCATTTGGCTTCCCTGACCACTTGAAAGATTTCTTGTATACACATPAA 4104
Db 6025 TCATCAATAGTT-----GATCATGTCTAGGTGAGGGCTAC 6060
Qy 4105 ATACAGAAACAAATGATGATGACTAAGAAAAAGTCATGCAATTAATCTCATCTGTTTAA 4164
Db 6061 CTGTACAGCCGAGCCCTGTGCTGCTCGCACTTAACATCTCCAGGCTTCAGTATCACTTC 6120
Qy 4165 GAAAGTTTAAATTTCTGTTAGGGTCAATCAAAAGCTGTCTGGCCATGTGGGCTG 4224
Db 6121 TGCTACTTAGACAGTTAGAGAGTTGACCAAACTTTTTC----- 6162
Qy 4225 TGGGCTCAGGTTGACAAAGCTCTTATTAAGTAATCTGTCAATAGATAGTTTGAAGCTGC 4284
Db 6163 -----AACCCCACTAAATTTAATTAAGCAAAAGACTGTGTAATTTGTGG 6207
Qy 4285 AAAACAGCCCAAGCATATATGGTGGCACTCGGATCCCAAGATCCAGCTCACTTCA 4344
Db 6208 GATACAGTGTGATTAATGA----- 6226
Qy 4345 GTCTCTGTCTCTGTGTTAAGAGGGGTGTCACTCTGCCCCAGCTTTTAAACAGCTTC 4404
Db 6227 -TCTATGTGTCATTTGCAAGGTTCATAATAGATATTAAGCCCATCAACAGCTTT 6285
Qy 4405 ATTAGTGTAGGTGACCTTGAAATGTATGCTGTGTGTGCTT--CTAGTCCAGAGAGCC 4463
Db 6286 ATGGGTGTGAATCAAGTAATATAGGTAGATGCTGTGTGTCTTAGGTCAAGAAAGGC 6345
Qy 4464 GTCAATTTAGCTTTTGGCAAAATCATACATACTAAGGAT-----TTAC 4511
Db 6346 ATGATTTAAGGTCTTGGCAAAATCATATTAATCTCATGCTAAAAATACATTATGTGAT 6405
Qy 4512 TATGAATGTTTCAAAATGCTTAAACTCGGTTCTGTCTCCATCAACTATCTTGCAG 4571
Db 6406 TATTAATCTTTTAAAGAGGTGATACTTGTGTTTGTGCTGACGAAAGCAATGTACCA 6465
Qy 4572 TTCT--AATTTGTCATTTAGAAACATGCGATTAATGTCTCAAAATCTTTTGCATTC 4628
Db 6466 GCTCTTCTTAATCTGTACCACTTTAGAAATGTCACTGTGCTCAAAATTTGGTTGTATTC 6525
Qy 4629 TTAATTTCAAGCTTGAGAGAGTGAAGATCAAAACATTTGAGAACTGGAATTTCTG 4688
Db 6526 TTATTTCAATGCTTGAGAGAGTGAAGATCAAGCGATGAGGAACTGTGAGCTGTG 6585
Qy 4689 TTTATGTCTGAGAAATGCTGATTTGACCAAGAGCAAGCTGAAATATGATTAATCTAA 4748
Db 6586 TTTATGTCTGTGAGAAATGCTGTGCTGTGAGCCGAGAAAGCTTGAAGAAAGCAATCTGC 6645
Qy 4749 CCCCCTTCCCTGTAGAAATTAACATTAAGTGGCCCAAAAGCATTTT 4797
Db 6646 TCTTCTGCTGCTTCTAAGAAAGCAATTAAGATCCCTGAATGAGACTTTT 6694
RESULT 9
AAA28818
ID AAA28818 standard; DNA; 5935 BP.
XX AAA28818;
AC
XX
DT 04-SEP-2000 (first entry)

Qy	1049	CTCCTTCCTCCCTCTTCCACAGACGCCCTTACCCTCACTCTCTCTTCCCTACCC	1108
Qy	1109	TAACTAGCAGGAAGTGTCTTGGCAGAGTGTATCAGAGTCA-----TTGGG	1161
Qy	1319	CTTCCCTCTTCTATCTCAGTAAGAACCCGAGGTCTCCTCTCTCTTCCACAAAGTGA	1378
Db	1379	GAGGGCCTCAGACCAACCACATCATAGGCCATTGAATAGGTACAAAGGCTTTGGC	1438
Qy	1162	ATCATAGATTTTGTCTTTTGTCTTGTACGTACATCTTGAGTTTATAGTGGTAATG	1221
Db	1439	TTCAATTGAGTAATCTTTGAGTTTGTATTAGTTAAGCTTTATTGTTTATTCATGAA	1498
Qy	1222	GGGTCTGGAATTAATGTACAGAACCCGACTTGGTTTGTCTTGGAAAAAGCACTC	1281
Db	1499	AGAAATCACTCAAAATCTGTAGAGTGAAGAAAGTGTGGAAACGAAAAAGCCTAGAT	1558
Qy	1282	AGGTTGCTGTA---GATGAGAAAGGTGTGGGAAAAATCTAGCTGTGGAAATGATCCA	1338
Db	1559	AGGAAACAGATCTGTGTAGTACAGTACTTATGGGGGGGGGGGCGAGGGGGGATATCCA	1618
Qy	1339	TTGAGTCTAAGTTTGAAGGGGAGGGGATGGCATGGAGAAATTAGAAGAGAAAGTGG	1398
Db	1619	CTGAGTCCAAAGTACTTGTGGAGAGAAATCCATGATGACAAAGTACTTGTGGGGAAAG	1678
Qy	1399	AAATGGGAAGGCTTAAGTGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG	1450
Db	1679	AAATGGCAGAGCAAGCAAGTGAAGGGAAAGAGAAAGATGAGAGAGGCTTCATATGGTGGG	1738
Qy	1451	TGTATGGGAAGCCCAAAATCGAGGCGGTGTAATCTGATGCCCTGAACTTTGAAC	1510
Db	1739	TGTGAAAGGTCACTCTTTTTCATGTGATGAGAGTTAAGAAAAATCAGTGTGTGAGTT	1798
Qy	1511	TATGAAAAAAGTTTGAAGTGTGGAGTGGGCCAGTAAAGGCCCTAGGACTTATGGAAGG	1570
Db	1799	TGATGTCTTCAACACACCCCACTATGTCAGACTGTGGAGACCTGGCAATTAGGGA-AGG	1857
Qy	1571	GCTTAATTTTTCATGAGATGTTTATGTATGATCTTTCTTGTCTAAGCATGCAATTTCTG	1630
Db	1858	CGGGCTTTTTCACAGAGAACTTATGTCTATCTCTGTGTCTACATCCCACTTTGAT	1917
Qy	1631	GAGATACATGAGGTTTATCTCTTACAGATTTGCAATTAATCTACCTCGCTCTTCCAC	1690
Db	1918	GAGGTTAAGCTCAGGTTTCTGTTCT-----ACGTTCTTGGCTAC	1956
Qy	1691	AAATGCCAACTCAGTAGATTTCCCAAGATGAAGAGAGTCTCTTTGAAGGAAGTGA	1750
Db	1957	TGTGGAATCTCAGTAGAGTCTCCCAAGACGAGACAGCTCTTCTGTAAGGAGGAGC	2016
Qy	1751	CTGATTCGTGGCGTCCAGAGGATTCAGAGCTCAGAAATCTAGGTCAGCTTGAATC	1810
Db	2017	CTGATTTCAAGTGTCTAGAGAACGAATAGCTCAGAAATCTAGAGTCAAGTGAATCT	2076
Qy	1811	TAGGTCATTTGGGCAAAATTACTAAGAGCTTAAATTCAGGTGAATTTGACTGTACTC	1870
Db	2077	AGGTACAGCGGGCAAAATAGCTGAAGCCTTATTCAGGTGAACGCTCAGCTGCTC	2136
Qy	1871	CATGGGTGTGAGGTTCAATAAGTTTCAGCAACAATTAAGTATGATGTGTATGTG	1930
Db	2137	AGATATCTAGAGTATTTGGGCTCCACCGATTAAGATTTCTTTAGTGA-GTCTCTTTTA	2195
Qy	1931	TTTTATAGCATATTTGAAGGTATGACTGTATATCCAGAGAGATGTGCAAAAGCTGAAG	1990
Db	2196	TTTTGACACATCAGTGTGACGACGACGATCCAGAAATGTCAAGAAAGCTGAAGG	2255
Qy	1991	ACACAGTAAAAAGGTGAGCTGATTAATGTCAATGTCTAATGTATGTCAATGTGAGACA	2050
Db	2256	AGACAGTAAAAAGGTATTTTGGCAAGCAATATCAATCAATCAATCAATCAATCAATCA	2315
Qy	2051	AATGTTGTTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	2110
Db	2316	GGAATTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	2373
Qy	2111	CTACACACAGGGGCAAT---ACCTTGGTGTCTGTATGATGATTAATATCTATATCTTA	2168
Db	2374	CTAGCTGTGCTCAATTAATCTAGTCTAGTGTGACCTGTGATCTAGCTGGGTCTATAGTCT	2433
Qy	2167	GATGTCACTTTCCAAATCTTGCAAATTTGATGAATTTGAACTGTGGGTCTTAACT	2226
Db	2434	TCAATCTGTGTCTAAATTT---GTATGTCAAAATTTGTGAGCTGTGCAAAAGCTTAACTC	2490
Qy	2227	GTCTAGTCAATACTCAGATTTCTGGGGAAATGTGAGGGAGAGATTAAGGCTGAATGC	2286
Db	2491	AGCAGTCTCATGAGCACTTGTCTGGAGATGCTTGTGACAGGTCAATGCTAGAAAGC	2550
Qy	2287	AGGTCTCTGAATCCCAAGCCAGCACTTTTCCGGGTGTGATACAGATTAAGTTTGTATC	2346
Db	2551	AGCATCCCTGATTTCCAGCTGTGAC-TTGCTGTGTGGCCACGATTAATTAATCTTAAGCT	2609
Qy	2347	CATTAAATCTTAGGAAATTTCAATTTCTTAATTAATCTAATGTAATCTGAAAGTACTTG	2406
Db	2610	GATTAAATTTTGGGAAA--GCCAAATTTCCACCACTCAATATTCGAAAGACATGCA	2467
Qy	2407	TTTAAAAACAGAAAAATGCTTATGGGCAAAATTTTATGAAGTCAATTTTGAAGCATTA	2466
Db	2668	TTGAAAACTAGAAA---GCTGGGCAACAACTTATAGATGATTTTGAAGCTCATTA	2723
Qy	2467	TGATTTCTTGAATCTTGAAGATTAATTAATCTGAAACATGAGAAAGAGCTGACCTTC	2526
Db	2724	ACTGATCTCTGAATGTGATCAAAATCAACCCAGAAATTAACAAAGAGCTGATTTGC	2783
Qy	2527	ATTAAGGCTTAATTTCTGAGTAAATAACCTTAT-----TTGAATATCATATA	2578
Db	2784	AAATGAGCAAGTATTTAGATCACTGTATTAACAGCTGTCACTTTAATTAATAATAG	2843
Qy	2579	TCT---ATCAGATATTGATTAATGTTTAAAGAGAGAGCAAC--CCGATCTCTTT	2634
Db	2844	TGTCTATTTAGCTGCTATTTAAGATTAACACAGAGTGAATATCTCCCATTTACTG	2903
Qy	2635	ATACAGTTCAATAGATTAATAATTTAGTAAGATTTATTAAGTTAAATGAAGTCT	2694
Db	2904	GGCTGTGTTCAATAGATTAATAATTAATCAATGATTAATTAATGATGTCAAGAAAGTA	2963
Qy	2695	TGAATGGTAAAGCTTTTCTTCTCTCTCTCTCCATCAAGACCTTCATCTGATTTCT	2754
Db	2964	TGAGTGTGAAC---CTTCTCTTACTTTTACTTCTTCTTCTTCTTCTTCTTCTTCT	3020
Qy	2755	CTTCACTCCCTCAACAAATCCCTAGGAGCATTTATCAATGTGGCTGTGTGATATTT	2814
Db	3021	TCTTCAACCCGTATCAAGCACTAAGAACCTTATCTGTCTGAGCATTTATATGACT	3080
Qy	2815	CTATAGGATGATTAATCATATGTGTGCTTATTTGTGAAAAAGACA--ACAATGAAGC	2872
Db	3081	TTACAGCAACAAATTTGCTGTGTGTCTTTTGGGAAAGGAAACGATGACGAGAGGC	3140
Qy	2873	TTAGACTAACAA-TAGTGACTCACCCCAAAACCGGAGATGATTTAGAGCACTGAAAGT	2931
Db	3141	TCAGGCTAGAAATCTGAGCTCACTAAGCAAGAGCATGTTATAGCAGAGAAAGT	3200
Qy	2932	GAGCTCTT--GCAAGAGGTACAACTAAATCTCAGAAACAT	

DB 3430 TGGGCTTGATGTTAGCATGCCAAGACACACTTCGATGCTGTGTAAAGATTAT 3489
QY 3231 TACTGATTTCACTTGTGTTGTTTGTAGAAAAGTGAAGTGAAGAGAAATCTCA 3290
DB 3490 TATTCATTACT-----TTGTCTTTGGAAAAGGTGAAGTGTGTGTAGAAAAGACTCA 3541

RESULT 10
ID AAS14878 standard; DNA; 5935 BP.
XX AAS14878;
AC AAS14878;
XX 19-DEC-2001 (first entry)
DT 19-DEC-2001 (first entry)
DE Mouse partial genomic DNA for T cell derived inducible factor, TIFbeta.
XX Mouse, T cell derived inducible factor; TIFbeta; ds; antiallergic;
KM antiaesthetic; cytokine; interleukin-9; IL-9; STAT transcription factor;
KM cancer; lymphoma; immune system disorder; allergy; asthma;
KM acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
KM thyroiditis; melanoma; hepatoma.
XX Mus musculus.
OS US2001024652-A1.
XX US2001024652-A1.
PD 27-SEP-2001.
XX 29-DEC-2000; 2000US-0751797.
PF 18-OCT-1999; 99US-0419568.
XX 26-OCT-1998; 98US-0178973.
PR 16-JUL-1999; 99US-0354243.
XX (DUMO/) DUMOUTIER L.
PA (LOUA/) LOUAHD J.
PA (RENA/) RENAULD J.
XX Dumoutier L, Louahed J, Renauld J;
PI WPI, 2001-638496/73.
XX New isolated nucleic acid molecules encoding T cell inducible factors,
PT useful as markers for expression or effect of interleukin (IL)-9 in a
PT subject and diagnosing susceptibility to asthma or allergy -
PS Claim 1; Page 21-23; 26pp; English.
XX The invention relates to an isolated nucleic acid molecule, which encodes
CC a T cell derived inducible factor (TIF) which are upregulated by the
CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor
CC activation. The TIF proteins (or their mutants) may be used to test IL-9
CC ant/agonists for their potency against lymphomas, immune system
CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
CC or inhibit differentiation of tissue types in which they are active and
CC therefore be used to develop treatments for melanomas and hepatomas.
CC The present sequence a partial genomic sequence for mouse TIFbeta.
XX Sequence 5935 BP; 1732 A; 1174 C; 1346 G; 1683 T; 0 other;
SQ

Query Match 13.6%; Score 650; DB 22; Length 5935;
Best Local Similarity 56.5%; Pred. No. 1.8e-160;
Matches 1863; Conservative 0; Mismatches 1285; Indels 152; Gaps 29;

QY 29 CTCCTTCCCGACGACAGTGTGCTCGAGTTAGATTGTCTGCAATGAGCGCCCTGAGAA 88
DB 356 CTCCTCTCAGTATCACTTTTGAACCTTGTCGATGCGTATGCTCTCTGAGAA 415
QY ATGTGAGCTCTTTCTTATAGGGAACCTGGCCACCAAGTCTCTCTTTTGTGGCCCT 148

DB 416 ATCTATAGATTTTTCCCTTATAGGGAAGTGTGGCCGAGCTGCTGCTCTCATGTCCCT 475
QY 149 CTGTGATAGGAGAGAGAGAGAGTGGCCCATAGTCTCCACCTGACGCTTGACAGTCCAA 208
DB 476 GTGGGCCCGAGAGCAATGTGCTGCCCATAAACCCGGGCAAGCTTGAGGTCCAA 535
QY 209 CTCGAGAGCCCTATATATACCAACCGACCTTCATGTGCTGAGATATATCATCTC 268
DB 536 CTCGAGAGCCGTCATATGTCACCGACCTTTATGTGTCGACAGAGATGACGTCCA 595
QY 269 AATCCGCTCTTTCGTTGATGATCTACTGGAATCCAAATGTTCTTAACCTTTCTTCA 328
DB 596 TCTCTTCTCCATACACCGCTTGCCATTTCTGAAACACTGGAACCTTTTAGGGCC 655
QY 329 GAGCATCTTAAGACTTTAGAACCCACTGTTATCCCTGAGGTAATATTTTCTG 388
DB 656 GCTTATCTCCGAGGTCTCACTACTATGTTTCTGTCT-----CTTTAGAG 703
QY 389 TTTTTCAGAGACTCTTGGGAATCTGCTTTTTTTTTCTGTAACCTTCTTCCAT 448
DB 704 ACTCTTAAAGACTGGATCTTTTCTATTTCTAATTTCAAGTCTGAGACATTTCTAT 763
QY 449 TTTGACCTTTATGATATATGATGATATTTTCCAAAGAGCGGCATTCATATCAT 508
DB 764 CTGGCCTTCAGAGACATATATCTGATTTTATCTACAGAGCGGCTTT--AGAAAGCA 821
QY 509 CTGATGATTTTTTTTCCCTTATAGCTCTGTCATTTGTTCTAACTATGACACATCTG 568
DB 822 CCGACAGCTGCAATCTTTCCATCTGTTGCTCTCTGAACTCACTCTCTGGC 881
QY 569 AATCTGCTTTAGTCTTTATGATGATGCTCTGAGGGAACGGAGTGGGCACTGCTAT 628
DB 882 TACTC-----CTGAACCCACTGCGACATATATCTTAC 916
QY 629 GATTAATTTTTTTCTATTTGCTCATGTCAGACCTTATGTTTCTTCTCTTCCAG 688
DB 917 TTACAGGCTTTCTTCATCTCTCTGTGTACCCAGCACTTAGAGTTTTC-TCTCTTCA 975
QY 689 GCTAGCTTGGCTGATTAACAACAAGAGCTGCTCATTTGGGAGAAACTGTTCCAGCA 748
DB 976 GCCAGCCTTCAGATTAACAACAAGAGCTGCTCATGAGGGAATACTGTTCCAGGA 1035
QY 749 GTCAGTGAAGCTACAGTTGTGACGAAGAGCGCTGTGCCATGGGTCTTGGGT 808
DB 1036 CTCAGTGAAGCTCTCAGCTGTGATGAGAGGCT-----TAGCTGCGGAGGT 1082
QY 809 GGTGTGATGATGTTTATGTTTATCCCTATGACCTTTGTTCCCTTCCACTG 868
DB 1083 GGTGAGCCCTCTGGATAG--TCTGAAGTATGACCTGCTGCTTCTTGTACTGCT 1138
QY 869 AGATAGTAGAGGCTGCTATCTGATGAGAGAGTGTCACTTCACTTGAAGAAGTGC 928
DB 1139 AGCTTAAGATAGAGTCTACGATGAGAGAGTGTCTCACTTCACTTGAAGAAGTGC 1198
QY 929 TGTTCCTTCAATCTATAGTGTTCACGCTTATATGAGAGAGTGTGCTTCTGAGCA 988
DB 1199 TGTCTCCCGACAGCAAGAGTGTCCGCTTATATCAGAGAGTGTGCTTCTGAGCA 1258
QY 989 GGCTCAGCAACAGGTTAGCAATGTGTAAGTTAGCTGTCCAGCTATGCCACCTACC 1048
DB 1259 AACTCAGCAATAGCTAGCTCTGTGTAAGTGTGCTGTGCTATGCTCTCTCT 1318
QY 1049 CTCCTTCCCTCTCCACAGAGACCCCTTACCCCACTCTCTCTTCCCTTCCCTCA 1108
DB 1319 CTCCTCTCTTATTTCAAGTAAAGACCGAGGCTGCTCTCTCTTCAACAAGTGA 1378
QY 1109 TAAGTACGAGAAAGAGTGTCTTGGACAGACTGTTATAGAGATCA-----TTGGG 1161
DB 1379 GGAAGGCTCAGACACACCATCATATGCGCACTGTAATAGTGCACAAAGCTTTGGC 1438
QY 1162 ATCATAGAGTATTTGTTTGTGTTGACTGATCATCTTATAGTTATAGTGAATG 1221
DB 1439 TTCAATTAGTATATCTTGAAGTTGATTAAGCTTTATTTGTTTATCATGAGA 1498

QY 1222 GGGCTCGAAGCTTAAGTGTACAGAGCCCGCATGGTCTTGGAAAAAGGCAATC 1281
DB 1499 AGAAATCAACTCAAAATTCGTAGGATGAGAAAGATGTGGAAACGAAAAAGGCGTAGAT 1558
QY 1282 AGGTGGCGTAA---GATGAGAAAGGTGTGGGAAAAATCTAGCTGTGAAATGATCCA 1338
DB 1559 AGGAAACAGATCTGCTGAGTACAGTACTTATGGGGGGGGGGGCGAGCATTCACA 1618
QY 1339 TTGAGTCTAAGTGTGAGGGGAGGGGATGCGATGAGAGAAATTTAGAGAGAAAGTGGG 1398
DB 1619 CTGAGTCCAGTACTGTGGGAGAGAAATCCACTGATGACAAAGTCTTGTGGGGGAGG 1678
QY 1399 AAATGGGAAGGCTTAAAGTCGTGGTGGGTGGGAGACTGTGCCC-----TGTGTA 1450
DB 1679 AATGGCACAGACGAAAGTTGAAGGAAAGAGAGATGAGAGGCGCTCAATGTGGGGG 1738
QY 1451 TGTGATGGGAGCGCAAAATGGGAGCGGTGTGAATGTATGCGCGCTGAACATTTGAAC 1510
DB 1739 TGTGAAGGTCACTCTTTTCCATGTATGAGAGATTAAGAAAAATCAGTGTGAGT 1798
QY 1511 TATGAAAAAAGTTTGAAGTGAAGTGGGCGCAGTAAAGGCCCTAGGACTTACGAAAGG 1570
DB 1799 TGAATGCTCAGACAGCCCACTATGCGAGACTGTGGGAGACTGGCAATTTAGGA-AGG 1857
QY 1571 GCTTAATTTTCACTAGATGATGTTTATGATGATCTTGTCTTACGATGCAATTTCTG 1630
DB 1858 CCGCGCTTTTCAACAGAAACTTATGCTCATCTTGTGCTACACTCCACCTTTGAT 1917
QY 1631 GAGATACGATGAGGTTTATTCCTTACAGAAATTGCAATACTCCGCTCTTTCCG 1690
DB 1918 GAGGTAAAGCTCAGGTTGCTT-----ACCGTCTTGTCTAC 1956
QY 1691 AAATGCAAACTCAGTATGATTTCCCAAGATGAGAGAGTCTCTTGAAGGAAGTGA 1750
DB 1957 TGGTGAATCTTCAAGTGAATTCCTCCAAAGAGAGACGCTCTTGTGAAGGAGGAC 2016
QY 1751 CTGATTTGCGGCTCCAGAGGAATTCAGAGCTCAGAAATCTAGTCACTGTTGAATC 1810
DB 2017 CTGGAATTCAGTCTCTAGAGAAACGAAATAGCTCAGAGATCTAGGTCAAGTGAATCT 2076
QY 1811 TAGGTATTTGGGCAAAATTTACTAAGACTTTAATTCAGGTGAATTTACTGTAATC 1870
DB 2077 AGGTACAGCGGCAAAATGACTGAACGCTCTATTCAGGTGAACGCTGACGTCCTC 2136
QY 1871 CATGGGTGAGAGTTCATAAAGTTTCAAGCAACATTAAGATGATGTTGTTATG 1930
DB 2137 AATATACTGAGATATGGGCTCCACCGGATTAAGTCTGTATGTA-GTCTGCTTTTA 2195
QY 1931 TTTTATAGCATATTGAAGTGAATGACTGTCATATCCAGAGATGTGCAAAAGCTGAAG 1990
DB 2196 TTTTGCAGACATCAGTGTGAGACCAACATCCAGAAAGATGCAAAAGCTGAAG 2255
QY 1991 AACAGTGAAGAAAGTGAAGTGAATGATGATCTCAATGCTAAGTGAAGAGACA 2050
DB 2256 AACAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2315
QY 2051 AATGTGTTTCTTCT 2110
DB 2316 GGGATTTCTTCT 2373
QY 2111 CTACCAACAGGCGGAT---ACTTGTGTCTGTGTATGATATATATATATATCTA 2166
DB 2374 CTACGTCTGTGTCTATCTACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2433
QY 2167 GATGTGATTTCCAAATCTTGAAGATTTGAAGTGTGAAGTGTGTGTGTGTGTGTGT 2226
DB 2434 TCAATCTGTGTCTAAATTT---GTAGTCAAAATCTGTGAGCTAGAGAAAGCTTAGCTC 2490
QY 2227 GTCTAGTCAATTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATG 2286
DB 2491 AGCGAGTCTCATGAGCACTTGTGCGAGGATGCTTGTGTGTGTGTGTGTGTGTGTGT 2550

QY 2287 AGGTCTCTGATTCCTCAAGCCAGCACTTTTCCCGGTGTGATCAATTTAGTTTGTGAC 2346
DB 2551 AGCATCCCTGATTTCCACACTCTGCAC-TTGGCTAGTGGCCAGGTGAATTTACTTAGCCT 2609
QY 2347 CATTAATTTCTAGGAAATTTCAATCTCTATATGATCTATGATCTGAGAGTACTTG 2406
DB 2610 GATTAAGTATTTGGGAAA---GCCAATTTCCACCGACTTACATTAATCCGAAGACATGCA 2667
QY 2407 TTTAAAAACAGAAATATGCTTATGAGCAATTTATTTGAAGTCAATTTGAAGTCAATTA 2466
DB 2668 TTGAAAATCTAGAA---GCTGGGCAAACTTACTAGAGATTTTGTGACTCAATTA 2723
QY 2467 TGCATTTCTTGAACCTTGAAGAAATTAATCTCAGAACTGAGAAAGAGCTGACCTGC 2526
DB 2724 ACTGATGCTCTGAATGTGATCAATTCACAGATTAACAAAGAGCTGGAATTTGC 2783
QY 2527 AATAGGCTAATTTCTGAGATTAATAACACTTA-----TTGAATTTCAATTA 2578
DB 2784 AATATGACAGATTTTGAATCACTGCTGATTAACAGCTGTGATCTTAATTAATTAATAG 2843
QY 2579 TCT---ATCAGATATTGATTTATGATTTTAAAGCAAGACAGACAAAC-CCCGATCTCTTT 2634
DB 2844 TGTCTATTTAGCTGCTATTTAAGATTTAAACAGAGAGTGAATACCTTCCCAATTTACG 2903
QY 2635 ATACAGTTCAAAATAGTAAATAATTAAGTAAAGATTTATTAATGTTAAATGAAGTCT 2694
DB 2904 GCGCTGTTTCAATGAGTAAATAATATCAGTATGATTAATTAATGATGATGAAAGTA 2963
QY 2695 TGAATTTGATGCTTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2754
DB 2964 TGAAGTGAAGACC---CTTCTCTTAACTTTTAACTTCTTAACTTAAATTAATTTTCT 3020
QY 2755 CTTTCACTCCCTCAACAAATCCCTAGGAGCATTTATTCATGATGAGTGGTGTGATCT 2814
DB 3021 TCTTACACCTCTGATCAAGCCACTGATGAAGCACTATCTGCTGCAAGCTATTAATGAT 3080
QY 2815 CTATAGTGAATGATCAATCATGTGCTTATTTGTTGTAAGAAAGACA--ACAATGAAGG 2872
DB 3081 TTACAGCAAAACAACTTCTGTGTGCTCTTGTGGGAAAGGAAAGGATACAGAGAGG 3140
QY 2873 TTAGCTAACA-TAGTATCTACCCCAAAACCGGAGAAATTAAGAGCTGTAAT 2931
DB 3141 TCAGGCTGCAAGTGTGACTCACTTAAGCAAGGAGCATGTGATGACAGAAAGT 3200
QY 2932 GACGCTCTT-GCAAGCAGTACCACTAATACTCAGAAATGAGAGCTCCAGTTGATG 2990
DB 3201 GAGGCTCTTCAAGTGTGTGCTTAAATGATCAAGAAAGGAGGCTGTGATGATG 3260
QY 2991 AATTTTCAAGTAAAGCTTAACTTAATTTCCCTTTTCTCTCTCTCTCTCTCTCTCTCT 3050
DB 3261 AATATGATGAATGATATACCTTATCTCC-----TTCTTATTAAGAACTAAACG 3313
QY 3051 GCGTTTCTCTGAGCATATTAATGATGATGATGATGATGATGATGATGATGATGATG 3110
DB 3314 TCTCTCTCTCTGTGTGTGAGCTGATTAACAAGCTGTGT---TTCTTTGAGTGTGATG 3371
QY 3111 CTGTGATTTTAAATTTGGAAGCCAGTCTCTGTTATTAAGAACTTATTAATGATGATG 3170
DB 3372 CTTTGCAATTTTCACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3429
QY 3171 GAGGCTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3230
DB 3430 TGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3489
QY 3231 TACTGATTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3290
DB 3490 TATTCATTTACT-----TTGTCTTTGGAAGTGAAGTGTGTGTGGAAGAACTCA 3541

RESULT 11
AAD30660
ID AAD30660 standard; DNA; 5935 BP.
XX

AC AAD30660;
 XX 21-MAY-2002 (first entry)
 XX Mouse TIF beta genomic DNA.
 XX T cell derived inducible factor; TIF; Interleukin-21; IL-21; mouse;
 XX STAT transcription factor; acute phase protein; inflammation; ds.
 XX Mus musculus.
 XX MO200210393-A2.
 XX 07-FEB-2002.
 XX 27-JUN-2001; 2001MO-US20485.
 XX 27-JUL-2000; 2000US-0626617.
 XX (LUDM-) LUDWIG INST CANCER RES.
 XX Dumoutier L, Renaud J;
 XX WPI; 2002-195964/25.
 XX Stimulating expression of STAT transcription factor and inducing
 XX production of acute phase protein in a cell, involves contacting a cell
 XX capable of expressing STAT with T cell derived inducible factors -
 XX Example 9; Page 61-64; 64pp; English.
 XX The invention relates to nucleic acid molecules encoding T cell
 XX derived inducible factors (TIFs) also known as interleukin-21 (IL-21).
 XX TIF polynucleotides are upregulated by the cytokine, IL-9. IL-TIF or
 XX IL-21 molecules are implicated in activation of STAT transcription
 XX factors, acute phase proteins and inflammation. The present sequence
 XX is mouse TIF beta genomic DNA.
 XX
 XX Sequence 5935 BP; 1732 A; 1174 C; 1346 G; 1683 T; 0 other;
 XX
 XX Query Match 13.6%; Score 650; DB 24; Length 5935;
 XX Best Local Similarity 56.5%; Pred. No. 1,8e-160;
 XX Matches 1863; Conservative 0; Mismatches 1285; Indels 152; Gaps 29;

DB 764 CTTGGCCCTCAGACACATATCTGATTTTATCTACAGAGCGCGTT--AGAAAGCA 821
 QY 509 CTGATGATTTTTTTCTTTTATGCTCTGTGCAATGTTTAACTCATGACACATCTG 568
 DB 822 CCCAGACTGCAATATCTTCATCTCTGTGCTCTCTTCTGAACTCATATCTCTTGGC 881
 QY 569 AATCTGCTTTTACTTTTATGATGCTCTGTGGGAGACGGGATGGGGGCATGTCAT 628
 DB 882 TATCT-----CTGAGACCACTGGCGACATCATCTCTAC 916
 QY 629 GTATATAATTTTTTCTATTGCTCAATGTCACACCCCTTACTTTTCTCTCTCCAG 688
 DB 917 TTACAGGCTTTCTTCATCTCTCTGTGACACCAAGCACTTAGGGTTTCTCTTACG 975
 QY 689 GCTAGCTTGCTGATTAACAACACAGAGCTGTCTCATTTGGGAGAACTGTTCCACGA 748
 DB 976 GCCAGCCTTGAGATTAACAACACAGAGCTGTGCTCATGGGAGAACTGTTCCGAGA 1035
 QY 749 CTCAGTGTAACTACAGTTGTGACGAACAGGCGGTGTGCTCCATGGGTACTTGGGGT 808
 DB 1036 GTCAGTGTAAGTCTCTCACTGTGATGACGAGGC-----TAGCTGCGGAGCT 1082
 QY 809 GGTGTGATGATGTTTATGCTTATCCCTTATGACCCCTTCTGTTTCCCTTCCACCTGC 868
 DB 1083 GGTGACCTCTGGAATG---TCTGACGTATGACCTCTCTCTCTTCTTGTCTACTGCT 1138
 QY 869 AGATGAGTGAAGCTGTGATCTGATGAGAGAGTGTGAACCTTACCTTGAAGAAGTGC 928
 DB 1139 AGGCTAAGATCAATGCTACTGATGAGAGAGTGTCAACTTCACTCTGAAAGCATTC 1198
 QY 929 TGTTCCTCAATGTGATGAGTTCAGCTTATATGACAGAGGTGTGCTCTCTGAGCA 988
 DB 1199 TGTCTCCCACTGACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1258
 QY 989 GGCCTCAGAAAGGCTTAAGCAATGATGATGATGATGATGATGATGATGATGATGATG 1048
 DB 1259 AACTGAGTAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1318
 QY 1049 CTCCTTCCCTCTTCCACAGAGACCCCTTACCCCACTCTCTCTCTCTCTCTCTCTCT 1108
 DB 1319 CTTCCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1378
 QY 1109 TAACTAGACAGAAAGAGTGTGCTGACAGAGTGTATCAGAGTCA-----TTTGGG 1161
 DB 1379 GAGGGCTCTGACACACACACATCATATGAGCACTGTAATAAGTCAAAAGGCTTTGGC 1438
 QY 1162 ATCATAGATATTTGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1221
 DB 1439 TTCAATGATGATTAATCTTGAATTTGATTTGATTAAGCTTATTTGTTTATTCATGGA 1498
 QY 1222 GGGCTGGAATTAAGTGTATGATGAGAGCCGATGTTGTTCTTGGAAAAAAGCACTC 1281
 DB 1499 AGAATCACTCAATTTCTGATGATGAGAAAGATGTTGGAGAGAAAAAGCCTTAAAT 1558
 QY 1282 AGTTGCTTAA---GATGAGAAAGTGTGGAAAAACATCTAGCTGTGAAATGATCCA 1338
 DB 1559 AGAGAAACAGATCTGCTAGTATGACTTATGAGGGGGGGGGGGGGGGGGGGGATATCCA 1618
 QY 1339 TTGACTTAAGTTGTTGAGGGGAGGGATGCGATGAGAGAAATTTAGAGAAAGTGGG 1398
 DB 1619 CTGAGTCCAGATCTTGTGGAGAGAAATCACTGATGATGATGATGATGATGATGATG 1678
 QY 1399 AAATGGAGGCTTAAGTGTGAGTGTGGGTGGGAGACTGTGTTGCC-----TGTGA 1450
 DB 1679 AATGCAACAGACAAAGTTGAGAGAAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1738
 QY 1451 TGTCTAGGAGACCAAAATGAGAGCGTGTGAACCTTATGATGCGCTGAACATTTGAAAC 1510
 DB 1739 TGTGAAGTCACTCTTTTCTTCTGATGATGAGAGTTAAGAAAAATCAGTGTGAGATT 1798
 QY 1511 TATGAAAAAAGTTTGAAGTGTGAGTGGGCGCCAGTAAAGCCCTAGAGCTTACTGAAGAG 1570

Db 1799 TGATGCTTCAGACACCCCACTATGAGAGACTGTGGAGACCTGGCAATTAGGGA-AGG 1857
 Qy 1571 GCTTAATTTTCACATAGATGTTTATGTAACATTCTTGTCTTAACATGCAATTTCG 1630
 Db 1858 CCGGGCTTTTCACACAGAAACCTTATGCTCATCTCTTGCTACACCTCCACCTTTGAT 1917
 Qy 1631 GAGATACGATGAGTGTATTTATCTTACAGAAATTTGCAATAAATCTACCTGGCTTTCCAC 1690
 Db 1918 GAGGTTAACTCAGGTTTCTTCT------ACGGTCTTGCTAC 1956
 Qy 1691 AATGCAAACTCAGTAGAATTTCCCAAGATGAGAGAGTCTCTTTAGAGGAAGTA 1750
 Db 1957 TGGTGAACCTTCAGTAGATTTCCCAAGAGAGAGACGCTCTTCTGTAAGAGAGGAC 2016
 Qy 1751 CTGAGATTCGGGCTCCAGAGGAATTAAGAGCTCAGGAATCTAGTCACTGTTGAATC 1810
 Db 2017 CTGAGATTCAGTCTCTAGAGAACGAAATAGCTCAGAGATCTAGGTCAACGTGAATCT 2076
 Qy 1811 TAGGTCAATGTTGGGCAAAATTAATAAGACTTTAATTCAGAGTAATGCTGTAACCTC 1870
 Db 2077 AGGTACAGCGGCAAAATGACTGACGCTCTTATTCAGGTGAACGGTCACTGCTC 2136
 Qy 1871 CATGGGTGAGGTTCAATMAAGTTTCAGACACACTTAAGATAGTATGTTGTTATG 1930
 Db 2137 AGATATCTGAGATATGGGCTCCACCGGATTAAGTTCTGTTAGTA-GTCTGCTTTTA 2195
 Qy 1931 TTTTATAGCATTTGAAGTGATGACCTGCAATTCAGAGAAATGCAAAAGCTGAAG 1990
 Db 2196 TTTTCAGACATCATGCTGTGACGACAGAACATCAGAAAGATGCAAGAGCTGAAG 2255
 Qy 1991 ACAGGTGAAAAGGTAGAGCTGATATCTGTAAGCTTAAGTCAATGCAATAGAGAGACA 2050
 Db 2256 AGACGTGAAAAGGTACTATGTTGGCAGACCAATACTAAGCCATTCAGTGAAGACGTG 2315
 Qy 2051 AATGTTGTTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2110
 Db 2316 GGGATTTCTTCTCTGCTTCCAGTCT--CTTCTAATTGTTAATCTTCTTCTTCTTCT 2373
 Qy 2111 CTACCAACAGGCGGCT--ACTTTGGTCTGTGATGATGATATATATATATATATAT 2166
 Db 2374 CTACTGCTGTGCTCACTACTCACTTAGCTGACCTGACCTAGCTGAGGCTATAGATCT 2433
 Qy 2167 GATGCACTTCCCAATCTTGCAATTTGTAATTTCTAGAACTGTTGGATCTTAGCTT 2226
 Db 2434 TCAATCTGTGTAAATTT--GTAGTCACAATTTCTGAGCTAGCAAAAAGCTTAGCTC 2490
 Qy 2227 GTCTAGTCAATTAACCTCAGATTTCTGGGATGGTCAAGGAGAGATAGGGCTAGATGC 2286
 Db 2491 AGCCAGTCTCATGACACTTGTGAGAGATGGCTTGTGACAGATCAATCTGAGAAAC 2550
 Qy 2287 AGGTCTCTGAAATCCAGACGACATTTCCCGTGTGATACAGATTAGTTTGTGATC 2346
 Db 2551 AGCATCCCTGAATCCCACTGTGAC-TTGCTAGTGGCCACGTGATATCTTAGCT 2609
 Qy 2347 CATTAATCTTAGGAAATTTCAATTTCTTATGACTATGATATGTAAGACTCTTG 2406
 Db 2610 GATTAAGTATTTGGAAA--GCCAATTCACACCGACCTAATATCCAGAAAGACATCA 2467
 Qy 2407 TTTAAAAACAGAAAATGCTATGGGCAATTTAATTTGAATCACTTTTGAAGCATTA 2466
 Db 2668 TTGAAACTGAAA--GCTGGGCAAACTTACTAGATGATTTTGTGCTCATTTAA 2723
 Qy 2467 TGCATTTGCTGAAACTTTGAAAGATAAACTCAGAACATGAGAAAGAGCTGATTC 2526
 Db 2724 ACTGATGCTGAAATGATCAATCAATCAACAGAAATTAACAAAAGAGCTGATTC 2783
 Qy 2527 AATAGGGCTAATTTCTGAGATTAATAACTTAT------TTGATATATCATATA 2578
 Db 2784 AATATGACAAATTTAGAAATCACTGTATTAACAGTCTCATCTTAATTAATTAATAG 2843
 Qy 2579 TCT--ATCAGATATGATTTAGTTTAAAGCAAGAGCAGACAAC--CCGATCTCTTT 2654
 Db 2844 TGTCTATTTAGCTGCTGCTATTTAAGATTAACACAGAGTGAATTACTTCCCAATTTACTG 2903

Qy 2635 ATACAGTTCAATAGATAAAATATTAATAGTAAGATTTATATAGTTAAATGAGATC 2694
 Db 2904 GGCTGTTTCAATAGATAAAATATCAGTATAGATTAATATATAGTCTATGAAAGTA 2963
 Qy 2695 TGAATTTGTAAGCTTTTCTTCTCTCTCTCCATCAAGACCTTCATTTAGTTCTT 2754
 Db 2964 TGAAGTGAACCC--CTTCTCTTACTTTTAACCTTCAATTTCTTATTAATTTTCTT 3020
 Qy 2755 CCTTCACTCCCTCAACAATCCCTGAGAGCAATTAATCAATGAGGCTGCTGATTT 2814
 Db 3021 TCTTACACCTGATCAAGACCACTATAGTAAAGCCTATCTGCTGCAAGCTATATATGACT 3080
 Qy 2815 CTATAGTAATGATCAATCATATGTGGCTATTTTGTGAAAAGACA--ACAATGAGAGC 2872
 Db 3081 TTACAGCAACAACTATGCTGTGTGCTCTTTGGGGAAGGGAACAGATAGCAGAGAGC 3140
 Qy 2873 TTAGCTAACAA-TAGTACTCACCCCAAAACCGAGGAATGATTAAGAGCAGTGAAGT 2931
 Db 3141 TCAGGCTAGCAAGTGTGACTCAACTTAAGCCAGAGGCAATGTGATAGCAGAGAAAGT 3200
 Qy 2932 GACGCTTT-GCAAGCAGTACAACTAAATCTCAGAAACATGAAGGCTCCAGTTGATG 2990
 Db 3201 GAGGCTTTCAAAAGTGGGTGTCTTAATGATATCAAGAAACAGAAAGCTGTGATG 3260
 Qy 2991 AATTTCAATACAGCTTAACCTTAATTTCCCTTTTCCCTCTGACTTTTAAAAA 3050
 Db 3261 AATATACATGTAAGATATCTACCTTATCTC-----TTCTTATAGAACTTAACCG 3313
 Qy 3051 GCGTTTCTCTGAGCATATTAATGAGTGAAGTCTTCTCTTCTTATTAATGAAG 3110
 Db 3314 TCTCTCTCTTGTGTGAGGCTGATTAACACGCTGTGT--TTCTTTGAGTGTTCATG 3371
 Qy 3111 CTTTGATTTTAATTTGTAAGCCCACTCTCTTGTATAGAACTATATCTAGACTG 3170
 Db 3372 CTTTGAGATTTTGAATGCTCTGCAAGTCTTGT--TAGAGGTTTGTATCTTGAACAC 3429
 Qy 3171 GAGGCTGAATGTAGCATGCGACAGACAAAGCATGCTTACATCTGCTTAAAAAT 3230
 Db 3430 TGGGCTTGATGTTAGATGCGCAAGGACACACTTCTGAATGCTGTGTAAGGTTAT 3489
 Qy 3231 TACTGATTTCACTGCTGTGTGTTCTTTAGAAAAGTGAAGTGTGAGAGAGAACTCA 3290
 Db 3490 TATTCATTTACT-----TTGTCTTGAAGGTGAAGTGTGTGAGAAAGAACTCA 3541

RESULT 12
 AAD27153
 ID AAD27153 standard; DNA; 5935 BP.
 XX AAD27153;
 AC
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Mouse T cell derived inducible factor (TIF) beta genomic DNA.
 XX
 KW T cell derived inducible factor; TIF; cytokine; interleukin-9; IL-9;
 XX protein therapy; STAT activation; differentiation; mouse; ds.
 OS Mus musculus.
 PN US6331613-B1.
 XX
 PD 18-DEC-2001.
 XX
 XX 18-OCT-1999; 99US-0419568.
 XX
 XX 26-OCT-1998; 98US-0178973.
 PR 16-JUL-1999; 99US-0354243.
 XX
 PA (LUDWIG-) LUDWIG INST CANCER RES.
 XX
 PI Dumoutier L, Louheid J, Renaud J;

QY 1811 TAGGTCATTGTGGGCAAAATTAAGCTTAATTCAGGGAATTTGACTGTAACCTC 1870
 DB 2077 AGGTACACAGCGGCAAAATTAAGCTTAATTCAGGGAATTTGACTGTAACCTC 2136
 QY 1871 CATGGGTGTGAGGTTCAATTAAGTTTCAGACAACTTAAGTATGCTGTTATG 1930
 DB 2137 AATATTAAGTATGAGGTTGAGGTTCCAGCGGATTAAGTTCTGTTAGTGA GTCTGCTTTTA 2195
 QY 1931 TTTTATAGCAATTAAGGATGATGATGATGATGATGATGATGATGATGATG 1990
 DB 2196 TTTTACAGACATGATGATGATGATGATGATGATGATGATGATGATGATG 2255
 QY 1991 AACAGTGAAGAAAGTATGATGATGATGATGATGATGATGATGATGATG 2050
 DB 2256 AACAGTGAAGAAAGTATGATGATGATGATGATGATGATGATGATGATG 2315
 QY 2051 AATGTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2110
 DB 2316 GGGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2373
 QY 2111 CTACACACAGGCGGATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2166
 DB 2374 CTACGTCGTGTCATTAAGTATGATGATGATGATGATGATGATGATGAT 2433
 QY 2167 GATGTCAGTTCCAAATCTGCAATTTGATGATTTGATGATTTGATGAT 2226
 DB 2434 TCMACTGTGTCTTAATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2490
 QY 2227 GTCTAGTCACATTAAGTATGATGATGATGATGATGATGATGATGATG 2286
 DB 2491 AGCCAGTCTCATGATGATGATGATGATGATGATGATGATGATGATGAT 2550
 QY 2287 AGGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2346
 DB 2551 AGCATCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2609
 QY 2347 CATTAATCTTAAGGAAATTTGATGATTTGATGATTTGATGATTTGAT 2406
 DB 2610 GATTAGTAATTTGGGAAATTTGATGATTTGATGATTTGATGATTTG 2466
 QY 2407 TTTAAAGACAGAAATGATGATGATGATGATGATGATGATGATGATGAT 2466
 DB 2668 TTGAAATCTAGAAAATTTGATGATTTGATGATTTGATGATTTGAT 2723
 QY 2467 TGCATGCTTTGAAATTTGATGATTTGATGATTTGATGATTTGATGAT 2526
 DB 2724 ACTGATGCTGTAATTTGATGATTTGATGATTTGATGATTTGATGAT 2783
 QY 2527 AATATGAGCTAATTTCTGATGATTTGATGATTTGATGATTTGATGAT 2578
 DB 2784 AATATGAGCTAATTTCTGATGATTTGATGATTTGATGATTTGATGAT 2843
 QY 2579 TCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2634
 DB 2844 TGTCTATTTAGCTGCTAATTTGATGATTTGATGATTTGATGATTTGAT 2903
 QY 2635 ATACAGGTTCAATTTGATGATTTGATGATTTGATGATTTGATGATTTG 2694
 DB 2904 GGCCTGTTCAATTTGATGATTTGATGATTTGATGATTTGATGATTTG 2963
 QY 2695 TGAATGTTAGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2754
 DB 2964 TGAATGTTAGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3020
 QY 2755 CTTTCACTCCCTCAACAATTTGATGATTTGATGATTTGATGATTTGAT 2814
 DB 3021 TCTTCACTCCCTCAACAATTTGATGATTTGATGATTTGATGATTTGAT 3080
 QY 2815 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2872
 DB 3081 TTACAGCAAAACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3140
 QY 2873 TTACAGCAAAACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2931

DB 3141 TCAGGCTAGCAAGTCTGATCTCAACCTTAAGCCAGAGCATGTTGATAGCAAGAAAGT 3200
 QY 2932 GACCTCTTTT-SCAAGCAGAGTCAACTAAATCTAGAAACATGAGGCTCCAGTTGATG 2990
 DB 3201 GAGCTCTTCAACAAGTGGTGTGCTTAAGTATCAGAAACAGAAAGCTCTGGTTGATG 3260
 QY 2991 AATTTTCAGTACAGCTTAACTTAATTCCTTCTTCTTCTTCTTCTTCTTCTT 3050
 DB 3261 AATATTCAGTAAAGTATCTACCTTATCTCC-----TCTCTTATGAAAGCTAAACG 3313
 QY 3051 GCGTTTCTCTGAGCATCATTTATAGTGTGATGCTTTCTTCTTCTTCTTCTTCTT 3110
 DB 3314 TCTCTCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3371
 QY 3111 CTTTGATGTTTAAATGTTGAAGCCAGCTTCTTCTTCTTCTTCTTCTTCTTCTT 3170
 DB 3372 CTTTGCAGATTTTACGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3429
 QY 3171 GAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3230
 DB 3430 TGGGCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3489
 QY 3231 TACTGATTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3290
 DB 3490 TATTCATTTACT-----TTGCTTTTGAAGGTGAAGTGTGTGTGTGAAGAACTCA 3541

RESULT 13
 ID AAA28839 standard; cDNA; 690 BP.
 AC AAA28839;
 DT 04-SEP-2000 (first entry)
 DE Human T cell inducible factor cDNA.
 KW TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;
 KW Anti-asthmatic; anti-allergic; cytoskeletal; inhibitor; antagonist;
 KW probe; chromosome 12q15; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 72..611
 FT /*tag= a
 PN W0200024758-A1.
 PD 04-MAY-2000.
 PE 18-OCT-1999; 99WO-US24424.
 PR 26-OCT-1998; 98US-0178973.
 PR 16-JUL-1999; 99US-0354243.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Dumoulier L, Louhed J, Renaud J;
 DR WPI; 2000-422495/36.
 DR P-PSDB; AAY92879.
 PT New nucleic acid molecule encoding a T cell derived inducible factor
 PT for treating asthma, an allergy or lymphoma
 PS Claim 1; Page 38; 46pp; English.
 CC This cDNA encodes a human T cell derived inducible factor (TIF). The gene
 CC was mapped to chromosome 12q15. The human TIF was identified based on
 CC homology to a murine TIF, which was identified by subtraction cloning
 CC from a murine lymphoma cell line BWS147 in the presence or absence of

FT CDS 72..611
FT /*tag= a
FT /product= "Human TIF protein"
XX
PN NO200210393-A2.
XX
PD 07-FEB-2002.
XX
PF 27-JUN-2001; 2001WO-US20485.
XX
PR 27-JUL-2000; 2000US-0626617.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Dumoutier L, Renaud J,
XX
DR WPI; 2002-195964/25.
DR P-PSDB; AA019237.
XX
XX
XX Stimulating expression of STAT transcription factor and inducing
PT production of acute phase protein in a cell, involves contacting a cell
PT capable of expressing STAT with T cell derived inducible factors .
XX
XX
PS Claim 6; Page 55-56; 64pp; English.
XX
CC The invention relates to nucleic acid molecules encoding T cell
CC derived inducible factors (TIFs) also known as Interleukin-21 (IL-21).
CC TIF polynucleotides are upregulated by the cytokine, IL-9. IL-TIF or
CC IL-21 molecules are implicated in activation of STAT transcription
CC factors, acute phase proteins and inflammation. The present sequence
CC is human TIF cDNA. The TIF gene is located on chromosome 12.
XX
SQ Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;

Query Match 5.4%; Score 258; DB 24; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.7e-57;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACAGCAGAACTTTTCAGAACAGGTTCTCTCCCGAGTCACCAAGTTGTCGAGTTAG 60
DB 1 TGCACAGCAGAACTTTTCAGAACAGGTTCTCTCCCGAGTCACCAAGTTGTCGAGTTAG 60
QY 61 AATTGCTGCATGCGCGCCCTGCAAGAAATCTGTAGGCTTTCTCTATGGGACCTGG 120
DB 61 AATTGCTGCATGCGCGCCCTGCAAGAAATCTGTAGGCTTTCTCTATGGGACCTGG 120
QY 121 CCACGAGCTGCTCTCTCTTTGGCCCTTTGTGTAAGAGAGAGACAGCTGGCCCATCA 180
DB 121 CCACGAGCTGCTCTCTCTTTGGCCCTTTGTGTAAGAGAGAGACAGCTGGCCCATCA 180
QY 181 GCTCCACTGACAGGTTTGAACAAGTCCAACTTCACAGCCCTATATCAACCAACGACCT 240
DB 181 GCTCCACTGACAGGTTTGAACAAGTCCAACTTCACAGCCCTATATCAACCAACGACCT 240
QY 241 TCATGCTGCTAAGAGG 258
DB 241 TCATGCTGCTAAGAGG 258

Search completed: July 19, 2003, 09:44:01
Job time : 709.876 secs

Db 121 CCACGAGCTGCTCTTCTTCTTGCCCTCTTGCTACAGGAGAGAGAGCTGGCCCATCA 180
Qy 181 GCTCCCACTGACAGGCTTGACACAGTCCAACTTCCAGAGCCCTATATACCAACCGCACCT 240
Db 181 GCTCCCACTGACAGGCTTGACACAGTCCAACTTCCAGAGCCCTATATACCAACCGCACCT 240
Qy 241 TCAATGCTGCTAAGAGAGTATACATCTCAATCTGCTCTTCTCTTGATCTACTTGA 300
Db 241 TCAATGCTGCTAAGAGAGTATACATCTCAATCTGCTCTTCTCTTGATCTACTTGA 300
Qy 301 ATCCAAATAGTCTTAACTTCTTCAAGAGCATCTCTAAGAGCTTAGAGAACCACTGT 360
Db 301 ATCCAAATAGTCTTAACTTCTTCAAGAGCATCTCTAAGAGCTTAGAGAACCACTGT 360
Qy 361 TTAATCCCTGAGGAGTAAATTTTCTGTTTTTTCAGAGACCTCTTGGAAATCTGCTTT 420
Db 361 TTAATCCCTGAGGAGTAAATTTTCTGTTTTTTCAGAGACCTCTTGGAAATCTGCTTT 420
Qy 421 TTTTTTTTCTGAACCTTCTCTCTTCCATTTTGGCCCTTATGATACATATGATATTTT 480
Db 421 TTTTTTTTCTGAACCTTCTCTCTTCCATTTTGGCCCTTATGATACATATGATATTTT 480
Qy 481 CCCAAAGAGGAGCATTCAGATATCCATGATGATTTTTTCTCTTATGCTGTG 540
Db 481 CCCAAAGAGGAGCATTCAGATATCCATGATGATTTTTTCTCTTATGCTGTG 540
Qy 541 CATTTGTTCTAACTGACACACATCTGAATCTGCTTTTATGCTTATGATGTTGCTCT 600
Db 541 CATTTGTTCTAACTGACACACATCTGAATCTGCTTTTATGCTTATGATGTTGCTCT 600
Qy 601 GGGGAGACGGGATGGGGACATGCTATGATATAATTTTTTTCTATTTGCTCAATGCTC 660
Db 601 GGGGAGACGGGATGGGGACATGCTATGATATAATTTTTTTCTATTTGCTCAATGCTC 660
Qy 661 AGACCCCTAGTCTTTCTCTCTCTTCCAGGCTAGCTTGGCTGATACAAACAGAGCTGTG 720
Db 661 AGACCCCTAGTCTTTCTCTCTCTTCCAGGCTAGCTTGGCTGATACAAACAGAGCTGTG 720
Qy 721 TCTCATTTGGGAGAACTGTTCCACGAGTCACTGATAGCTACAGTTGTGACGAAAGGG 780
Db 721 TCTCATTTGGGAGAACTGTTCCACGAGTCACTGATAGCTACAGTTGTGACGAAAGGG 780
Qy 781 CCGTGTGCCCTCACTGGGTACTTGGGGTGTGCTGATGATGTTTATGCTTATCCCTTA 840
Db 781 CCGTGTGCCCTCACTGGGTACTTGGGGTGTGCTGATGATGTTTATGCTTATCCCTTA 840
Qy 841 TGAACCTTTCTGTTTTCCCTTCCACCTGCAATGATGATGATGATGATGATGATGATG 900
Db 841 TGAACCTTTCTGTTTTCCCTTCCACCTGCAATGATGATGATGATGATGATGATGATG 900
Qy 901 GTGCTGAACCTTCAACCTTGAAGAGTGTCTTCCCTCAATCTGATAGTTCCAGCTTAT 960
Db 901 GTGCTGAACCTTCAACCTTGAAGAGTGTCTTCCCTCAATCTGATAGTTCCAGCTTAT 960
Qy 961 ATGACAGAGAGTGTGCTTCTGCGCAGGCTCAGCAACAGGCTTAAGCATATGTAAAGT 1020
Db 961 ATGACAGAGAGTGTGCTTCTGCGCAGGCTCAGCAACAGGCTTAAGCATATGTAAAGT 1020
Qy 1021 TGAAGCTCTAGAGCTAGCCCACTACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Db 1021 TGAAGCTCTAGAGCTAGCCCACTACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Qy 1081 CCCAACT 1140
Db 1081 CCCAACT 1140
Qy 1141 TGTATATAGAGATATTTGGGATGATAGATATTTGCTTTGCTTTATGATGATGATGATG 1200
Db 1141 TGTATATAGAGATATTTGGGATGATAGATATTTGCTTTGCTTTATGATGATGATGATG 1200
Qy 1201 TTGAGTTATATGAGTGAATGGGCTGGAACCTTAAGTATACAGAACCGGATGAGTTG 1260
Db 1201 TTGAGTTATATGAGTGAATGGGCTGGAACCTTAAGTATATGATGATGATGATGATG 1260

Qy 1261 TCTTGGAAAAAGGCACTCAGTGTGCTAAGATGAGAAAAAGTGTGGAAAAATATCTA 1320
Db 1261 TCTTGGAAAAAGGCACTCAGTGTGCTAAGATGAGAAAAAGTGTGGAAAAATATCTA 1320
Qy 1321 GCTGTGAAAAATGATCCATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 1321 GCTGTGAAAAATGATCCATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Qy 1381 ATTAAAGAGAAAGTGGGAAATGGGAGCTTAAAGTGGTGGTGGGAGACTGT 1440
Db 1381 ATTAAAGAGAAAGTGGGAAATGGGAGCTTAAAGTGGTGGTGGGAGACTGT 1440
Qy 1441 GGCCTGTTGATGCTCATGGGAGCCCAAAATGAGAGGGGTGGAACCTTGATCCCTCTGA 1500
Db 1441 GGCCTGTTGATGCTCATGGGAGCCCAAAATGAGAGGGGTGGAACCTTGATCCCTCTGA 1500
Qy 1501 CATTTGAAACTATGAAAAAAGTTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
Db 1501 CATTTGAAACTATGAAAAAAGTTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1560
Qy 1561 ACTGAAAGAGGCTTAATTTTCAATGAGATGTTTTATGATATTTCTGTTCTAAAGATG 1620
Db 1561 ACTGAAAGAGGCTTAATTTTCAATGAGATGTTTTATGATATTTCTGTTCTAAAGATG 1620
Qy 1621 CAATTTTCTGAGATACGATGAGGTTTTATCTCTTACAGAAATTTGCAATCTACCG 1680
Db 1621 CAATTTTCTGAGATACGATGAGGTTTTATCTCTTACAGAAATTTGCAATCTACCG 1680
Qy 1681 CTCTTTCCAAATCCAAATCCCTCAGTAGGATTTCCCAAGATGAGAGAGAGTCTCTGTA 1740
Db 1681 CTCTTTCCAAATCCAAATCCCTCAGTAGGATTTCCCAAGATGAGAGAGAGTCTCTGTA 1740
Qy 1741 AGGGAAGTACTGATGATTTGCGGCTCCAGGGAATTCAGAGCTCAGAAATCTAGTCA 1800
Db 1741 AGGGAAGTACTGATGATTTGCGGCTCCAGGGAATTCAGAGCTCAGAAATCTAGTCA 1800
Qy 1801 TGTGAAATCTAGATATTTGAGGCAAAATCTAAGAGCTTTAATCCAGGTGAATTTGT 1860
Db 1801 TGTGAAATCTAGATATTTGAGGCAAAATCTAAGAGCTTTAATCCAGGTGAATTTGT 1860
Qy 1861 ACTGATACCTCAATGGGTGAGGTTCAATAAAGTTACAGCAACATTAAGATAGTTATG 1920
Db 1861 ACTGATACCTCAATGGGTGAGGTTCAATAAAGTTACAGCAACATTAAGATAGTTATG 1920
Qy 1921 CTGTTATATGTTTATAGCATATGAAGGTGATGACCTGCAATCCAGAGAAATGTCAA 1980
Db 1921 CTGTTATATGTTTATAGCATATGAAGGTGATGACCTGCAATCCAGAGAAATGTCAA 1980
Qy 1981 AAGCTGAAGACACAGTGAAGAAAGTGAAGATGATGATGATGATGATGATGATGATGAT 2040
Db 1981 AAGCTGAAGACACAGTGAAGAAAGTGAAGATGATGATGATGATGATGATGATGATGAT 2040
Qy 2041 AGGAGAGCAAAATGTTGTTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2100
Db 2041 AGGAGAGCAAAATGTTGTTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2100
Qy 2101 CTGATTTCTCTACCAACAGGAGGATTAATTTGTTGTTCTGTGATGATGATATATCTATA 2160
Db 2101 CTGATTTCTCTACCAACAGGAGGATTAATTTGTTGTTCTGTGATGATGATATATCTATA 2160
Qy 2161 TATCTGATGATGATGATTTCCAAATCTTGGCAATTTGATGATTTAGAACTGTTGGATCT 2220
Db 2161 TATCTGATGATGATGATTTCCAAATCTTGGCAATTTGATGATTTAGAACTGTTGGATCT 2220
Qy 2221 TAGCTGTCTAGACATATACCTCAGATCTGAGGATGCTCAGTGGCAGAGATAGAGGCTA 2280
Db 2221 TAGCTGTCTAGACATATACCTCAGATCTGAGGATGCTCAGTGGCAGAGATAGAGGCTA 2280
Qy 2281 GAATGAGGATCTCTGAAATCCCAAGGCAACCTTTCCGGGTGATGATCAGATTAAGTTT 2340
Db 2281 GAATGAGGATCTCTGAAATCCCAAGGCAACCTTTCCGGGTGATGATCAGATTAAGTTT 2340

QY 2341 TGGTACATTAATCTTAGGGAATTTGAGATTCCATTTGACTAGTAATCTGAAG 2400
DB 2341 TGGTACATTAATCTTAGGGAATTTGAGATTCCATTTGACTAGTAATCTGAAG 2400
QY 2401 TACTGTTTAAAAAAGAAAAATGCTATGGCAATTTAATTTGAAGTCAATTTTGAAGT 2460
DB 2401 TACTGTTTAAAAAAGAAAAATGCTATGGCAATTTAATTTGAAGTCAATTTTGAAGT 2460
QY 2461 CATTAATGCAATGCTTTGAAACCTGGAAGATTAATCTGAAACAAATGAGAAAAAGCTGG 2520
DB 2461 CATTAATGCAATGCTTTGAAACCTGGAAGATTAATCTGAAACAAATGAGAAAAAGCTGG 2520
QY 2521 ACTTGCAATATAGGCTAATTTCTGAGATTAATCACTAATTTTGAATTAATCATATATC 2580
DB 2521 ACTTGCAATATAGGCTAATTTCTGAGATTAATCACTAATTTTGAATTAATCATATATC 2580
QY 2581 TATCAGATTAATGATTAATGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640
DB 2581 TATCAGATTAATGATTAATGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2640
QY 2641 GTTCAATATAGAGTAAATATATAGTAAAGATTTAATAGTAAATGAGAGCTGAAAT 2700
DB 2641 GTTCAATATAGAGTAAATATATAGTAAAGATTTAATAGTAAATGAGAGCTGAAAT 2700
QY 2701 GGTAAAGCTTTTCTTCTCTCTCTCCATCAAGACCTTCATTCATGTTCTTCTCTCA 2760
DB 2701 GGTAAAGCTTTTCTTCTCTCTCTCCATCAAGACCTTCATTCATGTTCTTCTCTCA 2760
QY 2761 CTCCCTCAACAAATCCCTTAGGAGAGATTTATCCATAGTGGGCTGCTGATCATTTCTATG 2820
DB 2761 CTCCCTCAACAAATCCCTTAGGAGAGATTTATCCATAGTGGGCTGCTGATCATTTCTATG 2820
QY 2821 TGAATGATACATCATGTCGCTATTTGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
DB 2821 TGAATGATACATCATGTCGCTATTTGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
QY 2881 ACAATAGTACATCAACCCCAAAACCGAGAGAGATTTAGAGAGAGAGAGAGAGAGAG 2940
DB 2881 ACAATAGTACATCAACCCCAAAACCGAGAGAGATTTAGAGAGAGAGAGAGAGAGAG 2940
QY 2941 GCAAGAGAGTACATTAATCTCAAGAAACATGAAAGGCTCCAGTTGATGAAATTTCACT 3000
DB 2941 GCAAGAGAGTACATTAATCTCAAGAAACATGAAAGGCTCCAGTTGATGAAATTTCACT 3000
QY 3001 AACAGGCTTAACCTTAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3060
DB 3001 AACAGGCTTAACCTTAATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3060
QY 3061 CTGAGCATCAATTAATGAGTGTGACTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3120
DB 3061 CTGAGCATCAATTAATGAGTGTGACTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3120
QY 3121 TTTAAATGTGAAGCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3180
DB 3121 TTTAAATGTGAAGCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3180
QY 3181 TGTGAGCATGCAAG 3240
DB 3181 TGTGAGCATGCAAG 3240
QY 3241 ATCTGCTGTTGTTGCTTTAGAAAAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 3300
DB 3241 ATCTGCTGTTGTTGCTTTAGAAAAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 3300
QY 3301 TGTGATTTTCAAGACCTTTAATCATTGAAAGATTAATCAATTTGCAATGGGTT 3360
DB 3301 TGTGATTTTCAAGACCTTTAATCATTGAAAGATTAATCAATTTGCAATGGGTT 3360
QY 3361 GGCATGTGAAGAGTATATGCTTTTGGTGTGAGTTCAGAAAAGAGAGAGAGAGAGAG 3420
DB 3361 GGCATGTGAAGAGTATATGCTTTTGGTGTGAGTTCAGAAAAGAGAGAGAGAGAGAGAG 3420
QY 3421 GCAATGTTGTTGAGAGAAAGATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480

DB 3421 GCAATGTTGTTGAGAGAAAGATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480
QY 3481 GTGTTTTGGAGGCAATTAATTCCTCTCTGTTGGGGGTAAAGAGAGAGAGAGAGAGAG 3540
DB 3481 GTGTTTTGGAGGCAATTAATTCCTCTCTGTTGGGGGTAAAGAGAGAGAGAGAGAGAG 3540
QY 3541 GTAAATGCAATGAG 3600
DB 3541 GTAAATGCAATGAG 3600
QY 3601 TCTTTGAGATGAGAAAGATCTTTTGGGCTTATGCAAAAGAGATGAGAAAGAGAGAG 3660
DB 3601 TCTTTGAGATGAGAAAGATCTTTTGGGCTTATGCAAAAGAGATGAGAAAGAGAGAG 3660
QY 3661 AAGGCGGAG 3720
DB 3661 AAGGCGGAG 3720
QY 3721 AGGTTTTCTTGAATTAATGCAATATGATTAATGATTAATGAGAGAGAGAGAGAGAG 3780
DB 3721 AGGTTTTCTTGAATTAATGCAATATGATTAATGATTAATGAGAGAGAGAGAGAGAG 3780
QY 3781 TTCACTTAATTTGGGTTCT 3840
DB 3781 TTCACTTAATTTGGGTTCT 3840
QY 3841 GAG 3900
DB 3841 GAG 3900
QY 3901 GAAAAAGCTTAATTTGATTTTCTTCCCAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 3960
DB 3901 GAAAAAGCTTAATTTGATTTTCTTCCCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3960
QY 3961 AAAAGGTGAATTAAGAAAAAGCTTAATGATTAATGATTAATGATTAATGATTAATG 4020
DB 3961 AAAAGGTGAATTAAGAAAAAGCTTAATGATTAATGATTAATGATTAATGATTAATG 4020
QY 4021 AGTGAAGATGTTTAAATCAG 4080
DB 4021 AGTGAAGATGTTTAAATCAG 4080
QY 4081 GAATGCTTGTGATCAACATTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4140
DB 4081 GAATGCTTGTGATCAACATTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4140
QY 4141 TGCATTAATCTCATCTGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4200
DB 4141 TGCATTAATCTCATCTGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4200
QY 4201 CTGTCCTGGGAG 4260
DB 4201 CTGTCCTGGGAG 4260
QY 4261 TGTCAATAGATGTTTGGAGCTCAAAACAGGCAAGAGAGAGAGAGAGAGAGAGAGAG 4320
DB 4261 TGTCAATAGATGTTTGGAGCTCAAAACAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 4320
QY 4321 CCCCAGATCCAGGCTCACTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4380
DB 4321 CCCCAGATCCAGGCTCACTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4380
QY 4381 TCTGCCAGCTTTTAAAGAGCTTCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4440
DB 4381 TCTGCCAGCTTTTAAAGAGCTTCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4440
QY 4441 GTGGCCTCTCAGTCCAG 4500
DB 4441 GTGGCCTCTCAGTCCAG 4500
QY 4501 AGGATATTACTATGAATGTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4560

Db 4501 AGGATATTAATGATGATGTTTACAAATGCTTAAACCTGTTCTGCTCCATCAACC 4560
Qy 4561 TAATCTGCAATTTCTAATTTGTTCACTTTAGAAAACATGSCATTAATGCTCAATACTT 4620
Db 4561 TAACTTGCATTTCTTAATTTGTTCACTTTAGAAAACATGSCATTAATGCTCAATACTT 4620
Qy 4621 TTGCAATTTCTTAATTTGTTCACTTTAGAAAACATGSCATTTAGAGAACTGG 4680
Db 4621 TTGCAATTTCTTAATTTGTTCACTTTAGAAAACATGSCATTTAGAGAACTGG 4680
Qy 4681 ATTGCTGTTAATTTGTTCACTTTAGAAAACATGSCATTTAGAGAACTGG 4740
Db 4681 ATTGCTGTTAATTTGTTCACTTTAGAAAACATGSCATTTAGAGAACTGG 4740
Qy 4741 ATAATAACCCCTTTCCCTCTGAGAAATTAACAATTAATGATGCTCCCAAGCATTTT 4797
Db 4741 ATAATAACCCCTTTCCCTCTGAGAAATTAACAATTAATGATGCTCCCAAGCATTTT 4797

RESULT 2

US-10-027-632-118181/c

Sequence 118181: Application US/10027632

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

POLYMERISMS IN THE HUMAN GENOME

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 118181

LENGTH: 1074

TYPE: DNA

ORGANISM: Human

US-10-027-632-118181

Query Match 22.4%; Score 1073.6; DB 15; Length 1074;

Best Local Similarity 99.9%; Pred. No. 1.6e-254;

Matches 1073; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2472 TGCTTGAACCTGGAAGATTAATCACTGAGAAATGAGAAAGAGCTGAGCTGATTA 2531
Db 1074 TGCTTGAACCTGGAAGATTAATCACTGAGAAATGAGAAAGAGCTGAGCTGATTA 1015
Qy 2532 GGGCTAATTTCTGAGATTAATCACTTATTTGATTAATCAATATATCTATGATAT 2591
Db 1014 GGGCTAATTTCTGAGATTAATCACTTATTTGATTAATCAATATATCTATGATAT 955
Qy 2592 GATTAATTTGATTAATCACTTATTTGATTAATCAATATATCTATGATAT 2651
Db 954 GATTAATTTGATTAATCACTTATTTGATTAATCAATATATCTATGATAT 895
Qy 2652 GATTAATTTGATTAATCACTTATTTGATTAATCAATATATCTATGATAT 2711
Db 894 GATTAATTTGATTAATCACTTATTTGATTAATCAATATATCTATGATAT 835
Qy 2712 TTTCTTCT 2771

Db 834 TTTCTTCT 775
Qy 2772 ATCCCTAGGAGAGATTTATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2831
Db 774 ATCCCTAGGAGAGATTTATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 715
Qy 2832 ATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2891
Db 714 ATCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 655
Qy 2892 TCACCCCAAAACCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2951
Db 654 TCACCCCAAAACCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 595
Qy 2952 CAATTAATATCTGAGAAATCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3011
Db 594 CAATTAATATCTGAGAAATCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 535
Qy 3012 CCTTAATTCCT 3071
Db 534 CCTTAATTCCT 475
Qy 3072 TTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3131
Db 474 TTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 415
Qy 3132 AGCCCAATTCCT 3191
Db 414 AGCCCAATTCCT 355
Qy 3192 CACAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3251
Db 354 CACAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 295
Qy 3252 TGCTTTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3311
Db 294 TGCTTTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 235
Qy 3312 AGACCTTAATTCCT 3371
Db 234 AGACCTTAATTCCT 175
Qy 3372 GAGTATTAATTCCT 3431
Db 174 GAGTATTAATTCCT 115
Qy 3432 CAGAGAAAGATCAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3491
Db 114 CAGAGAAAGATCAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 55
Qy 3492 AGGATTAATTCCT 3545
Db 54 AGGATTAATTCCT 1

RESULT 3

US-09-751-797-8

Sequence 8, Application US/09751797

Patent No. US20010024652A1

GENERAL INFORMATION:

APPLICANT: Dumoulier, Laure

APPLICANT: Louhe, Jamila

APPLICANT: Renaud, Jean-Christophe

TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible

FILE REFERENCE: LUD 5543.2

CURRENT APPLICATION NUMBER: US/09/751,797

CURRENT FILING DATE: 2000-12-29

PRIOR APPLICATION NUMBER: 09/419,568

PRIOR FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US09/178,973

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 8
LENGTH: 7445
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-751-797-8

Query Match 14.3%; Score 686; DB 10; Length 7445;
Best Local Similarity 53.8%; Pred. No. 3e-15;
Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

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2034 CTCTCTCTCACTTATCAACTGTGACACTGTGCACTTCTGATGAGCTGTCTGAGAA 2093
89 ATCTGTAGCTCTTCTCTTATGAGGACCTTGCCACAGCTGCTCTCTCTTGAGCCCT 148
2094 ATCTATGAGTCTTCTCTTATGAGGACCTTGCCGCGACGCTGCTCTCTCTTCCCT 2153
149 CTTGTACAGGAGAGACAGCTGCGCCATCAGCTCCCACTGCAAGCTTGACAAATCCAA 208
2154 GTGGGCGCCAGGAGCAATGCGCTGCCGCTCAACACCGGATGCAAGCTTGAGGTGCCAA 2213
209 CTTCCAGCAGCCCTATATACCAACCGCACTTCAGCTGCGCTAAGAGGTATACATCTC 268
2214 CTTCCAGCAGCCGATCATGTCACACCGCACTTATGCTGGCCAGAGGTACAGCTGCA 2273
269 AATCTGCTCTTCTGCTGTGATCTACTGGAATCCAAATAGTCTTAACTTTTCTTCA 328
2274 TCTCTTCTCTCATACCGCCCTTGCCATTTCTCTGAGACACTTGCAAACTCTTTAGGG 2333
339 GAGCATCTCTAAAGCTTTAGGAACCCACTGTTTATCCTGAGGGTATGATTAATTTCTG 388
2334 CCGTTATCTCCGAGGTCTCACTACTATGTTT-----TCTGCTCTTTAGAG 2382
389 TTTTTCAGACACTCTTGGGAATCGGCTTTTCTTTTCTTGAACCTTCTCTCCAT 448
2383 ACTCTTAAAGACTGGGCTTTTCTTATTTTCAAGTCTGAGACCATTTCTCTAT 2442
449 TTTGACCTTATGATCATATGATGATTTTCCCAAGAGCGGCCATTCAGTATCCAT 508
2443 CTTGGCTTCAAGACACATATCTGAAATTTTATCTACAGGGGCACTT--AGAAAGCCA 2500
509 CTGATGATTTTCTTCTTATGCTCTGCTGCTGCTTCTTAACTCATGACACATCTG 568
2501 CCCAGCATGCAATCTTCTCACTTCTGCTCTCTTCTGAACTCATATCTCTTGGC 2560
569 AATTCTGCTTTAGTCTTTATGATGTTGCTCTGGGAGACGGGATGGGCACTGTCTAT 628
2561 TAATC-----CTGAGACCCACTGCGACATACATCTCTAC 2595
629 GATTAATTTTCTTATTTGCTCAATGCCAGACCTTAAGCTTTCTCTCTCCAG 688
2596 TTACAGGCTTTCTTCACTCTCTTCTCAACCGACCTTAAGGCTTTCTCTCTTCAAG 2654
689 GCTAGCTTGGCTGATTAACAACAAGAGCTGCTCTCATTTGGGAGAACTGTTTCAAGGA 748
2655 GCCAGCTTGCAGATTAACAACAAGAGCTGCTCATGGGAGAACTGTTTCAAGGA 2714
749 GTGATGTAGCTACAGTTGTGACGAACAGGCGGTGCTGCTCATGGGATCTTGGGT 808
2715 GTGAGTGAAGTCTCTCACTGTGATGAGCAGGCG-----TAGCTGGGAGGCT 2761
809 GGTGAGTGAAGTGTAGGTCTTATCCCTTATGACCTTTCTGTTTCTCTCTCACTG 868
2762 GGTGAGCCTCTGGGATAG---CTGAGGATAGCCCTGCTCTTCTTGTACTCTG 2817
869 AGATGATGAGCGCTCTATCTGATGAGAGGCTGCTGAATCACCCTTGAAGAAGTGC 928
2818 AGGCTAAATATCATGCTCTACCTGATGAGAGGCTGCTGAATCACCCTGAGAGAGTTC 2877
929 TGTTCCTCAATCTGATGAGTTCAGCCTTATATGAGAGAGGTGCTCTCTGACCA 988

2878 TGCTCCCCAGTCAAGAGTTCAGCCCTACATGACGAGGTGACTCTTCTGTACCA 2937
989 GGCTCAACAAGGCTTAAGCACAATGTGAAGTTCAAGCTCTCAAGCTTATGCCACTACCC 1048
2938 AACTCAGCAATCAGCTCAGCTCTGTGTAAGTCACTGTGCTACCTATGCTCTCTCT 2997
1049 CTCCTTCCCTCTCTCAAGAGAACCCCTTACCCCAACTCTCTCTCTCTCTCTCTCC 1108
2998 CTCTCTCTTCTATTTCCAGTAAACCCGAGGTCTGCTCTCTCTCTCTCTCAAGGTGA 3057
1109 TAAGTACAGGAGAAAGTGTCTTGGCAGCAGGTATACAGAGTCA-----TTTGG 1161
3058 GAGGGCTCAGACACACCATCATATGAGCCACTGAATATAGTACAAAGCTTTGGC 3117
1162 ATCATAGATATTTGCTTTGCTTGTAGTCACTGATCATCTTGAATATAGTGAATG 1221
3118 TTCAATGTAGTATACCTTGTAGTGTATGAGGAAGCTTATTTGTTTATCATGAA 3177
1222 GGTCTGGAATTTAAGTACGAAGCCCACTTGTGTCTTCCGAAAAAGCAATC 1281
3178 AGAAATCAACTCAATTTCTGTAGATGAGAAAGATGTTGGAACGAAAAAGGCTTAGAT 3237
1282 A-----GGTTGGTAAATGAGAAAGTGTGG 1309
3238 AGAAGAAACGATCTGCTGATATATGATCTTATGGGGGAGCAGGGGCGATATCCATGA 3297
1310 GAAACATCTAGCTGTGAAATATGATTCATGATCTTAAATTTTGAAGGAGGAGATGG 1369
3298 GTACAGTACTTGTGGGAGAGAAATCCACTGATCAAGTACTTGTGGCATGAGATC 3357
1370 CATGAGAGAAATTTAGAGAGAAAGTGGAAATGGGAAGCTTAA-----1415
3358 CACTGTGCAAGTACTTGTGGGAGGAGAAATGGCAGACCAAAAGTTGAAGGAGAG 3417
1416 -----GTGGTGGTGGGTGGGAGACTGTGGCCCTGTGATGATGAGGA 1460
3418 AAGATGAGAGGCTCATGTGTGGGATGAAAGTCACTCTTTTCAATGATGAGAG 3477
1461 AGCCCAAAATCGAGGCTGTGAACTTGTATGCTGCACTTGAATGAAATGAAATGAA 1520
3478 AGTTAAGAAACAGT--GTGAGTGTGATGCTTCAACACCCCACTATGAAACAT 3536
1521 AGTTGATGAGTGGGCCCCAGTAAAGCCCTAGACCTTATCTGAAGAGGCTTAATTT 1580
3537 ATCCAGAGAGAGGCGGCAAGTGTGGAGAACCTGGCATTTAGGGA--AGGCGGCTTTT 3594
1581 CACATGAGATGTTTATATGATCTTCTGTTCTTGAAGCAATTTCTGAGATACGAT 1640
3595 CACAGAGAACTTATGCTCATCTTGTGCTACCTCCACCTTTGATGAGGTTCAAG 3654
1641 TGAGTTTATCTTCAAGATTTGCAATTAACCTCCGCTCTTCCAAATGCAAC 1700
3655 TCAAGTTGTTCT-----ACGTTCTTCTACTGTGTGAAC 3693
1701 CTCAGTGAATTTCCCAAGATGAAGAGAGTCTCTTGAAGGAAGTACATGATTTCTG 1760
3694 TTCAATGATTTCCCAAGAGAGAGAGAGTCTCTTGAAGGAGGAGCTGATTTCA 3753
1761 GGTCTCAAGGAAATTCAGAGTCAAGAAATCTAGTCACTGTGAATCTTAGTATTTG 1820
3754 GTGTCTTGAAGAGCAAAATGCTCAGAGATCTAGGTCAGAGAAATCTAGGTCACAG 3813
1821 TGGGCAAAATTTCAAGACTTAAATCCAGGGAATTTACTGTACTCTCAATGGGTG 1880
3814 GGGCAAAATGACTAGAGCTCTTATTCAGAGTGAAGGTCACTGCTCAATATACG 3873
1881 GAGTTCATTAAGTTTCAAGACAACTTAAGATAGTATGCTTATTTATTAAGCA 1940
3874 AGGTATTTGGGCTCCACCGGATTAAGTCTGTTAGGA--GTCTGCTTTATTTTGAAGA 3932
1941 TATGAGGTGATGACTCTCATATCTCAAGAGAAATGTCAAAAGCTGAAGACACAGTGA 2000
3933 CATAGCGGTGACGACCAAGATCCAGAAAGATGCAAGAGCTGAAGAGACAGTGA 3992

QY	2001	AAAGTGAAGACTGATTAAGTCAATGCTTAAGTCAATGCAATAGGAGAGACAAATTTGGTT	2060
Db	3993	AAAGTACTATTGGCAGACCAACAATACTAACCACTTACATGAG--GAGACGTGGGGAATTC	4050
QY	2061	TTCTTTCCCTTCTTTCTTCCCATCACTTTGATTTTTCACTTAATCTCTTACACAG	2120
Db	4051	TTTCTCTGCTTCCCAAGTCCCTTCTTAATTGTAACATTTTATTGAATCTGTCTACTAATCG	4110
QY	2121	GGCGATTA----CTTGGTGTCTGTGATATGATATATCTAATATCTAGATCTAGTT	2176
Db	4111	GTCAATTATCTGCTTAGCTGACCGCTGATCTAGCTGGGCTATATGATCTTTCAATCTGTG	4170
QY	2177	TCCAAATCTTCCAAATGTGAGAAATTTGAAATCTGATGGGATCTTAAGTGTCTAGTCAAC	2236
Db	4171	TCTAAATTT---GTAAGTCACAATTTCTGAACTGTAGCAAGAAAGCTTAAGTCTAGCCAGTCTC	4227
QY	2237	ATAACCTCAGATTCGAGGAGTGTCCAGTGGAGAGATAGGGCTAGATAGCAGTCTCTG	2296
Db	4228	ATGAGCACTTGTCTGGAGATGGCTGTGAGACAGGTCAATCTGAAAGACAGCATCTCTG	4287
QY	2297	AATCCCAAGCAGACACTTTTCCGGTGTGATACAGATTAAGTTTGGACCATTAATCT	2356
Db	4288	ATTCCCAAGCTGTCAAC-TTGCTCTAGTGGCCATGTGTATTAATCTTTGGCTGTATTAAGAT	4346
QY	2357	TAGGAAATTTTCAGATTCCTATTGACTCATGTAACTGAAAGATCACTTGTTTAAAAACA	2416
Db	4347	TTGGGAAA--GCCAGTTCCACGGACCTACATAATCTGAAAGAACATGCAATGAAAACTA	4404
QY	2417	GAAAAATGCTTAATGGGCATAATTTATTTGAATCAATTTTGAATCATTAATGCAATGCTT	2476
Db	4405	GAAA-----GCTGGGACACAAACTCTACAGATGATTTTGGACTCATTTAAACGAGATCTC	4460
QY	2477	TGAAACTTGGAAAGATTAACTCACAAACATAGAGAAAGAGCTGGACTGTGATAGAGCT	2536
Db	4461	TGAAATGTGGAAATTAACACCCAGAAATTAACAACAAAAGAGCTGATTTGCAAAATGAGACA	4520
QY	2537	AATTTCTGGA-----GTAAATAAACACTTATTTTGAATTAATCAATAATATCTACAGATA	2589
Db	4521	AGTATTTAGATCACTGSTATTTAATAGTATCACTTAATTAATAATATAGGCGCTAATATA	4580
QY	2590	TTGATTAATAGTTTAAAGCAAGACAGACAAAC--CCGATCTCTTTTAACAGTTCAAT	2648
Db	4581	TATATTTAAGATTAACACAGAGGTGATGCTCCCAATTTACTTGAGCGCTGTTCAAA	4640
QY	2649	AGACTAAAAAATTAATAGTAAGATTTTATTAATAGTAAATGGAAGTCTGAATGTGAAGT	2708
Db	4641	AGAGTAAAAAATATAGTCATGATGATTAATTAATAGTGCATGAAAGATGAGATGAAACC	4700
QY	2709	TTTTTTTCTCTCTCTCCCATCAAGACCTTCATTCAGTTCTTCTCTTACTCCCTCA	2768
Db	4701	TTTCTCTTACTTTTAACCTTCA-----TTTCTTAAGTTTTTTTTTTCTTCCACACCTTGA	4752
QY	2769	ACAAATCCCTTAGGAGCAATTAATCAATGATGGGCTGTGTAATTTCTAATGTAATGAT	2828
Db	4753	TCAAGCACTAGTAAGCACTATCTGCTGTAGCTAATATATGACTTTAACGACAAACAC	4812
QY	2829	ACCAATCAATGTGGCTTATTTGTGTGAAGAAACA--ACAATGGAAGCTTAAGCTAACATA	2886
Db	4813	ATTCTGTGTGTGGCTCTTTTGGGGAAGGGAAACAGATATGACAGAGGCTCAGGCTTAGAGT	4872
QY	2887	GTGACTCAACCCCAAAACCGAGAGATATTTATGAGAGCAAGTAAATGACGCTCT--GGACG	2945
Db	4873	CTGACTTGCCCTTAAGCCAGAGCGATGTTATATGCAAGAAAGTGAAGCTCTTTCGAGAG	4932
QY	2946	CAGGTACAATPAATACTCAGAAAATGAAAGGCTCCAGTTAGTGAATTTTCAATPAACA	3005
Db	4933	TGGGTGTCTTAAGTAATCAAGAAACAGGAAGCTCCGGTGTATGGAATTAATCAATPAAT	4992
QY	3006	GCTTAATCTTAATTTCCCTCTTTTCCCTCTTGAATTTTAAAAAAGCTTTCTTCTGAG	3065
Db	4993	ATTAACCTTAATCTCTCTTAATGAAAC-----TAAATGCTCTCTTTTCTTGTG	5042

QY	3066	CATCATTTAATGAGTGGACGCTGTTCTCTCTTTGATATAATGAAGGCGTTGATGTTTAA	3125
Db	5043	TGTAGGCTGATAAACACACTGTTT--TTCTTTTGAAGTGTTCATGGCTTTGTAGATTTTAA	5100
QY	3126	TTGTGAAGCCAGAGTCTCTGTGTATATAACATATATCTATAGACATGAGGGCTGAATGTTA	3185
Db	5101	GTCGCTCGCCAGTTCCTTGTTAGAG--GGTTGTTCCTTGTACACCTGGCGCTTGGATGTTA	5158
QY	3186	GCATGCCACAGACAAAGGCATGCTTTTACACATCTTGTCTTAAAAATTACGTATTCATCTT	3245
Db	5159	GCATGCCAAAGGACACACACTTCTGATATGCCGTGTAAAAAGGTTATATTCATTTACT--	5215
QY	3246	GCTTGTGTCTTTTGAAAAATGGAAGGTGAGAGAGGAATCTCATGTGCA-----	3296
Db	5216	-----TTGTCCTTTGGAAGGTGAAGCGTGTGTGGAAGAATCTCACAGAGATGTGTTCT	5270
QY	3297	-----TCTGTGTGATTTCAAGACCTTTATTCATCTTTGAAAGATTCATTT	3342
Db	5271	CTGTAGGAAAACTTTTTCCTTCCCTTTAAATGCTTATATTCACCTTTCAGTCAAC--TT	5327
QY	3343	TCATATTTTGCATGGGTGCGCATGTGGAGAGATGATATGCTTTTTCGTGTAGCTTCA	3402
Db	5328	TGACTTTTATACATGCTGTTCACATGAAAGAGTGTTAGGCCCGCGCTCATGCGTCTGGG	5387
QY	3403	GAAAGCA--CAGAGGGAGAGCAATGTTGTTTCAAGAAAGATCAACAGAGAGACAACTGT	3461
Db	5388	AAAGGACCAATAGGGAGAAAGGATGTATGCTGTGAGAAATCTGACCGGACGGGAAACGTGT	5447
QY	3462	CAGAGCTGTGAAATAGGGTGTGTTTGGAGGCAATTAATTCCTCTCTGTGTGGGGGTAAA	3521
Db	5448	CAGAGCTCCCCGGAAGCA-----CCACAGGTGTTAAGTAGG	5485
QY	3522	AGCAGAAAGCAGGTGTGGAGTAAAT--GCATGACAGACAGAGGGACGATTAACCTTAA	3580
Db	5486	AACGCTCAGGGTGGGCTCATGTATATGAATGGAACAGAGCGAGGAAGATTAAGTACAA	5545
QY	3581	AATTCCTTATATGCTTGGAGTCTTTGAGATAGAAAGAAATATCTTTTGGCTTATGTCA	3640
Db	5546	AGTTTCATAGGGTC--CGAGTCTTAAAGATACAAATATAGTGC--TTGGGCTTCATTA	5602
QY	3641	AAAGAGTATGGAAGG-----TGAAAGGGCGGAAGAAACAGAAAGGAAG	3688
Db	5603	AAGGAGTCTGGGAGGAGCAGGTGAGAGGGAATGGAAGGAAAAAACAATATAG	5662
QY	3689	AACCATGTATATATAGAGCAATGGTGCAAGGTTTTCTTGAATTAATGCAAAATATG	3748
Db	5663	AGGACTTGACACTTACAAATCTCTTACACAGCATTTTCTTGGACAAATCTTGAAGGT	5722
QY	3749	ATAGATTAGAGGAATTTCAAGTAGGAATGCTTTTCACTTGAATTTGGGTTTCTCT--T	3805
Db	5723	AGTGGATTAGGTATGTCAGAGGGGACCTTGCTTGGCAATTCGGTTTTGTCTCT	5782
QY	3806	CGATTAAAGTTGGGATCCTCATCTGCATTTGACT---TGAAGAGAAAGATGAATGT	3861
Db	5783	CCATTGAGGTTGAAGGTCACCTTTTTCACCTCGAATGAGAGGAAAGAGGGGTGT	5842
QY	3862	TAGGACCTATATCGGTTTTCTATTAATTAATGAAGCAATGGAAGAATTAATTTGGTATT	3921
Db	5843	TATATCTCTTACTCGGAGTTTACTATTTAAGCAATGGAACAGACCTGGGACCTCTT	5902
QY	3922	TTCCCAAAAAGTGAATACTTTCTTTTACTGTTTGTCAAAAAGTGAATAAGAAAAAG	3981
Db	5903	CTTGACAAAAAATGAAACCTGTGTGTTTGTCTGTGTGTTCTTTGTTAAGAAAGCAC	5962
QY	3982	CTTTAATGTATGTGTAATACATGTGTTCAAAAGTCATTTGATGAGATGTTTAAATCAG	4041
Db	5963	AGGCAAAAGCCGACCAATGGGTGGAATGTGGCTTTTGAGTCAAGGCTTTTGAGTTAG	6022
QY	4042	GAGGTGCATTCATTTGGCTTCCTGTGACACACTGAAAGAAATTTGCTTGTAACACAT	4101
Db	6023	CATTCATCAATAGTT-----GATCATGTCAAGGTGAGAGGC	6058
QY	4102	AAAAATACAGACATAGCTGATGAGTAAAAAAAGTCCATGATCAATTCATATCTGTTT	4161

Db 6059 TACCTGTCAGGCGGAGCCCTGCTGCTGCGACTTACATCTCCAGGCTTCAAGTACT 6118
 QY 4162 TAAGAAAGTTATGAAATTTCTGTAGGTCATTTCAAGCTGTCCTGCGCATGTGCGC 4221
 Db 6119 TCTGCTACTTACAGACAGTTAGAGGTTAGCAAACTTTTTC----- 6163
 QY 4222 CTGTGGGCTGCAAGTTGCAAGCTCTTTTAAGTAATCTGTCAATAGATGTTTGAGC 4281
 Db 6164 -----AACCCCACTAAATTTAATTGACAAACACGTGTAAATTG 6205
 QY 4282 TGCAAAACAGCCCAAGCATTAATGAGTGACCTGGATCCCAATCCAGCTCACT 4341
 Db 6206 TGGGATACAGTGTGATTAATGA----- 6227
 QY 4342 TCAGTCTCTGCTGCTGTGAAGAGGGGTGTCACTCTGCGCAGCTTTTAAAGC 4401
 Db 6228 -----TCTATGTGTGCAATGTGCAAGTTCAATAGATTAATAGCCCATCAAGC 6283
 QY 4402 TTCAATAGTGTAGGTGACCTGAAATGATGCTGTGTGCTTCTCAATCCAGAGA 4460
 Db 6284 TTATGGGTGTGAATGCAAGTAATAGATGATGCTGTGTGCTTGTAGGTGAGAAA 6343
 QY 4461 GCGGTCACTTTAAGCTTTGGCAAAATCAATCAATTAATAAGGATA-----T 4508
 Db 6344 GGGATGTTTAAAGTCTTGGGCAAAATCAATTAATTAATCAATGCTAAATAATCAATTAATGTT 6403
 QY 4509 TACATGAATGTTTAAAGTCTTAAACCTGCTTCTGCTCACTCAACTATCTG 4568
 Db 6404 GATTATTAATCTTTTAAAGAGGTGATCTGTTTGTGTGCTCAGCAAGCAATGTC 6463
 QY 4569 CAATTTCT---AATTGTCACTTTAGAAAACATGGCATTAATGCTCAAAATCTTTGCA 4625
 Db 6464 CCAAGCTTTCTTAAGTCACTGACCACTTTAGAAAATGCTACCTGCTCAAAATGGTTGTA 6523
 QY 4626 TTCTTATTTTCAAGCTTGAAGAGAGTGAAGATCAAGCAATTTGAGAACTGATTTG 4685
 Db 6524 TTCTTATTTTCAAGCTTGAAGAGAGTGAAGATCAAGGATTTGGGAACTGTGACCTG 6583
 QY 4686 CTGTTATGCTCTGAGAAATGCTGATTTGACCAAGCAAGCTGAAATAATTAAC 4745
 Db 6584 CTGTTATGCTCTGAGAAATGCTGCTGTGACGAGAAAGCTGAAACAGAGAAC 6643
 QY 4746 TAAACCCCTTCTCCTGCTAGAAATTAACATTAATGAGCCCAAGCAATTTT 4797
 Db 6644 TGCTCCTCTGCTCTTAATAAGAACATTAAGATCCGTGATGAGCTTTT 6695

 RESULT 4
 US-09-751-797-29
 ; Sequence 29, Application US/09751797
 ; Patent No. US20010024652A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumoulier, Laure
 ; APPLICANT: Leoued, Jamila
 ; APPLICANT: Renaud, Jean-Christophe
 ; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
 ; FILE REFERENCE: LUD 5543.2
 ; CURRENT APPLICATION NUMBER: US/09/751,797
 ; PRIOR FILING DATE: 2000-12-29
 ; PRIOR APPLICATION NUMBER: 09/419,568
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: US09/178,973
 ; PRIOR FILING DATE: 1998-10-26
 ; NUMBER OF SEQ ID NOS: 29
 ; SEQ ID NO 29
 ; LENGTH: 5935
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 US-09-751-797-29

Query Match 13.6%; Score 650; DB 10; Length 5935;
 Best Local Similarity 56.5%; Pred. No. 2e-149; Indels 152; Gaps 29;
 Matches 1863; Conservative 0; Mismatches 1285;

QY 29 CTCCTTCCCGACGACCAAGTTGCTCGAGTATGATGTCGAATGGCCGCCCTGAGAA 88
 Db 356 CTCCTCTCAGATTATCACTTTTGAACCTGTGGCATGGTATGGCTCTCTGAGAA 415
 QY 89 ATCTGTAGCTCTTCTTATGAGGACCTGCGCACAGCTGCTCTTCTTTGGCCCT 148
 Db 416 ATCTATAGATTTTCTTATGAGGACCTTGTGGCGCAGCTGCTCTTCTCAATGGCT 475
 QY 149 CTGTGTAAGGAGAGAGCGCTGCGCCATCACTCCACTGAGGCTTACAGTCAA 208
 Db 476 GTGGGCCGAGAGCAAAATGCGTCCCAATCAACCCGCTGAGCTTATAGGTCAA 535
 QY 209 CTTCAGACAGCCCTATATCAACAAGCAGCACTTCACTGCTGCTAAGAGTATATCTC 268
 Db 536 CTTCAGACAGCCCTATATCACTGTCACCGACCTTATGCTGCCAAGAGGTACAGTGA 595
 QY 269 AATCTGCTCTTCTGCTGATCTACTTGAATCCAAATATGTTCTTAACTTTCTCA 328
 Db 596 TCTCTTCTCCATACCGCTTGCCTTCTGTAAGCACTTGCAAACTCTTAAAGGAGC 655
 QY 329 GAGCATCTTAAGAGCTTGAAGAACCACTGTTATCCCTGAGGATGAATTTCTG 388
 Db 656 GCTTTATCTCCGAGGCTCACTAATGTTTCTGCT-----CTTTAGAG 703
 QY 389 TTTTTCAGAGCTCTTGGAAATGCGCTTTTCTTTTCTTGAATCTTCTCTTCAT 448
 Db 704 ACTCTTAAAGAGCTGATCTTTTCTTATTTCTTCAAGTCTCAGACATTTCTAT 763
 QY 449 TTTGAGCTTATGATATATATGATGAAATTTTCCAAAGACCGCAATTCAGTATCAT 508
 Db 764 CTGGCTTCAAGACATATATGATTAATTTATCAAGAGCGCGCTT--AGAAAGCA 821
 QY 509 CTGATGATTTTCTTATGCTCTGATGATTTTAACTATGACACATCTG 568
 Db 822 CCCAGACGCAATCTTTCATCTGTTGCTCTTCTTGAATCATATCTCTTGGC 881
 QY 569 AATTGCTTTTATGCTTATGATGTTGCTGAGGAGAGGAGTGGGACATGTTAT 628
 Db 882 TACT-----CTAGAACCACTGCGGACATATCTTAC 916
 QY 629 GATTAATTTTCTTATGCTCAATGTCAGACCCCTTATCTTCTCTTCCAG 688
 Db 917 TTAAGGCTTTCTTCACTCTTGTACCCAGGACCTTAGGTTTTC-TCTCTTCA 975
 QY 689 GCTAGCTTGGCTATTAACAACAGAGCTTCTCTCATTTGGGAGAACTGTTCCAGGA 748
 Db 976 GCCAGCTTGCATTAACAACAGAGCTTCTCTCATCGGAGAACTGTTCCAGGA 1035
 QY 749 GTGAGTAAAGCTAAGTGTGAGCAACAGGCGGTGTGCTGTCATGAGTACTTGGAGT 808
 Db 1036 GTAGGTAAAGCTCTCACTGTATGAGCAAGGCT-----TAGCTGCGGAGCT 1082
 QY 809 GGTGAGTATGATGTTAGGCTTATTCCTTATGACCTTTCTGTTTCCCTTCACTGC 868
 Db 1083 GTGAGACCTCTGGATG---TGTAGCTATGACCCCGCTGCTTCTGTCACTGC 1138
 QY 869 AGATGAGTGAAGCGCTGCTATGATGAGAGAGGTGCTGAACTTCACTTGAAGAGTGC 928
 Db 1139 AGCTAAGATGCTAGTGTACCTGATGAGAGAGGTGCTCACTTCACTTGAAGAGATTC 1198
 QY 929 TGTTCCTCATCTGATGATGTTGAGCTTATGAGAGAGAGGTGCTTCTGAGCA 988
 Db 1199 TGTTCCTCATCTGATGATGTTGAGCTTATGAGAGAGAGGTGCTTCTGAGCA 1258
 QY 989 GGTCAAGCAACAGCTTAAGACATGTTAAGTTCAAGCTTCAAGCTTATGCCAATCC 1048
 Db 1259 AATCAAGCAATCAAGCTTATGCTGTTAAGTCTGAGCTTCAAGCTTATGCTCTCT 1318
 QY 1049 CTCCTTCTCTTCCACAGAGACCCCTTATCCCACTCTCTCTCTTCCCTTACCC 1108

Db 1319 CTCTCTCTTCAATTCAGTAAGAACCCGAGGTCTCGCCCTCTCTCTTCAACAAGATGA 1378
Qy 1109 TAAGCTAGCAGAAAGATGTCTTGGCAGCAGTGTATCAGAGATCA-----TTTGGG 1161
Db 1379 GGAAGGCTCAGCACCCACCATCATAGGCCATTGAAATAGGTCAAAAGGCTTTGGC 1438
Qy 1162 ATCATAGAGATATGCTTTTCTTGTGACTGATCATCTGAGTTATAGTGTGAATG 1221
Db 1439 TTCAATTGAGTAATACTTTGAGTTTGTATGTAGTTAAGCTTATTTGTTTATCATGAA 1498
Qy 1222 GGGTCTGGAAGTATAGTATCAGAAAGCCGATGTGTCTTGGAAAAAAGCAATC 1281
Db 1499 AGAATCAACTCAATTCGTAGATGAGAAAGATGTGGAAACCAAAAAAGGCTAGAT 1558
Qy 1282 AGGTTGCGTAA---GATGAGAAAGTGTGGAAAAACATAGCTGTGAAATGATCCA 1338
Db 1559 AGAGAAACAGATCTGCTAGTACACTTATGAGGGGGGGGGGCGAGGGCGATATCCA 1618
Qy 1339 TTGAGTCAAGTGTGGAGGGGAGATGGCATGAGAGAAATTGAAAGAAAGTGGG 1398
Db 1619 CTGAGTCCAGTACTGTGGAGAGAAATCCACTGAGTACAGTACTGTGGGGGAAAG 1678
Qy 1399 AAATGGAAAGCTTAAATCGGTGGGTGGCGAGACTGTGCCC-----TGTGGA 1450
Db 1679 AATGGCAGAGCAAAAGTTAGAGGAAAGAGAAAGATGAGAGAGGCTCAATGTGTGGGG 1738
Qy 1451 TGTCAATGGGAGCCCAAAATCGGAGCGGTGTGAATCTGATCGCGCTCAACATTTGAAC 1510
Db 1739 TGTGAAGGTCACTCTTTTTCATGTATGAGAGATTAAAGAAATCAGTGTGAGTT 1798
Qy 1511 TATGAAAAAAAGTTGAGTGAAGTGGGCCCAATMAAGCCCTAGACCTTACTGAAAGG 1570
Db 1799 TGATGTCTTCAGACCCCACTAAGCAGACTGTGGAGACCTGGCATTTAAGGA-AGG 1857
Qy 1571 GCTTAATTTTCAATGAGATGTTTATATGATACATTTCTTGTCTAAGCATGCAATTTTCTG 1630
Db 1858 CGCGCTTTTACACGAGAACTTATATGCTCATCTTGTGTCTAACCCTCAACCTTTGAT 1917
Qy 1631 GAGATACGATTGAGGTTTATCTCTTCAAGATTTGACATTAACCTACCGCTCTTCCAC 1690
Db 1918 GAGGTTAAGCTCAGGTTTCGTTCT-----ACCGTTCTTGTCTAC 1956
Qy 1691 AAATGCAAACTCAGTAGATTTTCCCAAGATGAAGAGGCTCTTGTAAAGGAGTGA 1750
Db 1957 TGGTGAATCTTCAAGTAGATTTCCCAAGAGAGAGACAGCTCTTCTGTAAAGGAGGAC 2016
Qy 1751 CTGATTTCTGCGCTCAAGGAAATTCAGAGCTCAGGAAATCTAGTCACTGTGAATC 1810
Db 2017 CTGATTTCTAGTCTCTAGAGAAACGAAATAGCTCAGAAATCTAGTCAAGCTGAATCT 2076
Qy 1811 TAGGCTATGTTGGGCAAAATTAAGAGCTTTAATTCAGGTGAATTTGACTGACTC 1870
Db 2077 AGGTACAGCGGGCAAAATGACTGAAAGCTCTTATTCAGGTGAAGCTCAGCTGCTC 2136
Qy 1871 CATGGGTGAGGTTCAATAAGTTTCAACAACATTAAGTATGCTTGTATATG 1930
Db 2137 AGATTAATCTGAGGATTTGGGCTCCACCGGATTAAGATTTCTGTATGA-GTCTGCTTTTA 2195
Qy 1931 TTTTATAGCATTTTAAAGTATGATGACTGATATCAAGAGAAATGTGAAAAAGCTGAAG 1990
Db 2196 TTTTGCACACATCATGTGTGCGACAGAACATCTCAGAAAGATTCAGAAAGGCTGAAG 2255
Qy 1991 ACACAGTAAAAAGTAGACTGATTAAGTCAATGCTTAAGTCAATGATGAGAGACA 2050
Db 2256 AGACAGTAAAAAGTAACTATTGGAGAGCACAATCTAAGGCAATTCAGTAGAGAGCTG 2315
Qy 2051 AATGTTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2110
Db 2316 GGGATTTCTTCTCTGCTTCCAGTCT--CTTCTACTTTGTAACTTTTCTTGTGACTGT 2373
Qy 2111 CTACACACAGGCGATT---ACTTGGTGTGTGTATGATATATCTATATATCTA 2166

Db 2374 CTACTGTGCTCATTACTACTACTAGCTGACCTGATCTAGCTGGGTCTATGATCTT 2433
Qy 2167 GATGTCAAGTTTCCAAATCTTGCAAATTTGTGAATTTAGAACTGTGGATCTTACTT 2226
Db 2434 TCATCTGTGTCTAAATTT---GTAACTCAAAATTTGGAGCTGACGAAAGCTTAGCTC 2490
Qy 2227 GTCTAGTCAATTAATCTCAGATTTTGGGAGTGTCTAGTGTGCAAGATATAGGCTTGAATG 2286
Db 2491 AGCCAGTCTATGAGCACTTGTCTGGAGATGGCTTGTGACAGAGTCAATGCTGAAGAC 2550
Qy 2287 AGGTCTGTAATCCCAAGCAGCACTTTCCGGGTGTATACAGATTAGTTTGTGTAC 2346
Db 2551 AGCATCTCTGATTTCCAGCTGTGAC-TTGCTTGTGCGCCAGCTGTATTTACTTACGCT 2609
Qy 2347 CATTAATTTTGAAGAAATTTCAAGATTCATTAAGTCAATGAACTGAAAGATCTTG 2406
Db 2510 GATTAAATTTTGGGAAA---GCCAATTCACACGACCTACATTAATCCGAAAGACATGCA 2667
Qy 2407 TTTAAAAACAGAAAAATGCTATGAGCAATTTTGAAGTCAATTTTGAAGTCAATTA 2466
Db 2668 TTGAAAACTAGAAA---GCTGGGCACAAACTTCTAGAGATGATTTTGTGACTCATTA 2723
Qy 2467 TGCAATGCTTTGAACCTTGAAGAATAAATCAAGAAATGAGAAAAAGCTGAGCTGCG 2526
Db 2724 ACTGATCTCTGAAATGTGATCAATCAACCCAGAAATTAACAACAAAGAGCTGAGTTGC 2783
Qy 2527 ATATAGGCTTAATTTCTGAGTAAATAAATCTTAT-----TTGATATATCATATA 2578
Db 2784 AAATAGCAAGATTTAGATATCAGTGTATTAACAGTGTCACTTAAATTAATTAATAG 2843
Qy 2579 TCT---ATCAGATATTTATATGATTTTAAAGCAGAGCAGACAAAC-CCGATCTCTTT 2634
Db 2844 TGCTATTTAGTCTCTATTTAAGATTTAAACACAGAGTGTATTAATCTCCCAATTTACTG 2903
Qy 2635 ATACAGTCAATTAAGTAAATAATTAAGTAAAGATTAATTAAGTAAATGAAGTGC 2694
Db 2904 GCGCTGTTCATTAAGTAAATAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAA 2963
Qy 2695 TGAATGTAAAGCTTTTCTTCTCTCTCTCCCATCAAGACCTTCAATCTTACTTCTT 2754
Db 2964 TGAGTTGAAGAAC---CTTTCCTTACTTTTACTTACTTATTTCTTATTAATTTTCTT 3020
Qy 2755 CTCTACTCTCTCAACAAATCTCTAGGAGATTTATTCATGTGGGCTGTGTACATTT 2814
Db 3021 TCTTCAACCTCTGTATCAAGCACAATGAGCACTTATCTGTGAGACTATTAATGACT 3080
Qy 2815 CTATAGGATGATACATCATCATGAGCTATTTGGTGAAGAAAGACA--ACAATGAAGGC 2872
Db 3081 TTACAGCAACACAACTTGTGTGTGTGCTCTTTGGGAGGGAACAGATGACAGAGGC 3140
Qy 2873 TTAGACTTAACA--TAGTACTCACCACCAAAACCGAGAGATGATTAGAGCAGTGAAGT 2931
Db 3141 TCAGGCTAGCAAGTGTGAGTCAACCTAAGCCAGAGCAGTGTATAGCAGAGAAAGT 3200
Qy 2932 GAGCTCTT-CCAAAGAGTAACTAATATCTCAGAAACATGAAGGCTCCAGTTGATG 2990
Db 3201 GAGGCTCTTCAAGTGGGTGTGCTTAAGTATCAGAAACGAGAGGCTGTGTGATG 3260
Qy 2991 AATTTTCAAGTCAAGCTTAACCTTAATTCCTCTTCTTCTTCTTCTTCTTCTTCTTCT 3050
Db 3261 AATTAATCAAGTAAATCTACCTTATCTC-----TTTCTTATTAAGAGCTTAACCG 3313
Qy 3051 GCGTTTCTCTCTGAGATCATTTATGATGATGATGATGATGATGATGATGATGATGATG 3110
Db 3314 TCTCTCTCTCTGT 3371
Qy 3111 CTGTGATTTTAAATTTGTAAGCCAGTGTCTCTGTGTATGAACTATATCTAGACATG 3170
Db 3372 CTTTGCAAGATTTTGTAGTCTGTGCAAGTCTTGT--TAGAGGTTTGTGTACTTGAACCC 3429
Qy 3171 GAGGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3230
Db 3430 TGGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3489

QY 3231 TACTGATTTCAATCTGCTTGTCTTTAGAAAAAGTGAAGTGAAGAGCAATCTCA 3290
Db 3490 TATCATTTACT-----TTGTCTTTGAAAGGTGAAGTGTGTGTGAAGAACTCA 3541

RESULT 5
US-10-027-632-208140

/ Sequence 208140, Application US/10027632
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 208140
/ LENGTH: 637
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-208140

Query Match 12.8%; Score 611.8; DB 15; Length 637;
Best Local Similarity 99.2%; Pred. No. 1.4e-140;
Matches 632; Conservative 3; Mismatches 0; Indels 2; Gaps 2;

QY 3289 CATGATCTGTGTGATTTTCAAGACCTTTAATCA-TTTTGAAAGAAATCAATTCATA 3347
Db 1 CATGTGATCTGTGTGATTTTCAAGACCTTTAATCAATTTGAAAGAAATTCATATA 60
QY 3348 TTTGCAATGGCTTGCATGTGAAGAGTATATGCTTTTGTGCTGTGCTTCAAGAA 3407
Db 61 TTTGCAATGGCTTGCATGTGAAGAGTATATGCTTTTGTGCTGTGCTTCAAGAA 120
QY 3408 CACAGAGGAGAGCAATGTGTCA-GAGAAAGATCAACAGAGAGAAACTGTCAAG 3466
Db 121 CACAGAGGAGAGCAATGTGTCAAGAGAAATCAACAGAGAGAAACTGTCAAG 180
QY 3467 CTGTCTGAAATAGGGTGTGTTTGGAGGCAATTAATTCCTCTGTTGGGGGTAAGCA 3526
Db 181 CTGTCTGAAATAGGGTGTGTTTGGAGGCAATTAATTCCTCTGTTGGGGGTAAGCA 240
QY 3527 AACGCAAGTTGTGTAAGTAATGATACACAGCTGGGAGCATTAATCTTTAAATTTCT 3586
Db 241 AACGCAAGTTGTGTAAGTAATGATACACAGCTGGGAGCATTAATCTTTAAATTTCT 300
QY 3587 TTATAGCTTTGAGTCTTTGAGATAGAAAAGATATCTTTTGGCCTTATGTCAAAAGAA 3646
Db 301 TTATAGCTTTGAGTCTTTGAGATAGAAAAGATATCTTTTGGCCTTATGTCAAAAGAA 360
QY 3647 GATAGGAAAGTGAAGAGGCGGAGAAAGACAGAGAAAGCAATGATTAATATAGA 3706
Db 361 GATAGGAAAGTGAAGAGGCGGAGAAAGACAGAGAAAGCAATGATTAATATAGA 420
QY 3707 GAGCAATGTGACAAAGTTTCTTTGAAATTAATGCAATTTGATAGATTGAGAAATTC 3766
Db 421 GAGCAATGTGACAAAGTTTCTTTGAAATTAATGCAATTTGATAGATTGAGAAATTC 480

QY 3767 AGTAGGAAAGCTTTTCACTTAATTTGGGTTTCTCTGATTAAGTTGGGAATCTCA 3826
Db 481 AGTAGGAAAGCTTTTCACTTAATTTGGGTTTCTCTGATTAAGTTGGGAATCTCA 540
QY 3827 TCTGATTTGACTTGAGAGAGAAAGATGATGTTAGACCTAATCTGTTTCTATT 3886
Db 541 TCTGATTTGACTTGAGAGAGAAAGATGATGTTAGACCTAATCTGTTTCTATT 600
QY 3887 AACTAAGCAAGTGAAGAAAGCTTAATTTGATTTT 3923
Db 601 AACTAAGCAAGTGAAGAAAGCTTAATTTGATTTT 637

RESULT 6
US-10-027-632-208141

/ Sequence 208141, Application US/10027632
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 208141
/ LENGTH: 637
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-208141

Query Match 12.8%; Score 611.8; DB 15; Length 637;
Best Local Similarity 99.2%; Pred. No. 1.4e-140;
Matches 632; Conservative 3; Mismatches 0; Indels 2; Gaps 2;

QY 3289 CATGATCTGTGTGATTTTCAAGACCTTTAATCA-TTTTGAAAGAAATCAATTCATA 3347
Db 1 CATGTGATCTGTGTGATTTTCAAGACCTTTAATCAATTTGAAAGAAATTCATATA 60
QY 3348 TTTGCAATGGCTTGCATGTGAAGAGTATATGCTTTTGTGCTGTGCTTCAAGAA 3407
Db 61 TTTGCAATGGCTTGCATGTGAAGAGTATATGCTTTTGTGCTGTGCTTCAAGAA 120
QY 3408 CACAGAGGAGAGCAATGTGTCA-GAGAAAGATCAACAGAGAGAAACTGTCAAG 3466
Db 121 CACAGAGGAGAGCAATGTGTCAAGAGAAATCAACAGAGAGAAACTGTCAAG 180
QY 3467 CTGTCTGAAATAGGGTGTGTTTGGAGGCAATTAATTCCTCTGTTGGGGGTAAGCA 3526
Db 181 CTGTCTGAAATAGGGTGTGTTTGGAGGCAATTAATTCCTCTGTTGGGGGTAAGCA 240
QY 3527 AACGCAAGTTGTGTAAGTAATGATACACAGCTGGGAGCATTAATCTTTAAATTTCT 3586
Db 241 AACGCAAGTTGTGTAAGTAATGATACACAGCTGGGAGCATTAATCTTTAAATTTCT 300
QY 3587 TTATAGCTTTGAGTCTTTGAGATAGAAAAGATATCTTTTGGCCTTATGTCAAAAGAA 3646
Db 301 TTATAGCTTTGAGTCTTTGAGATAGAAAAGATATCTTTTGGCCTTATGTCAAAAGAA 360

QY 3647 GTATGAAAGGTGAAGGCGGAGAAAGCAAGAAAGAAACCATGATATATATAGA 3706
DB 361 GTATGAAAGGTGAAGGCGGAGAAAGCAAGAAAGAAACCATGATATATATAGA 420
QY 3707 GGACAAATGATGACAAAGGTTTCTTGAATATATGAAATATGATATAGAGAAATTC 3766
DB 421 GGACAAATGATGACAAAGGTTTCTTGAATATATGAAATATGATATAGAGAAATTC 480
QY 3767 AGTAGGAATGCTTTTCACTTGAATTTGGGTTTCTTCTTGAATATAGTTGGATCTCA 3826
DB 481 AGTAGGAATGCTTTTCACTTGAATTTGGGTTTCTTCTTGAATATAGTTGGATCTCA 540
QY 3827 TCTGCAATTTGACTTGGAGAGAAAGAAATGATATGATAGACCTATATCTGTTTCTATT 3886
DB 541 TCTGCAATTTGACTTGGAGAGAAAGAAATGATATGATAGACCTATATCTGTTTCTATT 600
QY 3887 AACTAAAGCAAGTGAAGAAAGCACTATTTGATATTTT 3923
DB 601 AACTAAAGCAAGTGAAGAAAGCACTATTTGATATTTT 637

RESULT 7
US-10-027-632-208142
; Sequence 208142, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208142
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-208142

Query Match 12.8%; Score 611.8; DB 15; Length 637;
Best Local Similarity 99.2%; Pred. No. 1,4e-140;
Matches 632; Conservative 3; Mismatches 0; Indels 2; Gaps 2;

QY 3289 CATGATCTGTGTGATTTTCAAGACCTTAATCCA-TTTTGAAGAAATCAATTCATA 3347
DB 1 CATGATCTGTGTGATTTTCAAGACCTTAATCCA-TTTTGAAGAAATCAATTCATA 60
QY 3348 TTTCGAATGGGTTGTCATGTGAAGAGATGATATGCTTTTGTGTGATCTTCAGAAAG 3407
DB 61 TTTCGAATGGGTTGTCATGTGAAGAGATGATATGCTTTTGTGTGATCTTCAGAAAG 120
QY 3408 CACAGAGGAGAGAGCAATGTTTCTCA-GAGAAAGATCAACAGAGAGAAACTGTCAAG 3466
DB 121 CACAGAGGAGAGAGCAATGTTTCTCAAGAAAGATCAACAGAGAGAAACTGTCAAG 180
QY 3467 CTGTCTGAATATAGGTTGTTTGGAGAGCATTAATTCCTCTGTGGGGGTAAAGCAG 3526
DB 181 CTGTCTGAATATAGGTTTGGAGAGCATTAATTCCTCTGTGGGGGTAAAGCAG 240

QY 3527 AACGCAAGTGTAGTAAATATGATGACAGACAGTAGGAGACATTAATCTTAAATCT 3586
DB 241 AACGCAAGTGTAGTAAATATGATGACAGACAGTAGGAGACATTAATCTTAAATCT 300
QY 3587 TTATAGCTTGGAGCTCTTTGAGATAGAAAGATATCTTTTGGCCTTATGTCAAAGAA 3646
DB 301 TTATAGCTTGGAGCTCTTTGAGATAGAAAGATATCTTTTGGCCTTATGTCAAAGAA 360
QY 3647 GTATGAAAGGTGAAGGCGGAGAAAGCAAGAAAGAAACCATGATATATATAGA 3706
DB 361 GTATGAAAGGTGAAGGCGGAGAAAGCAAGAAAGAAACCATGATATATATAGA 420
QY 3707 GGACAAATGATGACAAAGGTTTCTTGAATATATGAAATATGATATAGAGAAATTC 3766
DB 421 GGACAAATGATGACAAAGGTTTCTTGAATATATGAAATATGATATAGAGAAATTC 480
QY 3767 AGTAGGAATGCTTTTCACTTGAATTTGGGTTTCTTCTTGAATATAGTTGGATCTCA 3826
DB 481 AGTAGGAATGCTTTTCACTTGAATTTGGGTTTCTTCTTGAATATAGTTGGATCTCA 540
QY 3827 TCTGCAATTTGACTTGGAGAGAAAGAAATGATATGATAGACCTATATCTGTTTCTATT 3886
DB 541 TCTGCAATTTGACTTGGAGAGAAAGAAATGATATGATAGACCTATATCTGTTTCTATT 600
QY 3887 AACTAAAGCAAGTGAAGAAAGCACTATTTGATATTTT 3923
DB 601 AACTAAAGCAAGTGAAGAAAGCACTATTTGATATTTT 637

RESULT 8
US-09-751-797-24
; Sequence 24, Application US/09751797
; Patent No. US20010024652A1
; GENERAL INFORMATION:
; APPLICANT: Dumoulier, Laure
; APPLICANT: Renauld, Yamila
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
; FILE OF INVENTION: (trif) The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.2
; CURRENT APPLICATION NUMBER: US/09/751,797
; CURRENT FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 09/419,568
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 24
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-751-797-24

Query Match 5.4%; Score 258; DB 10; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.5e-53;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACAGAGAAATCTTCAAGACAGGTTCTCTCCCAAGTCAACAGTTGCTGAGTTAG 60
DB 1 TGCACAGAGAAATCTTCAAGACAGGTTCTCTCCCAAGTCAACAGTTGCTGAGTTAG 60
QY 61 AATTGCTCAGATGCGCGCGCTGCAAGAAATCTGTAGCTCTTCTTATAGGGAACCTGG 120
DB 61 AATTGCTCAGATGCGCGCGCTGCAAGAAATCTGTAGCTCTTCTTATAGGGAACCTGG 120
QY 121 CCACAGAGCTGCTCTCTTCTTGGCCCTTGTGACAGGAGAGAGAGAGAGAGAGAGAGAG 180
DB 121 CCACAGAGCTGCTCTCTTCTTGGCCCTTGTGACAGGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 GCTCCAGCTGAGGCTTGAAGAGTCAACTTCCAGAGAGCTTATATCAACAGAGAGCT 240

Db 181 GCTCCACTGACGCTTGACAACTCCAACTTCCAGAGCCCTATATCACCACCGACCT 240
Qy 241 TCATGCTGGCTAAGAGG 258
Db 241 TCATGCTGGCTAAGAGG 258

RESULT 9

US-09-870-574-1

Sequence 1, Application US/09870574

Patent No. US20020102723A1

GENERAL INFORMATION:

APPLICANT: Gurney, Austin L.

APPLICANT: Aggarwal, Sudeepa

APPLICANT: Xie, Ming-Hong

APPLICANT: Maruoka, Ellen M.

APPLICANT: Foster, Jessica S.

APPLICANT: Goddard, Audrey

APPLICANT: Wood, William I.

TITLE OF INVENTION: INTERLEUKIN-22 POLYPEPTIDES, NUCLEIC ACIDS ENCODING

FILE REFERENCE: P2806-1(US)

CURRENT FILING DATE: US/09/870,574

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: US 60/169,495

PRIOR FILING DATE: 1999-12-07

PRIOR APPLICATION NUMBER: PCT/US00/14042

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: PCT/US00/23328

PRIOR FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 1

LENGTH: 1152

TYPE: DNA

ORGANISM: Homo Sapien

US-09-870-574-1

Query Match 5.1%; Score 244; DB 11; Length 1152;

Best Local Similarity 100.0%; Pred. No. 1.4e-49;

Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTTGACAGAGGTTCTCTTCCCTCCAGTCCAGAGTGTGCTGAGTTAGATTGTCTGCAATG 74
Db 1 CTTGACAGAGGTTCTCTTCCCTCCAGTCCAGAGTGTGCTGAGTTAGATTGTCTGCAATG 60
Qy 75 GCGGCCCTGACAAATCTGTAGCTCTTCTTATGGGACCCCTGGCCACCAAGTGCCTC 134
Db 61 GCGGCCCTGACAAATCTGTAGCTCTTCTTATGGGACCCCTGGCCACCAAGTGCCTC 120
Qy 135 CTTCTCTTGGCCCTCTTGTACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
Db 121 CTTCTCTTGGCCCTCTTGTACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy 195 CTTGACAGGTCACCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
Db 181 CTTGACAGGTCACCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 255 GAGG 258
Db 241 GAGG 244

RESULT 10

US-10-063-588-153

Sequence 153, Application US/10063588

Publication No. US20030130483A1

GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT FILING DATE: US/10/063,588
PRIOR APPLICATION NUMBER: 2002-05-03
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-588-153

Query Match 5.1%; Score 244; DB 14; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTTGACAGAGGTTCTCTTCCCTCCAGTCCAGAGTGTGCTGAGTTAGATTGTCTGCAATG 74
Db 1 CTTGACAGAGGTTCTCTTCCCTCCAGTCCAGAGTGTGCTGAGTTAGATTGTCTGCAATG 60
Qy 75 GCGGCCCTGACAAATCTGTAGCTCTTCTTATGGGACCCCTGGCCACCAAGTGCCTC 134
Db 61 GCGGCCCTGACAAATCTGTAGCTCTTCTTATGGGACCCCTGGCCACCAAGTGCCTC 120
Qy 135 CTTCTCTTGGCCCTCTTGTACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
Db 121 CTTCTCTTGGCCCTCTTGTACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy 195 CTTGACAGGTCACCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
Db 181 CTTGACAGGTCACCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 255 GAGG 258
Db 241 GAGG 244

RESULT 11

US-10-066-867-153

Sequence 153, Application US/10066867

Publication No. US20020119130A1

GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Matanabe, Colin K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3230R1C1

CURRENT FILING DATE: US/10/066,867

CURRENT FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: 60/063435

PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/064215

PRIOR FILING DATE: 1997-10-29

PRIOR APPLICATION NUMBER: 60/082797

PRIOR FILING DATE: 1998-04-22

PRIOR APPLICATION NUMBER: 60/083495

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/085579

PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/088021

1	PRIOR FILING DATE: 1998-06-04
2	PRIOR APPLICATION NUMBER: 60/088029
3	PRIOR FILING DATE: 1998-06-04
4	PRIOR APPLICATION NUMBER: 60/088030
5	PRIOR FILING DATE: 1998-06-04
6	PRIOR APPLICATION NUMBER: 60/088734
7	PRIOR FILING DATE: 1998-06-10
8	PRIOR APPLICATION NUMBER: 60/088740
9	PRIOR FILING DATE: 1998-06-10
10	PRIOR APPLICATION NUMBER: 60/088811
11	PRIOR FILING DATE: 1998-06-10
12	PRIOR APPLICATION NUMBER: 60/088824
13	PRIOR FILING DATE: 1998-06-10
14	PRIOR APPLICATION NUMBER: 60/088825
15	PRIOR FILING DATE: 1998-06-10
16	PRIOR APPLICATION NUMBER: 60/088863
17	PRIOR FILING DATE: 1998-06-11
18	PRIOR APPLICATION NUMBER: 60/089105
19	PRIOR FILING DATE: 1998-06-12
20	PRIOR APPLICATION NUMBER: 60/089514
21	PRIOR FILING DATE: 1998-06-16
22	PRIOR APPLICATION NUMBER: 60/089553
23	PRIOR FILING DATE: 1998-06-17
24	PRIOR APPLICATION NUMBER: 60/089522
25	PRIOR FILING DATE: 1998-06-19
26	PRIOR APPLICATION NUMBER: 60/090246
27	PRIOR FILING DATE: 1998-06-22
28	PRIOR APPLICATION NUMBER: 60/090444
29	PRIOR FILING DATE: 1998-06-24
30	PRIOR APPLICATION NUMBER: 60/090688
31	PRIOR FILING DATE: 1998-06-25
32	PRIOR APPLICATION NUMBER: 60/090696
33	PRIOR FILING DATE: 1998-06-25
34	PRIOR APPLICATION NUMBER: 60/090862
35	PRIOR FILING DATE: 1998-06-26
36	PRIOR APPLICATION NUMBER: 60/091628
37	PRIOR FILING DATE: 1998-07-02
38	PRIOR APPLICATION NUMBER: 60/096012
39	PRIOR FILING DATE: 1998-08-10
40	PRIOR APPLICATION NUMBER: 60/096757
41	PRIOR FILING DATE: 1998-08-17
42	PRIOR APPLICATION NUMBER: 60/096949
43	PRIOR FILING DATE: 1998-08-18
44	PRIOR APPLICATION NUMBER: 60/096959
45	PRIOR FILING DATE: 1998-08-18
46	PRIOR APPLICATION NUMBER: 60/097954
47	PRIOR FILING DATE: 1998-08-26
48	PRIOR APPLICATION NUMBER: 60/097971
49	PRIOR FILING DATE: 1998-08-26
50	PRIOR APPLICATION NUMBER: 60/097979
51	PRIOR FILING DATE: 1998-08-26
52	PRIOR APPLICATION NUMBER: 60/098749
53	PRIOR FILING DATE: 1998-09-01
54	PRIOR APPLICATION NUMBER: 60/099741
55	PRIOR FILING DATE: 1998-09-10
56	PRIOR APPLICATION NUMBER: 60/099763
57	PRIOR FILING DATE: 1998-09-10
58	PRIOR APPLICATION NUMBER: 60/099792
59	PRIOR FILING DATE: 1998-09-10
60	PRIOR APPLICATION NUMBER: 60/099812
61	PRIOR FILING DATE: 1998-09-10
62	PRIOR APPLICATION NUMBER: 60/099815
63	PRIOR FILING DATE: 1998-09-10
64	PRIOR APPLICATION NUMBER: 60/100627
65	PRIOR FILING DATE: 1998-09-16
66	PRIOR APPLICATION NUMBER: 60/100662
67	PRIOR FILING DATE: 1998-09-16
68	PRIOR APPLICATION NUMBER: 60/100683
69	PRIOR FILING DATE: 1998-09-17
70	PRIOR APPLICATION NUMBER: 60/100684
71	PRIOR FILING DATE: 1998-09-17
72	PRIOR APPLICATION NUMBER: 60/100930
73	PRIOR FILING DATE: 1998-09-17

1	PRIOR APPLICATION NUMBER: 60/101279
2	PRIOR FILING DATE: 1998-09-22
3	PRIOR APPLICATION NUMBER: 60/101475
4	PRIOR FILING DATE: 1998-09-23
5	PRIOR APPLICATION NUMBER: 60/101733
6	PRIOR FILING DATE: 1998-09-24
7	PRIOR APPLICATION NUMBER: 60/101743
8	PRIOR FILING DATE: 1998-09-24
9	PRIOR APPLICATION NUMBER: 60/101916
10	PRIOR FILING DATE: 1998-09-24
11	PRIOR APPLICATION NUMBER: 60/101949
12	PRIOR FILING DATE: 1998-09-24
13	PRIOR APPLICATION NUMBER: 60/103449
14	PRIOR FILING DATE: 1998-10-06
15	PRIOR APPLICATION NUMBER: 60/103678
16	PRIOR FILING DATE: 1998-10-08
17	PRIOR APPLICATION NUMBER: 60/103679
18	PRIOR FILING DATE: 1998-10-08
19	PRIOR APPLICATION NUMBER: 60/103711
20	PRIOR FILING DATE: 1998-10-08
21	PRIOR APPLICATION NUMBER: 60/105000
22	PRIOR FILING DATE: 1998-10-20
23	PRIOR APPLICATION NUMBER: 60/105002
24	PRIOR FILING DATE: 1998-10-20
25	PRIOR APPLICATION NUMBER: 60/105861
26	PRIOR FILING DATE: 1998-10-27
27	PRIOR APPLICATION NUMBER: 60/106030
28	PRIOR FILING DATE: 1998-10-28
29	PRIOR APPLICATION NUMBER: 60/106464
30	PRIOR FILING DATE: 1998-10-30
31	PRIOR APPLICATION NUMBER: 60/106856
32	PRIOR FILING DATE: 1998-11-03
33	PRIOR APPLICATION NUMBER: 60/108087
34	PRIOR FILING DATE: 1998-11-17
35	PRIOR APPLICATION NUMBER: 60/112419
36	PRIOR FILING DATE: 1998-12-15
37	PRIOR APPLICATION NUMBER: 60/112422
38	PRIOR FILING DATE: 1998-12-15
39	PRIOR APPLICATION NUMBER: 60/112853
40	PRIOR FILING DATE: 1998-12-16
41	PRIOR APPLICATION NUMBER: 60/113011
42	PRIOR FILING DATE: 1998-12-16
43	PRIOR APPLICATION NUMBER: 60/112854
44	PRIOR FILING DATE: 1998-12-16
45	PRIOR APPLICATION NUMBER: 60/113300
46	PRIOR FILING DATE: 1998-12-22
47	PRIOR APPLICATION NUMBER: 60/113408
48	PRIOR FILING DATE: 1998-12-22
49	PRIOR APPLICATION NUMBER: 60/113430
50	PRIOR FILING DATE: 1998-12-23
51	PRIOR APPLICATION NUMBER: 60/113621
52	PRIOR FILING DATE: 1998-12-23
53	PRIOR APPLICATION NUMBER: 60/114223
54	PRIOR FILING DATE: 1998-12-30
55	PRIOR APPLICATION NUMBER: 60/115614
56	PRIOR FILING DATE: 1999-01-12
57	PRIOR APPLICATION NUMBER: 60/115627
58	PRIOR FILING DATE: 1999-01-20
59	PRIOR APPLICATION NUMBER: 60/116643
60	PRIOR FILING DATE: 1999-01-22
61	PRIOR APPLICATION NUMBER: 60/119285
62	PRIOR FILING DATE: 1999-02-09
63	PRIOR APPLICATION NUMBER: 60/119287
64	PRIOR FILING DATE: 1999-02-09
65	PRIOR APPLICATION NUMBER: 60/119525
66	PRIOR FILING DATE: 1999-02-10
67	PRIOR APPLICATION NUMBER: 60/119549
68	PRIOR FILING DATE: 1999-02-10
69	PRIOR APPLICATION NUMBER: 60/120014
70	PRIOR FILING DATE: 1999-02-11
71	PRIOR APPLICATION NUMBER: 60/129122
72	PRIOR FILING DATE: 1999-04-13
73	PRIOR APPLICATION NUMBER: 60/129674

PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/138387
PRIOR FILING DATE: 1999-06-09
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/175481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 60/191007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/199397
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/380139
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 09/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380138
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/380142

Query Match 5.1%; Score 244; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAACAGGTTCTCTTCCGACGACAGTGTCTGAGTAAGTGTCTGCAATG 74
DB 1 CTTGAGAACAGGTTCTCTTCCGACGACAGTGTCTGAGTAAGTGTCTGCAATG 60
QY 75 GCGGCCCTGAGAAATGTGAGCTCTTCTTATGGGAGACCTGGCCACAGCTGCTC 134
DB 61 GCGGCCCTGAGAAATGTGAGCTCTTCTTATGGGAGACCTGGCCACAGCTGCTC 120
QY 135 CTTCTCTTGGCCCTCTTGTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 194
DB 121 CTTCTCTTGGCCCTCTTGTATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 195 CTTGACAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
DB 181 CTTGACAGTCCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 255 GAGG 258
DB 241 GAGG 244

RESULT 12
US-10-066-500-125
Sequence 125, Application US/10066500
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
APPLICANT: Luc Desnoyers
APPLICANT: Dan L. Eaton
APPLICANT: Napoleone Ferrara
APPLICANT: Sherman Fong
APPLICANT: Wei-Qiang Gao
APPLICANT: Hanspeter Gerber
APPLICANT: Mary E. Gerltsen
APPLICANT: Audrey Goddard
APPLICANT: Paul J. Godowski
APPLICANT: Austin L. Gurney
APPLICANT: Ivar J. Kijavlin
APPLICANT: Jennie P. Macher
APPLICANT: Mary A. Napier
APPLICANT: James Pan
APPLICANT: Nicholas F. Paoni

APPLICANT: Margaret Ann Roy
APPLICANT: Timothy A. Stewart
APPLICANT: Daniel Tumas
APPLICANT: Colin K. Watanabe
APPLICANT: P. Mickey Williams
APPLICANT: William I. Wood
APPLICANT: Zemin Zang
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OR INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P310R1C7
CURRENT APPLICATION NUMBER: US/10/066,500
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059568
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066840
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: 60/066994
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/085998
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/087000
PRIOR FILING DATE: 1998-08-18
PRIOR APPLICATION NUMBER: 60/089601
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/089803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/089811
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/089812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100858
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106032
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/109304
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/139695
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/145070
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/063,547
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-547-153

Query Match 5.1%; Score 244; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAACAGGTTCTCTCCAGTGCAGGAGTTGCTGAGTTGAGTTGCTGCAATG 74
DB 1 CTTGAGAACAGGTTCTCTCCAGTGCAGGAGTTGCTGAGTTGAGTTGCTGCAATG 60
QY 75 GCCGCCCTGCAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACAGCTGCCTC 134
DB 61 GCCGCCCTGCAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACAGCTGCCTC 120
QY 135 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGAGCTGGCCCATCATGCTCCACTGCAGG 194
DB 121 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGAGCTGGCCCATCATGCTCCACTGCAGG 180
QY 195 CTTGACAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTATGCTGCTAG 254
DB 181 CTTGACAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTATGCTGCTAG 240
QY 255 GAGG 258
DB 241 GAGG 244

RESULT 14

US-10-063-616-153
Sequence 153; Application US/10063616
Publication No. US20030013855A1
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-616-153

Query Match 5.1%; Score 244; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAACAGGTTCTCTCCAGTGCAGGAGTTGCTGAGTTGAGTTGCTGCAATG 74
DB 1 CTTGAGAACAGGTTCTCTCCAGTGCAGGAGTTGCTGAGTTGAGTTGCTGCAATG 60

QY 75 GCCGCCCTGCAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACAGCTGCCTC 134
DB 61 GCCGCCCTGCAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACAGCTGCCTC 120
QY 135 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGAGCTGGCCCATCATGCTCCACTGCAGG 194
DB 121 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGAGCTGGCCCATCATGCTCCACTGCAGG 180
QY 195 CTTGACAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTATGCTGCTAG 254
DB 181 CTTGACAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTATGCTGCTAG 240
QY 255 GAGG 258
DB 241 GAGG 244

RESULT 15

US-10-063-502-153
Sequence 153; Application US/10063502
Publication No. US20030023042A1
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,502
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 153
LENGTH: 1152
TYPE: DNA
ORGANISM: Homo Sapien
US-10-063-502-153

Query Match 5.1%; Score 244; DB 15; Length 1152;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTGAGAACAGGTTCTCTCCAGTGCAGGAGTTGCTGAGTTGAGTTGCTGCAATG 74
DB 1 CTTGAGAACAGGTTCTCTCCAGTGCAGGAGTTGCTGAGTTGAGTTGCTGCAATG 60
QY 75 GCCGCCCTGCAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACAGCTGCCTC 134
DB 61 GCCGCCCTGCAGAAATCTGTAGCTCTTCTTATGGGAGCCCTGGCCACAGCTGCCTC 120
QY 135 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGAGCTGGCCCATCATGCTCCACTGCAGG 194
DB 121 CTTCTCTTGGCCCTCTTGTGTAACAGGAGAGAGAGCTGGCCCATCATGCTCCACTGCAGG 180
QY 195 CTTGACAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTATGCTGCTAG 254
DB 181 CTTGACAGTCCAACTTCCAGAGCCCTATATACCAACCGACCTTATGCTGCTAG 240
QY 255 GAGG 258
DB 241 GAGG 244

Search completed: July 20, 2003, 03:46:16
Job time : 692.702 secs

301 ATCCAATAGTTCCTTAACTTTTCTTCAGAGCATCTCTAAGAGCTTAGGAACCACTGT 360

Db 301 ATCCAAATAGTCTTAACTTTCTTCAAGACATCTTAAGACCTTTAGAACCCACTGT 360
Qy 361 TTAATCCCTGAGGATAGATAATTTCTGTCTTTTCAGAGACTCTTTGGGAATCGCTT 420
Db 361 TTAATCCCTGAGGATAGATAATTTCTGTCTTTTCAGAGACTCTTTGGGAATCGCTT 420
Qy 421 TTTTCTTTCTGAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db 421 TTTTCTTTCTGAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Qy 481 CCCAAGAGCGGCGCATTCAGTAATCCATCTGATGATTTTCTCTCTCTCTCTCTCT 540
Db 481 CCCAAGAGCGGCGCATTCAGTAATCCATCTGATGATTTTCTCTCTCTCTCTCTCT 540
Qy 541 CATTTCTTAACTCAATGACACATGTAATCTGCTTTAGCTTTAGTATGATGCTCT 600
Db 541 CATTTCTTAACTCAATGACACATGTAATCTGCTTTAGTATGATGATGCTCTCT 600
Qy 601 GGGGAGACGGGATGGGGACATGTCATGTAATTAATTTTCTATTTGCTCAATGCTC 660
Db 601 GGGGAGACGGGATGGGGACATGTCATGTAATTAATTTTCTATTTGCTCAATGCTC 660
Qy 661 AGACCTTATGCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 661 AGACCTTATGCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Qy 721 TCTCATTTGGGGAGAACTGTCCACAGGAGCTGTAAGTACAGTTGAGAGAAAGGG 780
Db 721 TCTCATTTGGGGAGAACTGTCCACAGGAGCTGTAAGTACAGTTGAGAGAAAGGG 780
Qy 781 CCGTGTGCCGTCATGGGTACTTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 781 CCGTGTGCCGTCATGGGTACTTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Qy 841 TGAACCTTTCTGTCTTCCCTTCCACCTGAGATGATGAGCGCTGCTATCTGATGAGCAG 900
Db 841 TGAACCTTTCTGTCTTCCCTTCCACCTGAGATGATGAGCGCTGCTATCTGATGAGCAG 900
Qy 901 GTGCTGAATCTCACTTGAAGAGAGTGTCTGCTCCCTCAATCTGATGATGATGATGAT 960
Db 901 GTGCTGAATCTCACTTGAAGAGAGTGTCTGCTCCCTCAATCTGATGATGATGATGAT 960
Qy 961 ATGACAGAGAGTGTGCT 1020
Db 961 ATGACAGAGAGTGTGCT 1020
Qy 1021 TGAAGCTCTAGGCTATAGCCCACTTACCCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Db 1021 TGAAGCTCTAGGCTATAGCCCACTTACCCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Qy 1081 CCCAATCT 1140
Db 1081 CCCAATCT 1140
Qy 1141 TGTATCAGAGATCATTTGGGATCATAGATATTTGCTTTGCTTTGATGATGATGATG 1200
Db 1141 TGTATCAGAGATCATTTGGGATCATAGATATTTGCTTTGCTTTGATGATGATGATG 1200
Qy 1201 TTGAGTTTATAGTGTGAAATGGGCTGTGAACTTAAGTGTACAGAAAGCCGATGTTTG 1260
Db 1201 TTGAGTTTATAGTGTGAAATGGGCTGTGAACTTAAGTGTACAGAAAGCCGATGTTTG 1260
Qy 1261 TCTTTCGAAAAAGGCACTCAGGTTGCGTAAATAGATAAGATGTTTGGAAAAACATCTA 1320
Db 1261 TCTTTCGAAAAAGGCACTCAGGTTGCGTAAATAGATAAGATGTTTGGAAAAACATCTA 1320
Qy 1321 GCTGTGAAATGATCATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 1321 GCTGTGAAATGATCATTTGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Qy 1381 ATTAGAAGAAAGTGGGAAATGGGAAAGCTTAAATCGTGTGTGTGTGTGTGTGTGTGT 1440
Db 1381 ATTAGAAGAAAGTGGGAAATGGGAAAGCTTAAATCGTGTGTGTGTGTGTGTGTGTGT 1440

Db 1381 ATTAGAAGAAAGTGGGAAATGGGAAAGCTTAAATCGTGTGTGTGTGTGTGTGTGTGT 1440
Qy 1441 GCCCTGTGATGTCAATGGGAAAGCCCAAAATCGAGGGGTGTAATCTGATCCGCTGAA 1500
Db 1441 GCCCTGTGATGTCAATGGGAAAGCCCAAAATCGAGGGGTGTAATCTGATCCGCTGAA 1500
Qy 1501 CATTTGAAACTATGAAAAAAGTTTGAATGAGTGGGCCCAATAAGAGGCTTGAAGCTT 1560
Db 1501 CATTTGAAACTATGAAAAAAGTTTGAATGAGTGGGCCCAATAAGAGGCTTGAAGCTT 1560
Qy 1561 ACTGAAGAGGCTTAAATTTTCAATGATGATGATGATGATGATGATGATGATGATG 1620
Db 1561 ACTGAAGAGGCTTAAATTTTCAATGATGATGATGATGATGATGATGATGATGATG 1620
Qy 1621 CAATTTCTGAGATACATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Db 1621 CAATTTCTGAGATACATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
Qy 1681 CTCTTTCCAAATGCAAACTCTCAGTAGGATTTCCCAAGATGAAGAGGCTCTCTGTA 1740
Db 1681 CTCTTTCCAAATGCAAACTCTCAGTAGGATTTCCCAAGATGAAGAGGCTCTCTGTA 1740
Qy 1741 AGGGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Db 1741 AGGGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
Qy 1801 TGTGAAATCTAGGCTATGTTGGGCAAAATCTAAGAGCTTAAATCCAGGCTGAATGT 1860
Db 1801 TGTGAAATCTAGGCTATGTTGGGCAAAATCTAAGAGCTTAAATCCAGGCTGAATGT 1860
Qy 1861 ACTGTACCTCAATGGGCTGAGGCTTCAATGATGATGATGATGATGATGATGATGATG 1920
Db 1861 ACTGTACCTCAATGGGCTGAGGCTTCAATGATGATGATGATGATGATGATGATGATG 1920
Qy 1921 CTGTGATTTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
Db 1921 CTGTGATTTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
Qy 1981 AAGCTGAAGACACAGTGAAGAAAGGTAGGACCTGATGATGATGATGATGATGATG 2040
Db 1981 AAGCTGAAGACACAGTGAAGAAAGGTAGGACCTGATGATGATGATGATGATGATG 2040
Qy 2041 AGGAGAGCAAAATGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2100
Db 2041 AGGAGAGCAAAATGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2100
Qy 2101 CTGTGATTTCTTCAACCAAGGCGGATTAATTTGGTGTGTGTGTGTGTGTGTGTGT 2160
Db 2101 CTGTGATTTCTTCAACCAAGGCGGATTAATTTGGTGTGTGTGTGTGTGTGTGTGT 2160
Qy 2161 TATCTAGATGCTAGTTTCCAAATCTTGAATTTGAAATCTGATGATGATGATGATG 2220
Db 2161 TATCTAGATGCTAGTTTCCAAATCTTGAATTTGAAATCTGATGATGATGATGATGATG 2220
Qy 2221 TAGCTTGTCTAGTCAATTAATCTGAGATTTGGGGATGCTGAGAGATGAGGCTTA 2280
Db 2221 TAGCTTGTCTAGTCAATTAATCTGAGATTTGGGGATGCTGAGAGATGAGGCTTA 2280
Qy 2281 GAAATCAGGCTCTCTGAAATCCCAAGCAGACTTTCCCGGTGTGTGTGTGTGTGTGT 2340
Db 2281 GAAATCAGGCTCTCTGAAATCCCAAGCAGACTTTCCCGGTGTGTGTGTGTGTGTGT 2340
Qy 2341 TGTGACAAATTAATCTTGAAGAAATTTGAGATTTCTATGATGATGATGATGATG 2400
Db 2341 TGTGACAAATTAATCTTGAAGAAATTTGAGATTTCTATGATGATGATGATGATGATG 2400
Qy 2401 TACTTGTTTAAAAACAGAAAAATGCTTATGAGGCAATTTATTTGAAGCATTTTGAAGT 2460
Db 2401 TACTTGTTTAAAAACAGAAAAATGCTTATGAGGCAATTTATTTGAAGCATTTTGAAGT 2460
Qy 2461 CATTAATCATTTGCTTGAATTTGAAAGAAATTAATCTGAAACATGAGAAAGAGCTGG 2520
Db 2461 CATTAATCATTTGCTTGAATTTGAAAGAAATTAATCTGAAACATGAGAAAGAGCTGG 2520

QY 2521 ACTGCATATAGAGGCTAATTTCTGGAGTATATACTTATTTGATATATCATATATATC 2580
Db 2521 ACTGCATATAGAGGCTAATTTCTGGAGTATATACTTATTTGATATATCATATATATC 2580
QY 2581 TATCGATATATGATATATAGTTTAAAGCAGAGCAGACACACCCGATCTCTTTATACG 2640
Db 2581 TATCGATATATGATATATAGTTTAAAGCAGAGCAGACACACCCGATCTCTTTATACG 2640
QY 2641 GTTCAATATAGATAAAAAATATTAGTATAGATTTATATAGTAAATGGAAGTCTGAAT 2700
Db 2641 GTTCAATATAGATAAAAAATATTAGTATAGATTTATATAGTAAATGGAAGTCTGAAT 2700
QY 2701 GGTAAAGCTTTTTTTTCTCTCTCTCTCCATCAAGACCTCCATCTAGTTTCTTCTTCA 2760
Db 2701 GGTAAAGCTTTTTTTTCTCTCTCTCTCCATCAAGACCTCCATCTAGTTTCTTCTTCA 2760
QY 2761 CTCCCTCAACAATCCCTAGAGGAGATTTATCATAGTGGGCTGGATCATTTCTATAG 2820
Db 2761 CTCCCTCAACAATCCCTAGAGGAGATTTATCATAGTGGGCTGGATCATTTCTATAG 2820
QY 2821 TGAATGATACATCATATGCTTATTTGGTAAAAAGAACACATATGAGGCTTAGACTA 2880
Db 2821 TGAATGATACATCATATGCTTATTTGGTAAAAAGAACACATATGAGGCTTAGACTA 2880
QY 2881 ACAATAGTACTACCCCAAAACCGAGAGATGATTTAGAGCAGTGAAGTACGCTCTT 2940
Db 2881 ACAATAGTACTACCCCAAAACCGAGAGATGATTTAGAGCAGTGAAGTACGCTCTT 2940
QY 2941 GCAAGCAGTCAACTAATACTCAGAAACATGAAAGCTCCAGTTGATGAAATTTTCACT 3000
Db 2941 GCAAGCAGTCAACTAATACTCAGAAACATGAAAGCTCCAGTTGATGAAATTTTCACT 3000
QY 3001 AACAGCTTAACCTTAATTTCCCTTTTCCCTCTTGAATTTTAAAAAGGCTTCTTC 3060
Db 3001 AACAGCTTAACCTTAATTTCCCTTTTCCCTCTTGAATTTTAAAAAGGCTTCTTC 3060
QY 3061 CTGAGCATCAATTAATGAGTGTACTGTTCTTCTTGAATTAATGAAAGCTTTAGAT 3120
Db 3061 CTGAGCATCAATTAATGAGTGTACTGTTCTTCTTGAATTAATGAAAGCTTTAGAT 3120
QY 3121 TTAATTTGTAAGCCCAATTTCTTGTATATGAACTATTTATATGACATGAGGCTGAA 3180
Db 3121 TTAATTTGTAAGCCCAATTTCTTGTATATGAACTATTTATATGACATGAGGCTGAA 3180
QY 3181 TGTAGCATGCAAGACAGCAGATCTTTACATCTTGTAAATAATTAATCTGATTTTC 3240
Db 3181 TGTAGCATGCAAGACAGCAGATCTTTACATCTTGTAAATAATTAATCTGATTTTC 3240
QY 3241 ATCTTGTCTTGTCTTTAGAAAAAGTGAAGTGAAGAGAGAGAACTCATGTGATCTG 3300
Db 3241 ATCTTGTCTTGTCTTTAGAAAAAGTGAAGTGAAGAGAGAGAACTCATGTGATCTG 3300
QY 3301 TGTGATTTTCAAGACCTTTAATCCATTTTGAAGAAATCAATTTCTATTTGCAATGGGT 3360
Db 3301 TGTGATTTTCAAGACCTTTAATCCATTTTGAAGAAATCAATTTCTATTTGCAATGGGT 3360
QY 3361 GCAATGTTTCAAGAGATTTATGCTTTTGTCTGAGCTTCAAGAAAGCAGAGAGAGAA 3420
Db 3361 GCAATGTTTCAAGAGATTTATGCTTTTGTCTGAGCTTCAAGAAAGCAGAGAGAGAA 3420
QY 3421 GCAATGTTTCAAGAGATTTATGCTTTTGTCTGAGCTTCAAGAAAGCAGAGAGAGAA 3480
Db 3421 GCAATGTTTCAAGAGATTTATGCTTTTGTCTGAGCTTCAAGAAAGCAGAGAGAGAA 3480
QY 3481 GTGCTTTTGGAGGATTAATTTCCCTCTCTGTTGGGGTAAAGCAGAAAGCAGGTTGGTA 3540
Db 3481 GTGCTTTTGGAGGATTAATTTCCCTCTCTGTTGGGGTAAAGCAGAAAGCAGGTTGGTA 3540
QY 3541 GTAAATGATGACAGACAGTGAAGAGATTAATCTTAAATTTCTTTATAGCTTTGAG 3600
Db 3541 GTAAATGATGACAGACAGTGAAGAGATTAATCTTAAATTTCTTTATAGCTTTGAG 3600

QY 3601 TCTTGGAGTAAAGAAATATCTTTTGGCCTTATGCAAAAGATGAGAAAGTGA 3660
Db 3601 TCTTGGAGTAAAGAAATATCTTTTGGCCTTATGCAAAAGATGAGAAAGTGA 3660
QY 3661 AAGGCGGAGAAAGCAGAAAGAAAGAACATATATATATAGAGACATGAGTGA 3720
Db 3661 AAGGCGGAGAAAGCAGAAAGAAAGAACATATATATATAGAGACATGAGTGA 3720
QY 3721 AGGTTTCTTGAATTAATGCAATATATATATATAGAGAAATTTCAATGAGAAATGCTT 3780
Db 3721 AGGTTTCTTGAATTAATGCAATATATATATATAGAGAAATTTCAATGAGAAATGCTT 3780
QY 3781 TTTCAATTAATTTGGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3840
Db 3781 TTTCAATTAATTTGGGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3840
QY 3841 GAGAGAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3900
Db 3841 GAGAGAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3900
QY 3901 GAAAGACTTATTTGATTTTCCACAAAGTGAATCTTTCTTTTACTGTTGTCA 3960
Db 3901 GAAAGACTTATTTGATTTTCCACAAAGTGAATCTTTCTTTTACTGTTGTCA 3960
QY 3961 AAAAGGTGAAATGAAAAACCTTAATGATTTGATGATGATGATGATGATGATGATGAT 4020
Db 3961 AAAAGGTGAAATGAAAAACCTTAATGATTTGATGATGATGATGATGATGATGATGAT 4020
QY 4021 AGTGAAGTGTTTTAAATCAGAGAGTGCATCAATTTGGCTTCCCTGAGCAGCTTGA 4080
Db 4021 AGTGAAGTGTTTTAAATCAGAGAGTGCATCAATTTGGCTTCCCTGAGCAGCTTGA 4080
QY 4081 GAATTTCTTGGTACACATATAATAACAAGATGATGATGATGATGATGATGATGATGAT 4140
Db 4081 GAATTTCTTGGTACACATATAATAACAAGATGATGATGATGATGATGATGATGATGAT 4140
QY 4141 TGCATTAATCTCATCTGTTTAAAGAAATTTGATGATTTCTGTTAGGCTCATCAAG 4200
Db 4141 TGCATTAATCTCATCTGTTTAAAGAAATTTGATGATTTCTGTTAGGCTCATCAAG 4200
QY 4201 CTGTCCTGGGCGATGCGGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 4260
Db 4201 CTGTCCTGGGCGATGCGGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 4260
QY 4261 TGTATAGATAGTTTGGAGCTGCAAAACAGGCAAGCATATAGGCTGCACTCGGAT 4320
Db 4261 TGTATAGATAGTTTGGAGCTGCAAAACAGGCAAGCATATAGGCTGCACTCGGAT 4320
QY 4321 CCCCAGATCCAGCTTCACTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4380
Db 4321 CCCCAGATCCAGCTTCACTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4380
QY 4381 TCTGCCAGCTTTTAAACAGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 4440
Db 4381 TCTGCCAGCTTTTAAACAGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 4440
QY 4441 GTGACCTCTCAGTCCAGAGACCTCAATTTTAACTCTTTGCAAAATCATCAATTAATA 4500
Db 4441 GTGACCTCTCAGTCCAGAGACCTCAATTTTAACTCTTTGCAAAATCATCAATTAATA 4500
QY 4501 AGGATATTAATGAAATGTTTCAAAATGCTTTAACTCGGTTCTGCTCAATCAAC 4560
Db 4501 AGGATATTAATGAAATGTTTCAAAATGCTTTAACTCGGTTCTGCTCAATCAAC 4560
QY 4561 TAACTTGCATTTCTAATTTGTTCACTTAAAGAAACATGAGCAATTAATGCTCAATCTT 4620
Db 4561 TAACTTGCATTTCTAATTTGTTCACTTAAAGAAACATGAGCAATTAATGCTCAATCTT 4620
QY 4621 TTGATTTCTTATTTTCAAGCTTGAAGAGATGAGAGATCAAAAGCATTTGAGAACTGG 4680
Db 4621 TTGATTTCTTATTTTCAAGCTTGAAGAGATGAGAGATCAAAAGCATTTGAGAACTGG 4680
QY 4681 ATTTGCTGTTTATGCTCTGAGAAATGCTGCAATTTGACAGAGCAAAAGCTGAAAAATGA 4740

Db 4601 ATTCTGTTATGCTCTGAGAAATGCTGATTTGACAGAGCAAGAGCTGAAAAATGA 4740
Qy 4741 ATAATAACCCCTTCCCTGCTAGAAATTAACATTAAGTGGCCCAAGCATTTT 4797
Db 4741 ATAATAACCCCTTCCCTGCTAGAAATTAACATTAAGTGGCCCAAGCATTTT 4797

RESULT 2
US-09-354-243B-25
; Sequence 25, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renaud, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
; TITLE OF INVENTION: (TfP)
; FILE REFERENCE: LUD 5543.1
; CURRENT APPLICATION NUMBER: US/09/354,243B
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 25
; LENGTH: 4797
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-354-243B-25

Query Match 100.0%; Score 4797; DB 4; Length 4797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACAGCAGAAATCTTCAGAACAGGTTCTCTCCCAAGTCACAGATTGCTGAGTTAG 60
Db 1 TGCACAGCAGAAATCTTCAGAACAGGTTCTCTCCCAAGTCACAGATTGCTGAGTTAG 60
Qy 61 AATTGTGCAATGGCCGCCCTGCAAGAAATCTGTAGAGCTTCTCTTAATGGGAGCCCTGG 120
Db 61 AATTGTGCAATGGCCGCCCTGCAAGAAATCTGTAGAGCTTCTCTTAATGGGAGCCCTGG 120
Qy 121 CCACAGAGTCCCTCTCTCTGTGGCCCTCTTGTGTAAGGAGAGAGAGCTGGCCCATCA 180
Db 121 CCACAGAGTCCCTCTCTCTGTGGCCCTCTTGTGTAAGGAGAGAGAGCTGGCCCATCA 180
Qy 181 GCTCCCACTGCAAGGCTTGCAAGTCCAACTTCAGAGCCCTATATACCAACCCACCT 240
Db 181 GCTCCCACTGCAAGGCTTGCAAGTCCAACTTCAGAGCCCTATATACCAACCCACCT 240
Qy 241 TCATGTGGCTAAGAGGATATCATCTCAATCTGCTCTTCTGTTGATCTACTTGA 300
Db 241 TCATGTGGCTAAGAGGATATCATCTCAATCTGCTCTTCTGTTGATCTACTTGA 300
Qy 301 ATCCAAATATGTTCTTAACCTTCTTCAGAGCATCTTAAGAGCTTTAGAAACCACTGT 360
Db 301 ATCCAAATATGTTCTTAACCTTCTTCAGAGCATCTTAAGAGCTTTAGAAACCACTGT 360
Qy 361 TTAATCCCTGAGGGATTAATTTCTGTTTTTTCAGAGACTCTTTGGAAATCTGGCTTT 420
Db 361 TTAATCCCTGAGGGATTAATTTCTGTTTTTTCAGAGACTCTTTGGAAATCTGGCTTT 420
Qy 421 TTTTCTTCTGAACTTCTCTCTGATTTTGGCCCTTAATGATACATATGATGATTTT 480
Db 421 TTTTCTTCTGAACTTCTCTCTGATTTTGGCCCTTAATGATACATATGATGATTTT 480
Qy 481 CCCAAGAGCGGCATTCAGTAATTCATGATGATTTTCTTTATGCTCTG 540
Db 481 CCCAAGAGCGGCATTCAGTAATTCATGATGATTTTCTTTATGCTCTG 540
Qy 541 CATGTCTTAACATCATGACACATCTGATTTCTGTTAGCTTTATGATGTTGCTCT 600

Db 541 CATGTCTTAACATCATGACACATCTGATTTCTGTTTATGCTTTATGATGTTGCTCT 600
Qy 601 GGGAGAGCGGATGGGACATGCTATGTAATAATTTTTTCTATTTGCTCAATGTC 660
Db 601 GGGAGAGCGGATGGGACATGCTATGTAATAATTTTTTCTATTTGCTCAATGTC 660
Qy 661 AGACCTTATGCTTTTCTCTCTTCAGAGCTAGCTTGGCTATACAAACAGAGCTTG 720
Db 661 AGACCTTATGCTTTTCTCTCTTCAGAGCTAGCTTGGCTATACAAACAGAGCTTG 720
Qy 721 TCTGATGGGAGAAAGCTTCCAGAGAGTGTAGCTACATCAAGTTGACAGAGG 780
Db 721 TCTGATGGGAGAAAGCTTCCAGAGAGTGTAGCTACATCAAGTTGACAGAGG 780
Qy 781 CCGTGTGCGCTTCATGAGGTAATTTGGGATGGTGTAGATGATGATTTAGCTTATCCCTTA 840
Db 781 CCGTGTGCGCTTCATGAGGTAATTTGGGATGGTGTAGATGATGATTTAGCTTATCCCTTA 840
Qy 841 TGACCTTTCTGTTTCCCTTCACCTGCAATGATGAGCGCTGATCTGATGAGCAG 900
Db 841 TGACCTTTCTGTTTCCCTTCACCTGCAATGATGAGCGCTGATCTGATGAGCAG 900
Qy 901 GTGCTGAATCTCACCTTGAAGAGTGTCTTCCTCAATCTGATGATGATGATGATGAT 960
Db 901 GTGCTGAATCTCACCTTGAAGAGTGTCTTCCTCAATCTGATGATGATGATGATGAT 960
Qy 961 ATGACAGAGTGTGAGCCCTTCTGCGCAGCTCAGACAGAGCTAAGCAGATGTAAGT 1020
Db 961 ATGACAGAGTGTGAGCCCTTCTGCGCAGCTCAGACAGAGCTAAGCAGATGTAAGT 1020
Qy 1021 TCAGCTCAGACCTATGCGCACTAAGCCTCTCTCTCTCTTCCACAGAGAGCCCTTAC 1080
Db 1021 TCAGCTCAGACCTATGCGCACTAAGCCTCTCTCTCTCTTCCACAGAGAGCCCTTAC 1080
Qy 1081 CCCAATCT 1140
Db 1081 CCCAATCT 1140
Qy 1141 TGTATCAGAGTCAATTTGGATCATAGATGATTTGCTTTGCTTTGCTTTGCTTTGCTTTG 1200
Db 1141 TGTATCAGAGTCAATTTGGATCATAGATGATTTGCTTTGCTTTGCTTTGCTTTGCTTTG 1200
Qy 1201 TTGATTTATAGTGTGATGATGGGATCTGGAATTAAGTGAATGATGATGATGATGATG 1260
Db 1201 TTGATTTATAGTGTGATGATGGGATCTGGAATTAAGTGAATGATGATGATGATGATG 1260
Qy 1261 TCTTCGAAAAAAGCACTAGGTTGCTTAAGTGAATGATGATGATGATGATGATGATG 1320
Db 1261 TCTTCGAAAAAAGCACTAGGTTGCTTAAGTGAATGATGATGATGATGATGATGATG 1320
Qy 1321 GCTGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 1321 GCTGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Qy 1381 ATTGAAGAGAAAGTGGAAATGGAGGCTTTAAAGTGGTGGTGGTGGTGGTGGTGGT 1440
Db 1381 ATTGAAGAGAAAGTGGAAATGGAGGCTTTAAAGTGGTGGTGGTGGTGGTGGTGGT 1440
Qy 1441 GCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
Db 1441 GCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
Qy 1501 CATTTGAATCATGAAAAAAGTTTGAATGATGATGATGATGATGATGATGATGATGATG 1560
Db 1501 CATTTGAATCATGAAAAAAGTTTGAATGATGATGATGATGATGATGATGATGATGATG 1560
Qy 1561 ACTGAAGAGGCTTAATTTTCAATGATGATGATGATGATGATGATGATGATGATGATG 1620
Db 1561 ACTGAAGAGGCTTAATTTTCAATGATGATGATGATGATGATGATGATGATGATGATG 1620
Qy 1621 CAATTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680

Db 1621 CAATTTCTGAGATAGAGTTGAGGTTTATTCCTTACAGAAATTTGCATTAACCTACTCCG 1680
Qy 1681 CTCTTTCCAAATGCAAACTCAGTAGAGATTTCCCAAAGATGAAGAGAGGCTCTTGT 1740
Db 1681 CTCTTTCCAAATGCAAACTCAGTAGAGATTTCCCAAAGATGAAGAGAGGCTCTTGT 1740
Qy 1741 AGGGAAGATGATGATTTCTGGCGCTCCAGGGAATTCAGAGCTCAGGAAATCTAGGTAC 1800
Db 1741 AGGGAAGATGATGATTTCTGGCGCTCCAGGGAATTCAGAGCTCAGGAAATCTAGGTAC 1800
Qy 1801 TGTGAAATCTAGGCTATGAGGCAAAATTAAGAGCTTAAATTCAGAGTAAATGCT 1860
Db 1801 TGTGAAATCTAGGCTATGAGGCAAAATTAAGAGCTTAAATTCAGAGTAAATGCT 1860
Qy 1861 ACTGACCTCCAGGAGTGTGAGGTTCAATAAGTTTCAGACAACAATTAAGATTAAG 1920
Db 1861 ACTGACCTCCAGGAGTGTGAGGTTCAATAAGTTTCAGACAACAATTAAGATTAAG 1920
Qy 1921 CTGTTATTTGTTTAAATGATATTTGAAGGTATGACCTGATATCCAGAGGAATGTGCA 1980
Db 1921 CTGTTATTTGTTTAAATGATATTTGAAGGTATGACCTGATATCCAGAGGAATGTGCA 1980
Qy 1981 AAGCTGAAGGACAGAGTAAAGATGAGATGATTAATGCTCAATGCTAAATGCTAAAT 2040
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Qy 2041 AGGAGAGACAAATGTTGTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 2100
Db 2041 AGGAGAGACAAATGTTGTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 2100
Qy 2101 CTGATTTCTCTTACACAGGCGCATTAATTGATGCTGATGATGATGATGATGATGATGAT 2160
Db 2101 CTGATTTCTCTTACACAGGCGCATTAATTGATGCTGATGATGATGATGATGATGATGAT 2160
Qy 2161 TATCTAATGTCAGTTTCCAAATCTTGCAATTTGATGATTTGAACTGTTGGAGCT 2220
Db 2161 TATCTAATGTCAGTTTCCAAATCTTGCAATTTGATGATTTGAACTGTTGGAGCT 2220
Qy 2221 TAGCTGTCTAGTACATTAACCTGATTCGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGG 2280
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Db 2281 GAAATGACAGTCTCTGATCCCAAGCCAGACCTTTCCCGGTGATGATGATGATGATGAT 2340
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Db 2341 TGGTACCATTAATTTCTAGGGAATTTCAAGATTCCTAATGATCATGTAATCTGAAGAG 2400
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Qy 2521 ACTTGCATATAGGCTAATTTCTGAGATTAATAACCTTAATTTTGAATTAATCATATATC 2580
Db 2521 ACTTGCATATAGGCTAATTTCTGAGATTAATAACCTTAATTTTGAATTAATCATATATC 2580
Qy 2581 TATCAGATATGATTAATGTTTAAAAAGCAGAGAGCAACCCCGATCTCTTTTATACAG 2640
Db 2581 TATCAGATATGATTAATGTTTAAAAAGCAGAGAGCAACCCCGATCTCTTTTATACAG 2640
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Db 3421 GCAATGTTTTCAGAGAAAGATCAACAGAGAGAGAACTGTCAAGCTGTCTGAATAGG 3480
Qy 3481 GTGGTTTTGGGAGGCAATTAATTCCTCTCTGTTGGGGTAAAGCAGAACGAGGTTGTA 3540
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Qy 3541 GTAAAAATGATCAGACAGATGAGGAGCAATAAATTTTAAAAATTTCTTTATAGCTTGGAG 3600
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Qy 3721 AGGTTTTTCTTGAATAATGCAATATGATAGATTAAGAGAAATTTAGTAGAGGAATGCTT 3780
Db 3721 AGGTTTTTCTTGAATAATGCAATATGATAGATTAAGAGAAATTTAGTAGAGGAATGCTT 3780
Qy 3781 TTCACTTGAATTTGGGTTCTCTTCTGATTAAGTTGGAGTCTCATCTGCAATTTGACTT 3840
Db 3781 TTCACTTGAATTTGGGTTCTCTTCTGATTAAGTTGGAGTCTCATCTGCAATTTGACTT 3840

QY 869 AGATGAGGCGCTGCTATCTGATGAAAGAGTGTCTGAATCTTCAACCTTGAAGAAGTGC 928
DB 2818 AGGCTAAAGATGATGCTACCTGATGAAGCAGGTCTCTCACTTCAACCTGGAAGACGTTC 2877
QY 929 TGTTCCTCAATCTGATAGTTCACAGCCTTATATGACAGAGGTGTGGCCTTCCGAGCA 988
DB 2878 TGTCTCCCAAGCAGACAGGTTCACAGCCTTACATGACAGAGGTGTGTACTTTCTGACCA 2937
QY 989 GCGTCAGCAACAGGCTAAGACACATGTGTAAGTTCAGCTCTGACCTTATGCCCACCTACCC 1048
DB 2938 AACTCAGCAATAGCTCAGCTCTGTGTAGTCTGACCTGTGCTACCTATGCTCTCTCT 2997
QY 1049 CT 1108
DB 2998 CT 3057
QY 1109 TAAGTACAGCAAGAGTGTCTGACAGAGTGTATTCAGAGTCA-----TTTGGG 1161
DB 3058 GAGAGGCTCAGACACACACCACTATAGGCCACTTGAATAGTTCACAAAGCTTTGGC 3117
QY 1162 ATCATAGATATTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTG 1221
DB 3118 TTCAATGATGATATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 3177
QY 1222 GGGTCTGAACTTAAGTGAAGAAAGCCGCACTGTTGTCTTGGAAAAAGCAATC 1281
DB 3178 AGAATCAACTCAATCTGTAGATGAGAAAGATGTGGAAACAAAAAGCCTAGAT 3237
QY 1282 A-----GGTTCGTAAAGTGAAGAAAGTGTGG 1309
DB 3238 AGAGAAACAGATCTGCTGATGATGATCTTATGAGGAGAGAGGAGGAGCAATTCACATGA 3297
QY 1310 GAAACATCTAGCTGTGAAATGATCCATTGAGTCTAAGTGTGTAGGAGGAGGAGATG 1369
DB 3298 GTACAGATCTTGTGTGGAGAGAAATCCATGAGTACAAAGTACTTGTGTGTGTGTGTGT 3357
QY 1370 CATGAGAGAAATTAAGAAAGAAAGTGGGAAATGGGAAAGCTTAA----- 1415
DB 3358 CACTGAGTACAAGTCTGTGGGAGGAGGAAATGSCACAGACAAAGTGAAGGAGAG 3417
QY 1416 -----GTGGGT 1460
DB 3418 AAGATGAGAGGCTCATGT 3477
QY 1461 AGCCACAATCTGAGGCGGTGTGAATCTGATGCCCTGAACTTTGAAACTGTAAGAAA 1520
DB 3478 AGTTAAGAAAACAGT-GTGTGATTTGATGTCTTCAACACCCCACTATGAAACAT 3536
QY 1521 AGTTGAGTGAAGTGGCCAGTAAAGCCCTAGACTTACTGAAGAGGCTTAATTT 1580
DB 3537 ATCCACGAGAGCGGCGAGACTGTGGAGACCTGCACTTAAAGGA--AGGCGCGCTTTT 3594
QY 1581 CACATGAGATGTTTATGATCACTTTCTTGTCTTAAGCATGCAATTTCTGAGATACAT 1640
DB 3595 CACACGAAACCTTATGCTCATCTTGTGTCACTCCACCTTTATGAGGTTCAGC 3654
QY 1641 TGAGGTTTATCTCTTACAGATTTGCAATTAACCTCTCGCTTTCCACAAAGCAAC 1700
DB 3655 TCAAGTTTCTTTCT-----ACCGTCTTGTCTACCTGTGTGAAC 3693
QY 1701 CTCAGTAGATTTTCCCAAGATGAAGAGGCTCTTGTAAAGGAAGTCACTGATTTCTG 1760
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QY 1761 GCGTTCAGGGAATTCAGAGCTCAGAAATCTAGCTCACTGTGAAAATCTAGTCAAC 1820
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QY 1821 TGGGCAAAATTAAGAGCTTATTCAGGTGATGATGATGATGATGATGATGATGATGATG 1880
DB 3814 GGGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3873
QY 1881 GAGTTCATAAGTTTCAAGACACACATTAAGATGATGATGATGATGATGATGATGATG 1940

DB 3874 AGGATTTGGGCTCCACCGGATTAAGATCTGTGTGTGA-GTCTGCTTTTATTTTGCACCA 3932
QY 1941 TATTGAAGTATGACTGCTATCTCAGAGAAATGTGAAAAAGCTGAAGACACAGTAA 2000
DB 3993 CATGAGCGGTACACAGCAACATCTCAGAGAAATGTGAAAAAGCTGAAGACAGTAA 3992
QY 2001 AAAGTATGACTGATTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATG 2060
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QY 2061 TTTCT 2120
DB 4051 TTTCT 4110
QY 2121 GCGCATTA-----CTTGT 2176
DB 4111 GTCCATTAAGT 4170
QY 2177 TCCAAATCTTGCMAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2236
DB 4171 TCTAAATTT---GTAACTCAATCTGTGAGCTGACAGAAAGCTTACCTCAGCTCAGCTC 4227
QY 2237 ATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2296
DB 4228 ATGAGCACTGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 4287
QY 2297 AATCCCAAGCAGACCTTTCCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2356
DB 4288 ATTCAGCTGCTGAC-TTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4346
QY 2357 TAGGAAATTTCAATCTCTATGATGATGATGATGATGATGATGATGATGATGATGATG 2416
DB 4347 TTGGAA--GCCAGTTCCAGAGACCTAATCTGATGATGATGATGATGATGATGATGATG 4404
QY 2417 GAAAAATGCTATGAGGCAATTTATTTGATGATGATGATGATGATGATGATGATGATGATG 2476
DB 4405 GAAA-----GCTGGCACAACCTTACTAGATGATGATGATGATGATGATGATGATGATG 4460
QY 2477 TGAATCTGAAAGATTAATCTCAGAACATGAGAAAGAGCTGATGATGATGATGATGATG 2536
DB 4461 TGAATGAGCAAAATCAACCAAGATTAACAAAGAGCTGATGATGATGATGATGATGATG 4520
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DB 4521 AGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4580
QY 2590 TTGATTAATGTTAAAGCAAGACAGCAAC--CCGATCTTTTATACAGTTCAAT 2648
DB 4581 TATATTTAAGATTAACCAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 4640
QY 2649 AGATTAAGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2708
DB 4641 AGATTAAGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4700
QY 2709 TTTTCT 2768
DB 4701 TTTCT 4752
QY 2769 ACAAATCCCTAGGAGCATTTATCATGATGATGATGATGATGATGATGATGATGATGATG 2828
DB 4753 TCAAGCAGCTAGTAAAGACCTATCTGCTGTAGCTATTAATTAAGCAACAAAC 4812
QY 2829 ACCATCATGTGCTATTTTGTGAAAGAA--ACAATGAGAGCTTACCTAACATA 2886
DB 4813 ATTCTGTGTGCTCTTTTGGGAAAGGAAAGATGACAGAGAGCTCAGCTGACAGT 4872
QY 2887 GTGACTCAACCCCAAAACCGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 2945
DB 4873 CTGACTTGCCTTAAGCAGAGGATGATGATGATGATGATGATGATGATGATGATGATG 4932
QY 2946 CAGGTACAATTAATCTCAGAAACATGAGAGCTCAAGTGTGATGATGATGATGATGATG 3005

D	b	4933	TGGGTGCTTAAGTATCAGAAACAGGAAGGCTCCGGTTGATGAATATACGTAAGAT	4992
Q	y	3006	GCTTAACCTTAATTCCTCCCTTTTTCCTTGACTTTAAAAAAAGCTTTCCTCGAG	3065
D	b	4993	ATCTACCCCTTATCTCTTCATGAAACC-----TAAATGCTCTTTTCTGTG	5042
Q	y	3066	CATCATTTAANGATGTGACGTGTTCTCTCTGTATATAATGAAGGCTTGTAGTTTAA	3125
D	b	5043	TGTAGGCTGTAAACACACTTGT--TTCCTTGAAGTGTCAATGGCTTGTGAATTTT	5100
Q	y	3126	TTGGAAGCCAGTCTCTGTTATATAGAACATATATAGACATGAGGGCTGATGTTA	3185
D	b	5101	GTCGTCTGCCAGTTCCTGTTAGAG--GGTTGTACTTACACCTGGGCTGGATGT	5158
Q	y	3186	GCATGCACACAGACAGGCGATGCTTACACATCTTGTAATAAATACTGATTTCACTT	3245
D	b	5159	GCATGCCAAAGGCGACACACTTCTGAATGCCGTGTAAAGGTTATATCAATTAC--	5215
Q	y	3246	GCTTGTGTTCTTTAAGAAAGTGAAGTGTGAGAGAGCAATCTCATGTGA-----	3296
D	b	5216	-----TTGTTCTTGAAAGGTGAAGCGTGTGTGAAGAAACATCACAGGAGTGTCT	5270
Q	y	3297	-----TCTGTGATTTCAAGACCTTAATCCATTTTGAAGAAATCAAT	3342
D	b	5271	CTGTAGGAAAACTTTTTTTTCCCTTAAATGCTTAATACACTTTCACTGACAC--TT	5327
Q	y	3343	TCATATTTTGCATGCGGTGCCATGTGGAAGAGTATTAGCTTTTTCCTGTGACTTCA	3402
D	b	5328	TGACTTTTATATCATGCTGTCAATGAAGAAGTGTTTAGGCCCGCTCTCATGGCTGGG	5387
Q	y	3403	GAAAGCA-CAGAGGGAGAGCAATGTGTTCACAGAAAGATCAACAGAGGACAACTGT	3461
D	b	5388	AAAAGCACCAATAGGGGAGGAAGTATATGCTGAAATCTGACCGGACGGAAACGTGT	5447
Q	y	3462	CAGAGCTGTGGAATAGGGGTGTTTGGAGGCAATTAATCCCTCGTGGGGGTAA	3521
D	b	5448	CAGAGCTCCCCGAAGACA-----CCACAGGTCTTAAGTAGG	5485
Q	y	3522	AGCAGAAACGCGAGTGTGTAATTAAT-GCATGACAGACAGTAGGGGACGATAACTTAA	3580
D	b	5486	AACAGTCCAGGCTGGGCTCATGTATATAGAAATGGAACAGAGGAGAAAGATTAAC	5545
Q	y	3581	AATTCCTTATAGTCTTGGAGTCTTTAGATAGAAAAGATATCTTTTGGCCTTATGTCA	3640
D	b	5546	AGTTTCATAGGGTCT-CGGAGCTTAAAGATCAAAATAGCTGCT--TTGGGCTTATACA	5602
Q	y	3641	AAAGAAATATGGAAG-----TGAAGGGCGGAAGAAAGCAGAAAGAGAG	3688
D	b	5603	AAGGAAGCTGGGAAGGCGACAGTGAAGAGGAAATGAAAGGGAAGAAACAGATGAG	5662
Q	y	3689	AACCATGTATATATAGAGCAATATGGAACAAGGTTTCTGAAATATATGCAAAATATG	3748
D	b	5663	AGGACTTGAAACAGCTCAAAATCTCTACACACATTTTCTTGGAAACAATCTGAAGGT	5722
Q	y	3749	ATATATAGAGAAATTCAGTAGGGAATGCTTTTCACTGAATTTGGTTCCTCT--T	3805
D	b	5723	AGTGGATTAGGTGATGACAGGGGGACTTGCTTGGCATTTGAATCTGGGTTTGTCTCT	5782
Q	y	3806	CGATTAACTTTGGGATCTCTCATCTGCATTTTAACT---TGAAGAGAAAGAAATGAATGT	3861
D	b	5783	CCATTGAAGTTGAAGCGCTCACCTTTTACCCTGGAATGAGAGGAGAAAGAGGGGTGT	5842
Q	y	3862	TAGGACCTATATCTGTTTCTATTAATAAGCAAGTGAAGAAAGAACTTATTTGGTATTT	3921
D	b	5843	TATGACTCTTACTTGGAGTTTATCTAGTTTACGCATATGGAACAGACACTCGGACCTCT	5902
Q	y	3922	TTCCCAAAAAGTGAAACTTTTCTTAACTGTTTGTCAAAAAGGTGGAATAGAAAAAG	3981
D	b	5903	CTTGACAAAAAATGGAAACTGTGTTGTGCTGTTGTGTTCTTTGTAAAGAAACAC	5962
Q	y	3982	CCTTAATGTATTTGGTAATACATGTTCAAAAGTCAATTTGAGTAGAGATGTTTAAATCAG	4044
D	b	5963	AGGCAAGCCGACACATAGGGTTAATATGTGGTCTTTTGAAGCAAGGCTTTTGAATGAG	6022

QY 4042 GAGTGTCCATTCATTGGCTTCCCTGGACACACTGGAAAGAAATGTGCTTGTAACACAT 4101
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 QY 4102 AAAATACAGAAACAATAGCTGATGACTAAAAAAGTCATGCAATAAATCATACTGTTT 4161
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 QY 4162 TAAAGAAAGTTATGAATTTCTGTTAGGGTGCAATTCAAAGCTGTCTCGGGCCATGTGGGC 4221
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 QY 4222 CTGTGGGGGTGAGGTGGACAGCTCTTATAGAAATCTGATCATAGATAGTTTGGAGC 4281
 Db 6164 -----AACCCCACTAAAAATTAATTTAGCAAAAGACTGTGTAATTTG 6205
 QY 4282 TGCAAAACAGGCCAACGACATATAGGGTGGCACTGGGATCCCCACAGATCCACCTCACT 4341
 Db 6206 TGGGATACAGTGTGTAATATGA----- 6227
 QY 4342 TCACTCTCTTCTGCTGTGGTTAAGAAAGGGGTGTCACTCTGCCACGTTTAAACAGC 4401
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 Db 6524 TTCTTATTTTCAATCTGTGAAGAGTGGAGATCAAGGCGATTTGGGGCAACTGGAACTTG 6583
 QY 4686 CTGTTTATGTCTCTTGAAGAAATGCCCTGCATTTACACCGAGCAAGCTGAAAATGAATTAAC 4745
 Db 6584 CTGTTTATGTCTCTTGAAGAAATCTTGCTGTGCGAAGAAAGCTTGAAGAAACGAAGAC 6643
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 Db 6644 TGCTCTTCTCTGCTCTTCTTAAAAAGAAACAATATGATCCTCGAATGACTTTT 6695

RESULT 4
 US-09-419-568F--8
 ; Sequence 8, Application US/09419568F
 ; Patent No. 6331613
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumoutier, Laure
 ; APPLICANT: Louned, Jamila
 ; APPLICANT: Renaud, Jean-Christophe
 ; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible F
 ; TITLE OF INVENTION: (Tlfs) The Proteins Encoded, and Uses Thereof
 ; FILE REFERENCE: LUD 5543.2
 ; CURRENT APPLICATION NUMBER: US/09/419, 568F
 ; CURRENT FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: US09/354,243
 ; PRIOR FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: US09/178,973
 ; PRIOR FILING DATE: 1998-10-26
 ; NUMBER OF SEQ ID NOS: 29
 ; SEQ ID NO 8

LENGTH: 7445
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-419-568F-8

Query Match 14.3% Score 686; DB 4; Length 7445;

Best Local Similarity 53.8%; Pred. No. 1,3e-182;
Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;

QY 29 CTCCTTCCCACTACCAAGTGTCTGAGTTAGATTGTCTGCAATGAGCCGCCCTGCAGAA 88
Db CTCCTCTCACTTAACTGTTGACATGTGCGATCTCTATAGCTCTCTGCGAA 2093
QY 89 ATCTGAGCTCTTCTTATGAGGACCTTGGCCACAGCTGCTCTCTTGGCCCT 148
Db ATCTAGAGTTTTCCTTATGAGGACCTTGGCCACAGCTGCTCTCTCAATGGCCCT 2153
QY 149 CTGTGTAAGAGGAGGAGAGCTGGCCATCAGCTCCACCTGCAGGCTTACAGTCCAA 208
Db GTGGGCCAGAGAGGAGAGCTGGCCATCAGCTCCACCTGCAGGCTTACAGTCCAA 2213
QY 209 CTTCAGCAGCCCTATATACCAACGACCTTCATGCTGAGTAAAGAGTATCATCTC 268
Db CTTCAGCAGCCCTATATACCTCAACCGACCTTATGCTGCGCAGAGGATCAGCTGCA 2273
QY 269 AATCTGCTCTTCTGCTGATCTACTTGAATCCAAATAGTTCTTAACTTTCTTCA 328
Db TCTCTTCTCTCATACCGCTTGCCATTTCTCTGAAGCATTCGAACTCTTAGGGG 2333
QY 329 GAGCATCTCAAGAGCTTGAAGAACCCACCTGTTATCCCTGAGGATGATTAATTTCTG 388
Db CGCTTATCTCCGAGCTCACTACTATGTTT-----TCTGCTCTTTAGAG 2382
QY 389 TTTTTCAGAGACTCTTGGGAATCTGGCTTTTCTTCTTGAATCTCTCTTCAT 448
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RESULT 5

US-09-354-243B-8
 ; Sequence 8, Application US/09354243B
 ; Patent No. 6359117
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumoutier, Laure
 ; APPLICANT: Leuhed, Jamila
 ; APPLICANT: Renaldi, Jean-Christophe
 ; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
 ; TITLE OF INVENTION: (Tifs)
 ; FILE REFERENCE: LUD 5543.1
 ; CURRENT APPLICATION NUMBER: US/09/354, 243B
 ; PRIOR APPLICATION NUMBER: US09-07-16
 ; PRIOR FILING DATE: 1999-07-16
 ; NUMBER OF SEQ ID NOS: 29
 ; SEQ ID NO 8
 ; LENGTH: 7445
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; FEATURE:
 US-09-354-243B-8

Query Match 14.3%; Score 686; DB 4; Length 7445;
 Best Local Similarity 53.8%; Pred. No. 1,36-182;

Matches 2644; Conservative 0; Mismatches 1875; Indels 393; Gaps 44;
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RESULT 7
 US-09-419-568F-29
 ; Sequence 29. Application US/09419568F
 ; Patent No. 6331613
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumoutier, Laure
 ; APPLICANT: Louhed, Jamila

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; APPLICANT: Renault, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
; FILE OF INVENTION: (Tifs) The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LND 5543.2
; CURRENT APPLICATION NUMBER: US/09/419,568F
; PRIOR APPLICATION NUMBER: US09/354,243
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO: 29
; LENGTH: 5935
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; US-09-419-568F-29

Query Match      13.6%; Score 650; DB 4; Length 5935;
Best Local Similarity 56.5%; Pred. No. 1.5e-112;
Matches 1863; Conservative 0; Mismatches 1285; Indels 152; Gaps 29;

QY 29 CTCCTTCCCGATACCAAGTTCGAGTTAGATTTGTCGATATGCGCCCTGCAAA 88
DB 356 CTCCTTCCCGATACCAAGTTCGAGTTAGATTTGTCGATATGCGCCCTGCAAA 415
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DB 416 ATCTATGATTTTCTCTTATGAGGACCCGCGCCACGAGCTGCTCTTGGCCCT 475
QY 149 CTGGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 208
DB 476 GTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 535
QY 209 CTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 268
DB 536 CTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595
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DB 596 TCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 655
QY 329 GAGCATCTCTAAGAGCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 388
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QY 389 TTTTTCAGAGAGCTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 448
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DB 822 CCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 881
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DB 1036 GTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1082

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RESULT 8
US-09-354-243B-29
Sequence 29, Application US/09354243B
Patent No. 6359117
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
TITLE OF INVENTION: (ntfs)
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 29
LENGTH: 5935
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-354-243B-29

Query Match 13.6%; Score 650; DB 4; Length 5935;
Best Local Similarity 56.5%; Pred. No. 1,5e-172;
Matches 1863; Conservative 0; Mismatches 1285; Indels 152; Gaps 29;

QY 29 CTCCTTCCCAGTACACAGTGTCTGAGTGAATGTCTGCAATGCGCGCTCGAGAA 88
DB 356 CTCCTCTCAGTATTAACAATTTTGACATTTGCGCATCGTGATGCTGTCTCGAGAA 415
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3372 CTTTGAGATTTTCAAGTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3429
3171 GAGGCTGAAGTGAAG 3230
3430 TGGGCTTGAATTTGAG 3489
3231 TACTGATTTCACTTGTGTTGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3290
3490 TATTCATTTACT-----TTGTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3541

RESULT 9
US-09-419-568F-24
; Sequence 24, Application US/09419568F
; Patent No. 6331613
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
; FILE REFERENCE: LND 5543.2
; CURRENT APPLICATION NUMBER: US/09/419,568F
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US09/354,243
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 24

LENGTH: 690
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-419-568F-24

Query Match 5.4%; Score 258; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.1e-62;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACAGCAGATCTTTCAGACAGGTTCTCTTCCCAATCAGGTTGCTGAGTTAG 60
DB 1 TGCACAGCAGATCTTTCAGACAGGTTCTCTTCCCAATCAGGTTGCTGAGTTAG 60
QY 61 AATTGCTGCAATGGCCGCTGACAGAAATCTGTGAGCTTTTCTTATGGGAGCCCTGG 120
DB 61 AATTGCTGCAATGGCCGCTGACAGAAATCTGTGAGCTTTTCTTATGGGAGCCCTGG 120
QY 121 CCACCAAGCTGCTCTCTTCTTCTTGGCTTGTATACAGGAGAGAGAGAGAGAGAGAG 180
DB 121 CCACCAAGCTGCTCTCTTCTTCTTGGCTTGTATACAGGAGAGAGAGAGAGAGAGAG 180
QY 181 GCTCCACTGACAGGCTTGAAGTCAAGTTCAGAGAGCCCTATATCAACCAAGCCGACCT 240
DB 181 GCTCCACTGACAGGCTTGAAGTTCAGAGAGCCCTATATCAACCAAGCCGACCT 240
QY 241 TCATGCTGCTAAGAGG 258
DB 241 TCATGCTGCTAAGAGG 258

RESULT 10
US-09-354-243B-24
Sequence 24, Application US/09354243B
Patent No. 6359117

GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
TITLE OF INVENTION: Renald, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Pe
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 24
LENGTH: 690
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-354-243B-24

Query Match 5.4%; Score 258; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.1e-62;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACAGCAGATCTTTCAGACAGGTTCTCTTCCCAATCAGGTTGCTGAGTTAG 60
DB 1 TGCACAGCAGATCTTTCAGACAGGTTCTCTTCCCAATCAGGTTGCTGAGTTAG 60
QY 61 AATTGCTGCAATGGCCGCTGACAGAAATCTGTGAGCTTTTCTTATGGGAGCCCTGG 120
DB 61 AATTGCTGCAATGGCCGCTGACAGAAATCTGTGAGCTTTTCTTATGGGAGCCCTGG 120
QY 121 CCACCAAGCTGCTCTCTTCTTCTTGGCTTGTATACAGGAGAGAGAGAGAGAGAGAG 180
DB 121 CCACCAAGCTGCTCTCTTCTTCTTGGCTTGTATACAGGAGAGAGAGAGAGAGAGAG 180
QY 181 GCTCCACTGACAGGCTTGAAGTTCAGAGAGCCCTATATCAACCAAGCCGACCT 240
DB 181 GCTCCACTGACAGGCTTGAAGTTCAGAGAGCCCTATATCAACCAAGCCGACCT 240

DB 181 GCTCCACTGACAGGCTTGAAGTTCAGAGAGCCCTATATCAACCAAGCCGACCT 240
QY 241 TCATGCTGCTAAGAGG 258
DB 241 TCATGCTGCTAAGAGG 258

RESULT 11
US-09-178-973B-9
Sequence 9, Application US/09178973B
Patent No. 6274710

GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
TITLE OF INVENTION: Renald, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543
CURRENT APPLICATION NUMBER: US/09/178,973B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus
US-09-178-973B-9

Query Match 2.7%; Score 127.6; DB 4; Length 1111;
Best Local Similarity 72.2%; Pred. No. 8.3e-26;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 29 CTCCTTCCCAATCAGGCTTCTGAGTTAGATTTCTGCAATGCGCCCTGAGAA 88
DB 7 CTCCTCTCAGTTATCACTTTTACACTTGTGAGATGGATGGCTCTGAGAA 66
QY 89 ATCTGAGCTCTTCTTATATGAGGAGCCCTGGCCACACTGCTCTTCTTGGCCCT 148
DB 67 ATCTAGAGTTTCTTATATGAGGAGCTTGGCCGCGCAGCTGCTCTTCTTATGCTCT 126
QY 149 CTGTGACAGGAG 208
DB 127 GTGGGCGCAG 186
QY 209 CTTCAG 258
DB 187 CTTCAG 236

RESULT 12
US-09-419-568F-9
Sequence 9, Application US/09419568F
Patent No. 6331613

GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
TITLE OF INVENTION: Renald, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus
US-09-419-568F-9

Query Match 2.7%; Score 127.6; DB 4; Length 1111;
Best Local Similarity 72.2%; Pred. No. 8.3e-26;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

29 CTCCTCCCAAGTCCAGTGTCTGAGTGAATTGTCGCAATGGCCGCTGACAGAA 88
7 CTCCTCTCAGTTATCACTTTTGACACTGTGGGATGGTGAATGCTGTCTGACAGAA 66
89 ATCTGTAGCTCTTTCTTATGGGAGACCTGGCCACAGCTGCTCTTCTTTGGCCCT 148
67 ATCTATAGTTTTCCTTATGGGAGCTTTGGCCGACGCTGCTCTTCTTATGGCCCT 126
149 CTGGTACAGGAG 208
127 GTGGGCCAGGAG 186
209 CTCACAG 258
187 CTCACAG 236

RESULT 13

US-09-354-243B-9
Sequence 9, Application US/09354243B
Patent No. 6359117

GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
TITLE OF INVENTION: (TIFFS)
FILE REFERENCE: LUD 5543.1
CURRENT APPLICATION NUMBER: US/09/354,243B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 9
LENGTH: 1111
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-354-243B-9

Query Match 2.7%; Score 127.6; DB 4; Length 1111;
Best Local Similarity 72.2%; Pred. No. 8.3e-26;
Matches 166; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

29 CTCCTCCCAAGTCCAGTGTCTGAGTGAATTGTCGCAATGGCCGCTGACAGAA 88
7 CTCCTCTCAGTTATCACTTTTGACACTGTGGGATGGTGAATGCTGTCTGACAGAA 66
89 ATCTGTAGCTCTTTCTTATGGGAGACCTGGCCACAGCTGCTCTTCTTTGGCCCT 148
67 ATCTATAGTTTTCCTTATGGGAGCTTTGGCCGACGCTGCTCTTCTTATGGCCCT 126
149 CTGGTACAGGAG 208
127 GTGGGCCAGGAG 186
209 CTCACAG 258
187 CTCACAG 236

RESULT 14
US-09-178-973B-7
Sequence 7, Application US/09178973B
Patent No. 6274710
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure

APPLICANT: Louhed, Jamila
APPLICANT: Renauld, Jean-Christophe
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
TITLE OF INVENTION: (TIFFS)
FILE REFERENCE: LUD 5543
CURRENT APPLICATION NUMBER: US/09/178,973B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 7
LENGTH: 1119
TYPE: DNA
ORGANISM: Mus musculus
US-09-178-973B-7

Query Match 2.6%; Score 126; DB 4; Length 1119;
Best Local Similarity 71.7%; Pred. No. 2.3e-25;
Matches 165; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

29 CTCCTCCCAAGTCCAGTGTCTGAGTGAATTGTCGCAATGGCCGCTGACAGAA 88
9 CTCCTCTCAGTTATCACTTTTGACACTGTGGGATGGTGAATGCTGTCTGACAGAA 68
89 ATCTGTAGCTCTTTCTTATGGGAGACCTGGCCACAGCTGCTCTTCTTTGGCCCT 148
69 ATCTATAGTTTTCCTTATGGGAGCTTTGGCCGACGCTGCTCTTCTTATGGCCCT 128
149 CTGGTACAGGAG 208
129 GTGGGCCAGGAG 188
209 CTCACAG 258
189 CTCACAG 238

RESULT 15

US-09-419-568F-7
Sequence 7, Application US/09419568F
Patent No. 6331613

GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Factors
TITLE OF INVENTION: (TIFFS) The Proteins Encoded, and Uses Thereof
FILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/419,568F
CURRENT FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US09/354,243
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US09/178,973
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 7
LENGTH: 1119
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
US-09-419-568F-7

Query Match 2.6%; Score 126; DB 4; Length 1119;
Best Local Similarity 71.7%; Pred. No. 2.3e-25;
Matches 165; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

29 CTCCTCCCAAGTCCAGTGTCTGAGTGAATTGTCGCAATGGCCGCTGACAGAA 88
9 CTCCTCTCAGTTATCACTTTTGACACTGTGGGATGGTGAATGCTGTCTGACAGAA 68
89 ATCTGTAGCTCTTTCTTATGGGAGACCTGGCCACAGCTGCTCTTCTTTGGCCCT 148
69 ATCTATAGTTTTCCTTATGGGAGCTTTGGCCGACGCTGCTCTTCTTATGGCCCT 128